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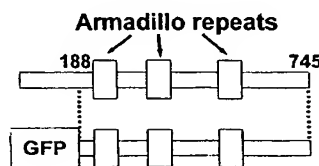
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(54) Title: MODULATORS OF ANGIOGENESIS

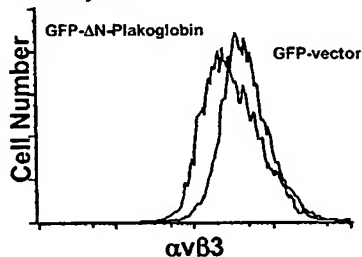
GFP-ΔN-Plakoglobin Expression in Endothelial Cells Downregulates αvβ3 Surface Levels

Functional Screening Hit

Plakoglobin
GFP-ΔN-Plakoglobin



FACS Analysis



(57) Abstract: The present invention relates to regulation of angiogenesis. More particularly, the present invention is directed to nucleic acids encoding "angiogenesis regulatory proteins and nucleic acids" which are involved in modulation of angiogenesis. The invention further relates to methods for identifying and using agents, including small organic molecules, antibodies, peptides, cyclic peptides, nucleic acids, antisense nucleic acids, RNAi, and ribozymes, that modulate angiogenesis via modulation of angiogenesis regulatory proteins and nucleic acids; as well as to the use of expression profiles and compositions in diagnosis and therapy of diseases related to angiogenesis.

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TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG)

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

Modulators of Angiogenesis

CROSS-REFERENCES TO RELATED APPLICATIONS

This application is a continuation-in-part of Application No. 10/231,956 filed
5 August 30, 2002, which is herein incorporated by reference for all purposes.

FIELD OF THE INVENTION

The present invention relates to regulation of angiogenesis. More particularly,
the present invention is directed to nucleic acids encoding "angiogenesis regulatory proteins
10 and nucleic acids" which are involved in modulation of angiogenesis. The invention further
relates to methods for identifying and using agents, including small organic molecules,
antibodies, peptides, cyclic peptides, nucleic acids, antisense nucleic acids, RNAi, and
ribozymes, that modulate angiogenesis via modulation of angiogenesis regulatory proteins
and nucleic acids; as well as to the use of expression profiles and compositions in diagnosis
15 and therapy of diseases related to angiogenesis.

BACKGROUND OF THE INVENTION

Angiogenesis is typically limited in a normal adult to the placenta, ovary,
endometrium and sites of wound healing. However, angiogenesis, or its absence, plays an
20 important role in the maintenance of a variety of pathological states. Some of these states are
characterized by neovascularization, *e.g.*, cancer, diabetic retinopathy, glaucoma, and age
related macular degeneration. More specifically, pathological states characterized by
neovascularization include lymphoma, hematologic cancers, melanoma, breast cancer, lung
cancer, prostate cancer, colon cancer, ovarian cancer, liver cancer, Kaposi's sarcoma,
25 metastatic disease, rheumatoid arthritis, psoriasis, and benign proliferative disorders
including hemangiomas. Others, *e.g.*, stroke, infertility, heart disease, ulcers, delayed wound
healing, and scleroderma, are diseases of angiogenic insufficiency. Therefore, there is a need
to identify nucleic acids encoding proteins involved in the regulation of angiogenesis, to
identify, *e.g.*, modulators of angiogenesis, as well as new therapeutic and diagnostic
30 applications.

BRIEF SUMMARY OF THE INVENTION

The present application identifies, for the first time, a number of proteins and DNA molecules involved in regulation of angiogenesis, *e.g.*, angiogenesis regulatory proteins and DNA molecules. The invention further relates to methods for identifying and using agents, including small organic molecules, antibodies, peptides, cyclic peptides, nucleic acids, antisense nucleic acids, RNAi, and ribozymes, that modulate angiogenesis via modulation of angiogenesis regulatory proteins and DNA molecules; as well as to the use of expression profiles and compositions in diagnosis and therapy of diseases related to insufficient or increased angiogenesis.

In one aspect, the present invention provides a method for identifying a compound that modulates angiogenesis, the method comprising the steps of:

(i) contacting the compound with an angiogenesis regulatory nucleic acid, or an angiogenesis regulatory polypeptide or a fragment thereof encoded by a nucleic acid, wherein the nucleic acid hybridizes under stringent conditions to a second nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ ID NO:523; and (ii) determining the functional effect of the compound upon the nucleic acid or polypeptide.

In one embodiment, the functional effect is determined in vitro. In another embodiment, the functional effect is a physical effect. In another embodiment, the functional effect is determined by measuring ligand or substrate binding to the polypeptide. In another embodiment, the functional effect is a chemical effect. In another embodiment, the functional effect is determined by measuring an enzymatic activity.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell. In a further embodiment, the functional effect is a physical effect. In another embodiment, the functional effect is determined by measuring ligand or substrate binding to the polypeptide. In a further embodiment, the functional effect is a chemical or phenotypic effect. In another embodiment, the functional effect is determined by measuring an enzymatic activity. In another embodiment, the host cell is an endothelial cell. In a further embodiment, the functional effect is determined by measuring $\alpha v \beta 3$ expression or haptotaxis, or chemotaxis, or co-culture tube formation.

In one embodiment, modulation is inhibition of angiogenesis.

In one embodiment, the polypeptide is recombinant. In another embodiment, the nucleic acid comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ ID NO:523.

In another embodiment, the polypeptide comprises a sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:33, SEQ ID NO:44, SEQ ID NO:58, SEQ ID NO:64, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:77, SEQ ID NO:82, SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:121, SEQ ID NO:129, SEQ ID NO:140, SEQ ID NO:154, SEQ ID NO:164, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:203, SEQ ID NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, SEQ ID NO:331, SEQ ID NO:341, SEQ ID NO:352, SEQ ID NO:366, SEQ ID NO:378, SEQ ID NO:385, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:420, SEQ ID NO:429, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID

NO:457, SEQ ID NO:463, SEQ ID NO:482, SEQ ID NO:485, SEQ ID NO:494, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:520, SEQ ID NO:522, and SEQ ID NO:524.

In one embodiment, the compound is an antibody, an antisense molecule, a small organic molecule, or a peptide.

5 In another aspect, the present invention provides a method for identifying a compound that modulates angiogenesis, the method comprising the steps of (i) contacting the compound with a nucleic acid, or a polypeptide or a fragment thereof encoded by a nucleic acid, wherein the nucleic acid hybridizes under stringent conditions to a second nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:3, SEQ
10 ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID
15 NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID
20 NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ ID NO:523; (ii) determining the functional effect of the compound upon the nucleic acid or polypeptide; and (iii) expressing the nucleic acid or polypeptide in a cell, contacting the nucleic acid or polypeptide with the compound, and determining the
25 phenotypic or chemical effect upon the cell.

In another aspect, the present invention provides a method of modulating angiogenesis in a subject, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as a modulator of angiogenesis using the methods described herein. In one embodiment, the subject is a human. In a further
30 embodiment, the compound is an antibody, an antisense molecule, a small organic molecule, a peptide, or an RNAi molecule. In another embodiment, the compound inhibits angiogenesis.

In another aspect, the present invention provides a method of modulating angiogenesis in a subject, the method comprising the step of administering to the subject a

therapeutically effective amount of a polypeptide, the polypeptide encoded by a nucleic acid that hybridizes under stringent conditions to a second nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:165, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:218, SEQ ID NO:232, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:340, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, and SEQ ID NO:498.

In another aspect, the present invention provides a method of modulating angiogenesis in a subject, the method comprising the step of administering to the subject a therapeutically effective amount of a nucleic acid that hybridizes under stringent conditions to a second nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ ID NO:523.

In another aspect, the present invention provides the nucleic acid sequences of SEQ ID NO:165, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, and SEQ ID NO:330.

In another aspect, the present invention provides the amino acid sequences of SEQ ID NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, and SEQ ID NO:331.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 provides a schematic diagram of an assay for modulators of angiogenesis.

Figure 2 provides results of an experiment demonstrating the effect of a plakoglobin-GFP fusion protein expression on levels of the cell surface marker $\alpha\beta3$.

Plakoglobin is an exemplar angiogenesis regulatory protein. Human umbilical vein endothelial (HUVEC) cells were transfected with a vector expressing the plakoglobin-GFP fusion protein or a control vector, expressing GFP only. Cells were incubated with APC-labeled antibodies directed against the cell surface marker $\alpha\beta3$. The X-axis depicts cell number and the Y-axis depicts the amount of $\alpha\beta3$ -APC antibody derived fluorescence.

Cells transfected with the plakoglobin-GFP fusion protein construct exhibit lower $\alpha\beta3$ expression levels than control cells.

Figure 3 also provides results of an experiment demonstrating the effect of a plakoglobin-GFP fusion protein (*i.e.*, GFP- Δ N-plakoglobin) expression on levels of the cell surface marker $\alpha\beta3$. The figure also depicts the presence of armadillo repeats in the functional screen hit, GFP- Δ N-plakoglobin.

Figure 4 demonstrates that GFP- Δ N-Plako expression downregulates vitronectin receptors ($\alpha\beta3$ and $\alpha\beta5$) but not the fibronectin receptor ($\alpha5\beta1$).

Figure 5 demonstrates that expression of GFP- Δ N-Plakoglobin downregulates endogenous catenin levels, as well as expression of endogenous plakoglobin and VE-cadherin.

Figure 6 demonstrates that GFP- Δ N-Plakoglobin expression upregulates surface levels of the laminin receptor, $\alpha6\beta4$.

Figure 7 provides provides results of an experiment demonstrating the effect of a HoxB2-GFP fusion protein expression (*i.e.*, Δ N-HoxB2) on levels of the cell surface marker $\alpha\beta3$. Cells transfected with the Δ N-HoxB2-GFP fusion protein construct exhibit lower $\alpha\beta3$ expression levels than control cells. The figure also provides the structure of the functional screen hit, demonstrating that the homeodomain is present in Δ N-HoxB2.

Figure 8 demonstrates that Δ N-HoxB2 downregulates both α v and $\beta3$ integrin subunit surface expression, as well as $\alpha\beta5$ surface expression.

Figure 9 demonstrates that Δ N-HoxB2 Inhibits Proliferation in HUVECs, a primary cell line.

Figure 10 demonstrates that full length HoxB2 phenocopies Δ N-HoxB2 in the downregulation of $\alpha\beta 3$.

5 Figure 11 provides provides results of an experiment demonstrating the effect of a SUSP-1 GFP fusion protein expression (*i.e.*, GFP-SUSP-1) on levels of the cell surface marker $\alpha\beta 3$. Cells transfected with the GFP-SUSP-1 fusion protein construct exhibit lower $\alpha\beta 3$ expression levels than control cells. The figure also provides the structure of the functional screen hit, demonstrating that GFP-SUSP-1 is an N-terminal fusion in the sense
10 orientation and that a cDNA insert is present before the wild-type start codon.

Figure 12 demonstrates that the GFP-SUSP-1 screening hit does not affect proliferation when expressed in HUVEC (human umbilical vein endothelial cells), PASMC (pulmonary artery smooth muscle cells), and NHDF (normal human dermal fibroblasts).

15 Figure 13 provides expression analysis of SUSP-1 mRNA in a variety of cell lines.

Figure 14 demonstrates that SUSP-1 siRNAs inhibit SUSP-1 mRNA expression.

Figure 15 provides a new sequence determination for a nucleic acid encoding an ABC transporter protein.

20 Figure 16 provides a new sequence determination for a nucleic acid encoding an HSPA5 protein.

Figure 17 provides a new sequence determination for a nucleic acid encoding a protein disulfide isomerase.

25 Figure 18 provides a new sequence determination for a nucleic acid encoding a novel protein from human chromosome 1.

Figure 19 provides a new sequence determination for a nucleic acid encoding a novel protein from human chromosome 3.

Figure 20 provides a new sequence determination for a nucleic acid encoding a novel protein from human chromosome 17

30 Figure 21 provides a new sequence determination for a nucleic acid encoding a novel protein from human chromosome 8.

Figure 22 provides a new sequence determination for a nucleic acid encoding a novel protein from human chromosome 9.

Figure 23 provides a new sequence determination for a nucleic acid encoding a 1/226 protein.

Figure 24 provides a new sequence determination for a nucleic acid encoding an FLJ10688 protein.

5 Figure 25 provides a new sequence determination for a nucleic acid encoding a KIAA1583 protein.

Figure 26 provides a new sequence determination for a nucleic acid encoding a KIAA1814 protein.

10 Figure 27 provides a new sequence determination for a nucleic acid encoding a novel protein from human chromosome 4.

Figure 28 provides a new sequence determination for a nucleic acid encoding a peroxidasin/melanoma antigen related protein.

Figure 29 provides a new sequence determination for a nucleic acid encoding a WD40/SOCS box protein.

15 Figure 30 provides provides results of an experiment demonstrating the effect of a $\Delta 5FADS$ antisense screening hit (*i.e.*, GFP- $\Delta 5FADS$ or D5ADS) on levels of the cell surface marker $\alpha v \beta 3$. Cells transfected with the GFP- $\Delta 5FADS$ antisense construct exhibit lower $\alpha v \beta 3$ expression levels than control cells. The figure also provides the structure of the functional screen hit, demonstrating that GFP- $\Delta 5FADS$ is in the antisense orientation and
20 that a the anti sense portion of the $\Delta 5FADS$ nucleic acid is about 300 base pairs long.

Figure 31 demonstrates that the GFP-D5FADS antisense screening hit does not affect cell proliferation.

Figure 32 demonstrates that $\Delta 5FADS$ siRNAs inhibit $\Delta 5FADS$ mRNA expression.

25 Figure 33 demonstrates that $\Delta 5FADS$ siRNAs inhibit haptotaxis.

Figure 34 demonstrates that $\Delta 5FADS$ siRNAs inhibit SDF-1 induced chemotaxis in Jurkat cells.

Figure 35 demonstrates that $\Delta 6FADS$ is a functional screening hit. The figure shows that $\Delta 6FADS$ transcript is spliced to the KIAA1583 functional screen hit.

30 Figure 36 demonstrates tha $\Delta 6FADS$ mRNA levels are straongly reduced in cells that express the antisense KIAA1583 functional screen hit.

Figure 37 that $\Delta 6FADS$ siRNAs inhibit $\Delta 6FADS$ mRNA expression and also reduce $\alpha v \beta 3$ surface expression.

DETAILED DESCRIPTION OF THE INVENTION

Introduction

Using a functional assay, angiogenesis regulatory proteins and nucleic acids have been identified and cloned from a green fluorescent protein (GFP) fusion library.

5 Primary endothelial cells were transduced with retroviral cDNA/GFP fusion libraries. Transduced cells were selected and assayed for alterations consistent with inhibition of angiogenesis, e.g. downregulation of cell surface expression of $\alpha v \beta 3$ or downregulation of haptotaxis.

10 Using the screen described above, fifty-two proteins and/or DNA molecules were shown for the first time to regulate angiogenesis. Thirty-four of the proteins and/or DNA molecules are known, while fifteen of the proteins and/or DNA molecules are completely novel. However, this is the first demonstration of a function in regulation of angiogenesis for these molecules.

15 The ABC transporter is involved in peroxisome biogenesis. Relevant sequence data for the protein, nucleic acids encoding the ABC transporter, and related sequences include the nucleic acid accession number NM_000033, SEQ ID NO:3; protein accession number NP_000024, SEQ ID NO:4; a new sequence determination, SEQ ID NO:2; and the functional screen hit, SEQ ID NO:1. The protein has an ATP-binding domain. The gene encoding the ABC transporter is linked to a genetic disease, adrenoleukodystrophy
20 (Mosser *et al.*, *Nature* 361:682-3 (1993)). An antisense version of the ABC transporter gene, e.g., SEQ ID NO:1, was identified as a functional hit in the screen for modulators of angiogenesis.

25 PCB1, a poly (rC) binding protein functions as a translational co-activator and also binds 3' UTRs of RNA, most likely through KH domains, thereby regulating RNA stability. Relevant sequence data for the protein, nucleic acids encoding PCB1, and related sequences include the nucleic acid accession number NM_006196, SEQ ID NO:32; protein accession number NP_006187, SEQ ID NO:33; and the functional screen hit, SEQ ID NO:5-31. An antisense version of the gene encoding PCB1 was identified as a functional hit in the screen for modulators of angiogenesis.

30 SLC1A5, an amino acid transporter, has ten transmembrane spanning segments. Relevant sequence data for the protein, nucleic acids encoding PCB1, and related sequences include the nucleic acid accession number NM_005628, SEQ ID NO:43; protein accession number NP_005619, SEQ ID NO:44; and the functional screen hit, SEQ ID

NO:34-42. An antisense version of the gene encoding SLC1A5 was identified as a functional hit in the screen for modulators of angiogenesis.

Chromobox homolog 6 is involved in chromatin regulation. Relevant sequence data for the protein, nucleic acids encoding chromobox homolog 6, and related sequences include the nucleic acid accession number NM_014292, SEQ ID NO:57; protein accession number NP_055107, SEQ ID NO:58; and the functional screen hit, SEQ ID NO:44-56. An antisense version of chromobox homolog 6 was identified as a functional hit in the screen for modulators of angiogenesis.

Cytochrome C oxidase subunit 1 is encoded by a mitochondrial gene and transfers electrons from cytochrome C to O₂ (Ingman *et al.*, *Nature* 408:708-713 (2000); (Leninger, *Principles of Biochemistry* (1984); Stryer, *Biochemistry* (1995)) Relevant sequence data for the protein, nucleic acids encoding cytochrome C oxidase, and related sequences include the nucleic acid accession number NC_001807, SEQ ID NO:63; protein accession number NP_536845, SEQ ID NO:64; and the functional screen hit, SEQ ID NO:59-62. A sense version of the gene encoding cytochrome C oxidase, encoding a 21 amino acid peptide, was identified as a functional hit in the screen for modulators of angiogenesis.

Δ -5 fatty acid desaturase (FADSD5 or Δ 5FADS) introduces double bonds into a fatty acyl chain. The protein is involved in arachadonic acid synthesis and has a fatty acid desaturase domain and a heme-binding domain. Relevant sequence data for the protein, nucleic acids encoding Δ -5 fatty acid desaturase, and related sequences include the nucleic acid accession number NM_013402, SEQ ID NO:68; protein accession number NP_037534, SEQ ID NO:69; and the functional screen hit, SEQ ID NO:65-67. An antisense version of Δ -5 fatty acid desaturase gene was identified as a functional hit in the screen for modulators of angiogenesis.

The dynactin p27 subunit protein was shown to be an angiogenesis regulatory protein. The protein has an RGD domain. Relevant sequence data for the protein, and the nucleic acid encoding dynactin p27 subunit protein, include the nucleic acid accession number NC_006571, SEQ ID NO:70; and protein accession number NP_006562.1, SEQ ID NO:71. An antisense version of the gene encoding dynactin p27 subunit protein was identified as a functional hit in the screen for modulators of angiogenesis.

Elongation factor 1 alpha (EF1 α) was shown to be involved in regulation of angiogenesis. Relevant sequence data for the protein, nucleic acids encoding EF1 α , and related sequences include the nucleic acid accession number NC_001402, SEQ ID NO:76;

protein accession number NP_001393, SEQ ID NO:77; and the functional screen hit, SEQ ID NO:72-75.

Elongation factor 4 gamma (eIF4 γ) is a translation elongation factor. The protein also has a guanine nucleotide binding domain and a W2 domain. Relevant sequence data for the protein, nucleic acids encoding cytochrome C oxidase, and related sequences include the nucleic acid accession number NM_001418, SEQ ID NO:81; protein accession number NP_001409, SEQ ID NO:82; and the functional screen hit, SEQ ID NO:78-80. An antisense version of the eIF4 γ gene was identified as a functional hit in the screen for modulators of angiogenesis. The antisense hit encodes a 21 amino acid peptide that may also be useful as a therapeutic or to modulate angiogenesis.

The filamin A protein binds integrin and regulates actin polymerization. Relevant sequence data for the protein, nucleic acids encoding filamin A, and related sequences include the nucleic acid accession number NM_001456, SEQ ID NO:86; protein accession number NP_001447, SEQ ID NO:87; and the functional screen hit, SEQ ID NO:83-85. A sense version of the filamin A gene was identified as a functional hit in the screen for modulators of angiogenesis.

Inactivation of the gene encoding the G α 13 protein causes a severe vascular phenotype in mice due to an inhibition of angiogenesis (vasculogenesis was apparent). This protein couples to the thrombin receptor. Thrombin and G α 13 protein activate Rho and tyrosine-phosphorylation of focal adhesion proteins FAK, Paxillin, and p130Cas. G α 13 also interacts with the cytoplasmic domain of adherins, leading to increased levels of β -catenin and transcriptional activation. Relevant sequence data for the protein, the nucleic acid encoding the G α 13 protein, and related sequences include the nucleic acid accession number NM_006572, SEQ ID NO:89; protein accession number NP_006563.1, SEQ ID NO:90; and the functional screen hit, SEQ ID NO:88. A sense version of the G α 13 gene was identified as a functional hit in the screen for modulators of angiogenesis.

The HOXB2 protein is a transcription factor. Relevant sequence data for the protein, nucleic acids encoding HOXB2, and related sequences include the nucleic acid accession number NM_002145, SEQ ID NO:120; protein accession number NP_002136, SEQ ID NO:121; and the functional screen hit, SEQ ID NO:91-119. A sense version of the HOXB2 gene was identified as a functional hit in the screen for modulators of angiogenesis.

HSPA5, a member of the HSP70 family of proteins has a role in protein folding and assembly in the endoplasmic reticulum. Expression of the protein is glucose regulated. The protein has an ATPase domain which is fused in frame to GFP in the

functional screen hit. Relevant sequence data for the protein, nucleic acids encoding HSPA5, and related sequences include the nucleic acid accession number NM_005347, SEQ ID NO:128; protein accession number NP_005338, SEQ ID NO:129; a new sequence determination, SEQ ID NO:127; and the functional screen hit, SEQ ID NO:122-126.

5 Interferon gamma receptor 1 (IFN γ 1) is a cytokine receptor that induces antiangiogenic genes. Relevant sequence data for the protein, nucleic acids encoding IFN γ 1, and related sequences include the nucleic acid accession number NM_000416, SEQ ID NO:139; protein accession number NP_000407, SEQ ID NO:140; and the functional screen hit, SEQ ID NO:130-138. An antisense version of the IFN γ 1 gene was identified as a
10 functional hit in the screen for modulators of angiogenesis.

Importin α 4 (karyopherin α 3) is a subunit of the nuclear localization signal receptor. Relevant sequence data for the protein, nucleic acids encoding importin α 4, and related sequences include the nucleic acid accession number NM_002267, SEQ ID NO:153; protein accession number NP_002258.1, SEQ ID NO:154; and the functional screen hit, SEQ
15 ID NO:141-152. An antisense version of the importin α 4 gene was identified as a functional hit in the screen for modulators of angiogenesis.

The lysosomal pepstatin-insensitive protease (CLN2) is encoded by a gene associated with juvenile neuronal ceroid lipofuscinosis disease. Relevant sequence data for the protein, nucleic acids encoding CLN2, and related sequences include the nucleic acid
20 accession number NM_000391, SEQ ID NO:163; protein accession number NP_000382, SEQ ID NO:164; and the functional screen hit, SEQ ID NO:155-162. An antisense version of the CLN2 gene was identified as a functional hit in the screen for modulators of angiogenesis.

A novel protein disulfide isomerase was shown to have a role in angiogenesis.
25 Relevant sequence data for the nucleic acid encoding the novel protein disulfide isomerase, includes SEQ ID NO:165. An antisense version of gene encoding the novel protein disulfide isomerase was identified as a functional hit in the screen for modulators of angiogenesis. The antisense hit encodes a 45 or 32 amino acid peptide that may also be useful as a therapeutic or to modulate angiogenesis.

30 Microtubule-associated protein 4 (MAP4) binds tubulin and may link microtubules to other elements of the cytoskeleton. See *e.g.*, Chapin & Bulinski, *J. Cell. Sci* 98:27-36 (1991); and Chapin *et al.*, *Biochemistry* 34:2289-2301 (1995). Four isoforms of MAP4 are known. Relevant sequence data for the proteins, nucleic acids encoding MAP4 isoforms, and related sequences include the nucleic acid accession numbers NM_002375,

NM_030884, NM_030885, and NM_030883; SEQ ID NOs:169, 171, 173, and 175; protein accession numbers NP_002366, NP_112146, NP_112147, and NP_112245; SEQ ID NOs:170, 172, 174, and 176; and the functional screen hit, SEQ ID NO:166-168. An antisense version of MAP4 was identified as a functional hit in the screen for modulators of angiogenesis.

Neural precursor cell expressed developmentally down regulated 5 (Nedd5) is a septin GTPase. Relevant sequence data for the protein, nucleic acids encoding Nedd5, and related sequences include the nucleic acid accession number NM_004404, SEQ ID NO:183; protein accession number NM_004395, SEQ ID NO:184; and the functional screen hit, SEQ ID NO:177-182. A sense version of the Nedd5 gene was identified as a functional hit in the screen for modulators of angiogenesis.

A novel tyrosine/serine/threonine kinase was found to be involved in angiogenesis. The protein is also a breast cancer antigen. Relevant sequence data for the protein, nucleic acids encoding the novel kinase, and related sequences include the nucleic acid accession number NM_044379, SEQ ID NO:202; protein accession number XP_044379, SEQ ID NO:203; and the functional screen hit, SEQ ID NO:185-201. A sense version of the gene encoding the novel kinase was identified as a functional hit in the screen for modulators of angiogenesis.

A novel protein encoded by a gene on human chromosome 1 was found to be involved in angiogenesis. The chromosome 1 DNA sequence identified was previously identified as intron 1 of the JAK1 gene. Relevant sequence data for chromosome 1 DNA sequence include a new sequence determination, SEQ ID NO:210; and the functional screen hit, SEQ ID NO:204-209. The functional screen hit is believed to be in the antisense orientation.

A novel protein encoded by a gene on human chromosome 3 was found to be involved in angiogenesis. The chromosome 3 DNA sequence was previously identified as H41 exon 2/3 and part of intron 1. Relevant sequence data for the chromosome 3 DNA sequence include a new sequence determination, SEQ ID NO:218; and the functional screen hit, SEQ ID NO:211-217. The functional screen hit is in the sense orientation.

A novel protein encoded by a gene on human chromosome 17 was found to be involved in angiogenesis. Relevant sequence data for the chromosome 17 DNA sequence include a new sequence determination, SEQ ID NO:227; and the functional screen hit, SEQ ID NO:219-226. The functional screen hit is believed to be in the antisense orientation.

A novel protein encoded by a gene on human chromosome 8 was found to be involved in angiogenesis. Relevant sequence data for the chromosome 8 hit include a new sequence determination, SEQ ID NO:232; and the functional screen hit, SEQ ID NO:228-231. The functional screen hit is believed to be in the antisense orientation or encodes a nine amino acid peptide that may also be useful as a therapeutic or to modulate angiogenesis.

A novel protein encoded by a gene on human chromosome 9 was found to be involved in angiogenesis. The chromosome 9 DNA sequence was previously identified as intronic DNA from the RXRa gene. Relevant sequence data for chromosome 9 hit include a new sequence determination, SEQ ID NO:248; and the functional screen hit, SEQ ID NO:233-247. The functional screen hit is believed to be in the antisense orientation.

A novel protein (1/226) that binds to PAK2 in a yeast two hybrid screen was found to be involved in angiogenesis. Relevant sequence data for the novel 1/226 hit include a new sequence determination, SEQ ID NO:274; and the functional screen hit, SEQ ID NO:249-273. The functional screen hit is in the sense orientation.

Another novel protein FLJ10688 contains fibronectin domains and binds to STAT-6 in a yeast two hybrid screen. Relevant sequence data for the protein, nucleic acids encoding FLJ10688, and related sequences include the nucleic acid accession number NM_018179, SEQ ID NO:286; protein accession number NP_060649, SEQ ID NO:287; a new sequence determination, SEQ ID NO:285; and the functional screen hit, SEQ ID NO:275-284. The functional screen hit is in the sense orientation.

Another novel protein KIAA0217 contains an RNA recognition motif. Relevant sequence data for the protein, nucleic acids encoding KIAA0217, and related sequences include the nucleic acid accession number XM_040265, SEQ ID NO:297; protein accession number NP_040265, SEQ ID NO:298; and the functional screen hit, SEQ ID NO:288-296. The functional screen hit is in the antisense orientation.

Another novel protein KIAA1583 is homologous to PDZ-RGS, which regulates Ephrin B signaling. Relevant sequence data for the protein, nucleic acids encoding KIAA1583, and related sequences include the nucleic acid accession number AB046803, SEQ ID NO:308; protein accession number BAB13409, SEQ ID NO:309; a new sequence determination, SEQ ID NO:307; and the functional screen hit, SEQ ID NO:299-306. The functional screen hit is in the antisense orientation. The KIAA1583 transcript is spliced to the transcript of the $\Delta 6$ -fatty acid desaturase enzyme, also located on chromosome 11q12. The antisense KIAA1583 functional screen hit, inhibits expression of $\Delta 6$ -fatty acid desaturase mRNA. In addition, a $\Delta 6$ -fatty acid desaturase specific siRNA decreased $\Delta 6$ -fatty

acid desaturase message levels and inhibited tube formation in a co-culture assay. Thus, $\Delta 6$ -fatty acid desaturase is also an angiogenesis regulatory protein and the protein and its related nucleic acids can be used in the screening methods of the present invention. Compounds identified in such screens can be used in the therapeutic methods described herein.

5 Representative $\Delta 6$ -fatty acid desaturase amino acid sequence data is found at accession numbers NP_004256, SEQ ID NO:522; and AAD31282, SEQ ID NO:524. Related nucleic acid sequence data is found at accession numbers NM_004265, SEQ ID NO 521; and AF134404, SEQ ID NO:523.

A novel protein, KIAA1814, was found to be involved in angiogenesis.

10 Relevant sequence data for functional screen hit include the nucleic acid accession number XM_046822, SEQ ID NO:318; protein accession number XP_046822, SEQ ID NO:319; a new sequence determination, SEQ ID NO:317; and the functional screen hit, SEQ ID NO:310-316. The functional screen hit is in the sense orientation.

A novel protein encoded by a gene on human chromosome 4 was found to be
15 involved in angiogenesis. Relevant sequence data for functional screen hit include a new sequence determination, SEQ ID NO:320.

Another novel protein identified as an angiogenesis regulatory protein is related to a peroxidasin/melanoma antigen. The protein has peroxidase, vWF, Ig, and leucine rich domains. Relevant sequence data for the protein, nucleic acids encoding the novel
20 protein, and related sequences include the nucleic acid accession number XM_056455, SEQ ID NO:324; protein accession number XP_056455, SEQ ID NO:325; a new sequence determination, SEQ ID NO:323; and the functional screen hit, SEQ ID NO:321-322. The functional screen hit is in the sense orientation comprising a fusion to the peroxidase domain.

Another novel protein identified herein as an angiogenesis regulatory protein
25 is a novel WD40/SOCS box protein. Relevant sequence data for the protein, nucleic acids encoding the novel WD40/SOCS box protein, and related sequences include the nucleic acid accession number NM_018639, SEQ ID NO:330; protein accession number NP_061109, SEQ ID NO:331; a new sequence determination, SEQ ID NO:329; and the functional screen hit, SEQ ID NO:326-328. The functional screen hit is in the antisense orientation.

30 A Numb-like protein contains adapter and PTB domains and is involved in regulation of angiogenesis. Relevant sequence data for the protein, nucleic acids encoding the Numb-like protein, and related sequences include the nucleic acid accession number NM_004756, SEQ ID NO:340; protein accession number NP_004747, SEQ ID NO:341; and

the functional screen hit, SEQ ID NO:332-339. The functional screen hit is in the sense orientation.

Protein p130CAS (Crk-associated substrate) was identified as an angiogenic regulatory protein. p130 CAS is an adapter protein and has SH3 domains. (Dorssers *et al.*, *Mol. Endocrinol.* 7:870-878 (1993); Brinkman *et al.*, *J. Natl. Cancer Inst.* 92:112-120 (2000)). Relevant sequence data for the protein, nucleic acids encoding FLJ10688, and related sequences include the nucleic acid accession number NM_014567, SEQ ID NO:351; protein accession number NP_055382, SEQ ID NO:352; and the functional screen hit, SEQ ID NO:342-350. The orientation of this functional screen hit is antisense.

Perlecan, a basement membrane component, was identified as an angiogenesis regulatory protein. (Nicole *et al.*, *Nat. Genet.* 26:(4) 480-483 (2000)). Relevant sequence data for the protein, nucleic acids encoding perlecan, and related sequences include the nucleic acid accession number NM_005529, SEQ ID NO:365; protein accession number NP_005520, SEQ ID NO:366; and the functional screen hit, SEQ ID NO:353-364. The functional screen hit is in the antisense orientation.

The T cell activation protein PGR-1, was identified as an angiogenesis regulatory protein. Relevant sequence data for the protein, nucleic acids encoding PGR-1, and related sequences include the nucleic acid accession number NM_033296, SEQ ID NO:377; protein accession number NP_150638, SEQ ID NO:378; and the functional screen hit, SEQ ID NO:367-376. The functional screen hit is in the sense orientation.

Phosphoribosyl pyrophosphate synthetase associated protein 1 (PRPSAP1), was identified as an angiogenesis regulatory protein. PRPSAP1 regulates a nucleotide synthesis pathway. Relevant sequence data for the protein, nucleic acids encoding PRPSAP1, and related sequences include the nucleic acid accession number NM_002766, SEQ ID NO:384; protein accession number NP_002757, SEQ ID NO:385; and the functional screen hit, SEQ ID NO:379-383. The functional screen hit is in the sense orientation.

Plakoglobin, a member of the catenin family, was identified as an angiogenesis regulatory protein. Plakoglobin binds to E-cadherin, N-cadherin, and desmoglein proteins. Relevant sequence data for the protein, nucleic acids encoding plakoglobin, and related sequences include the nucleic acid accession numbers NM_002230, SEQ ID NO:406, NM_021991, SEQ ID NO:408; protein accession numbers NP_002221, SEQ ID NO:407, NP_068831, SEQ ID NO:409; and the functional screen hit, SEQ ID NO:386-405. Two functional screen hits were identified: one in the sense orientation, fused to GFP; and one in the antisense orientation.

Plasminogen activator inhibitor 1 (SERPINE1 or PAI-1) was identified as an angiogenesis regulatory protein. PAI-1 is a protease inhibitor. Relevant sequence data for the protein, nucleic acids encoding PAI-1, and related sequences include the nucleic acid accession number NM_000602, SEQ ID NO:419; protein accession number NP_000593, SEQ ID NO:420; and the functional screen hit, SEQ ID NO:410-418. The functional screen hit is in the antisense orientation.

Proteosomal subunit Y, an $\text{INF}\gamma$ regulated proteosomal subunit, was identified as an angiogenesis regulatory protein. Relevant sequence data for proteosomal subunit Y includes the functional screen hit, SEQ ID NO:421. The functional screen hit is in the antisense orientation.

Rap2B was identified as an angiogenesis regulatory protein. Rap2B is a member of the RAS family of GTPases. Relevant sequence data for the protein, nucleic acids encoding Rap2B, and related sequences include the nucleic acid accession number XM_003032, SEQ ID NO:428; protein accession number XP_003032, SEQ ID NO:429; and the functional screen hit, SEQ ID NO:422-427. The functional screen hit is in the antisense orientation.

Semaphorin 3F was identified as an angiogenesis regulatory protein. Semaphorin 3F is a ligand for NP2. Relevant sequence data for the protein, nucleic acids encoding semaphorin 3F, and related sequences include the nucleic acid accession number U38276, SEQ ID NO:437; protein accession number AAB18276, SEQ ID NO:438; and the functional screen hit, SEQ ID NO:430-436. The functional screen hit is in the antisense orientation.

SPARC was identified as an angiogenesis regulatory protein. Relevant sequence data for the protein, nucleic acids encoding SPARC, and related sequences include the nucleic acid accession number NM_003118, SEQ ID NO:439; and protein accession number NP_003109, SEQ ID NO:440.

ssDNA binding protein-1 was identified as an angiogenesis regulatory protein. Relevant sequence data for the protein, nucleic acids encoding ssDNA binding protein-1, and related sequences include the nucleic acid accession number NM_018070, SEQ ID NO:445; protein accession number NP_060540, SEQ ID NO:446; and the functional screen hit, SEQ ID NO:441-444. The functional screen hit is in the sense orientation.

Sumo protease (SUSP-1) was identified as an angiogenesis regulatory protein. Relevant sequence data for the protein, nucleic acids encoding SUSP-1, and related sequences include the nucleic acid accession number NM_015571, SEQ ID NO:456; protein

accession number NP_056386, SEQ ID NO:457; and the functional screen hit, SEQ ID NO:447-455. The functional screen hit is in the sense orientation and includes the 5' untranslated region of the gene.

5 Pantophysin, a synaptophysin homolog, was identified as an angiogenesis regulatory protein (Zhong *et al.*, *Biochim. Biophys. Acta* 1129:235-238 (1992)). Pantophysin was previously shown to be involved in vesicle trafficking. Relevant sequence data for the protein, nucleic acids encoding pantophysin, and related sequences include the nucleic acid accession number NM_006754, SEQ ID NO:462; protein accession number NP_006745, SEQ ID NO:463; and the functional screen hit, SEQ ID NO:458-461. The functional screen
10 hit is in the antisense orientation.

Thrombospondin, a known regulator of angiogenesis, was also identified as a sense hit fused to the laminin domain. Relevant sequence data for the protein, nucleic acids encoding thrombospondin, and related sequences include the nucleic acid accession number NM_0003246, SEQ ID NO:481; protein accession number NP_003237, SEQ ID NO:482; and the functional screen hit, SEQ ID NO:464-480.
15

Transgelin 2 was identified as an angiogenesis regulatory protein. Relevant sequence data for the protein, nucleic acids encoding transgelin 2, and related sequences include the nucleic acid accession number NM_003564, SEQ ID NO:484; protein accession number NP_003555, SEQ ID NO:485; and the functional screen hit, SEQ ID NO:483. The
20 functional screen hit is in the sense orientation.

Vigilin was identified as an angiogenesis regulatory protein. Relevant sequence data for the protein, nucleic acids encoding vigilin, and related sequences include the nucleic acid accession number NM_005336, SEQ ID NO:493; protein accession number NP_005327, SEQ ID NO:494; and the functional screen hit, SEQ ID NO:486-492. The
25 functional screen hit is in the sense orientation.

Vimentin was identified as an angiogenesis regulatory protein. Relevant sequence data for the protein, nucleic acids encoding vimentin, and related sequences include the nucleic acid accession number NM_003380, SEQ ID NO:496, XM_167414, SEQ ID NO:498; protein accession number NP_003371, SEQ ID NO:497, XP_167414, SEQ ID
30 NO:499; and the functional screen hit, SEQ ID NO:495.

Vinexin (SCAM-1) was identified as an angiogenesis regulatory protein. SCAM-1 is an adaptor protein and has an SH3 domain. Relevant sequence data for the protein, nucleic acids encoding SCAM-1, and related sequences include the nucleic acid accession number NM_005775, SEQ ID NO:519; protein accession number NP_005766,

SEQ ID NO:520; and the functional screen hit, SEQ ID NO:500-518. The functional screen hit is in the antisense orientation.

Some of the functional screen hits can be grouped together on the basis of other cellular functions. For example, plakoglobin, the Gα13 protein, and p130CAS protein all appear to function in cell adhesion. The Δ-5 fatty acid desaturase, the ALD protein (ABC transporter), cytochrome C oxidase, and the novel peroxidasin protein all may be important in arachadonic acid synthesis. The novel protein disulfide isomerase may be involved in collagen biosynthesis. Pantophysin, HSPA5, and dynactin p27, may all be involved in vesicle trafficking. Without wishing to be bound by theory, regulation of any of these cellular functions may influence the angiogenesis pathway. In addition, without wishing to be bound by theory, both the proteins and/or the nucleic acids identified in the assays are regulators of angiogenesis, *e.g.*, by antisense activity, by overexpression of a functional protein, or as dominant negative inhibitors, or small peptide inhibitors.

Angiogenesis assays described herein reveal for the first time that expression of a nucleic acid molecule encoding the above described angiogenesis regulatory proteins exerted a negative effect on αvβ3 surface expression. In addition, endothelial cells expressing the sequences were strongly inhibited in their haptotactic response to vitronectin, which is an indicator of an anti-angiogenic phenotype. Without wishing to be bound by theory, it appears that the angiogenesis regulatory proteins or fragments of those proteins, peptides derived from the proteins, or peptides and inhibitory DNA or RNA molecules derived from DNA encoding the proteins, provide an anti-angiogenic phenotype. Thus, in addition to their use in screens for modulators of angiogenesis, the angiogenesis regulatory proteins or fragments of those proteins, peptides derived from the proteins, or peptides and inhibitory DNA or RNA molecules derived from DNA encoding the proteins, can also be used as therapeutics for treatment of neovascularization or for treatment of angiogenic insufficiency.

The angiogenesis regulatory proteins, nucleic acids, and other members of the angiogenesis pathway therefore represent targets for the development of angiogenic drugs, preferably anti-angiogenic drugs, *e.g.*, anti-angiogenic drugs for treatment of neovascularization. Neovascularization can be caused by pathologic states including cancer, diabetic retinopathy, glaucoma, age related macular degeneration, lymphoma, hematologic cancers, melanoma, breast cancer, lung cancer, prostate cancer, colan cancer, ovarian cancer, liver cancer, Kaposi's sarcoma, metastatic disease, rheumatoid arthritis, psoriasis, and benign proliferative disorders including hemangiomas. The angiogenesis regulatory proteins,

nucleic acids, and other members of the angiogenesis pathway also represent targets for the development of angiogenic drugs for treatment of angiogenic insufficiency, e.g., stroke, infertility, heart disease, ulcers, delayed wound healing, and scleroderma, are diseases of angiogenic insufficiency. Modulators include small organic molecules, nucleic acids, peptides, cyclic peptides, antibodies, antisense molecules, RNAi molecules, and ribozymes. The nucleic acids and proteins of the invention are also useful for diagnostic applications, using, e.g., nucleic acid probes, oligonucleotides, and antibodies.

Definitions

By “disorder associated with angiogenesis” or “disease associated with angiogenesis” herein is meant a disease state which is marked by either an excess or a deficit of vessel development. Angiogenesis disorders associated with increased angiogenesis include, but are not limited to, cancer and proliferative diabetic retinopathy. Pathological states for which it may be desirable to increase angiogenesis include stroke, heart disease, infertility, ulcers, and scleredema. An increase in angiogenesis may also be desirable in transplantation or for artificial or *in vitro* growth of organs.

The following table (Table 1) presents the angiogenesis regulatory proteins and nucleic acids identified in a screen for such proteins and nucleic acids. Accession numbers and SEQ ID NOs are also provided for each angiogenesis regulatory protein. While the angiogenesis regulatory proteins and nucleic acids are referred to as SEQ ID NOs throughout the present application, the term SEQ ID NO encompasses orthologues and homologues of each angiogenesis regulatory proteins or nucleic acids identified by a SEQ ID NO.

TABLE 1: ANGIOGENESIS REGULATORY PROTEINS AND NUCLEIC ACIDS

Name	Nucleic Acid Accession Number	Nucleic Acid SEQ ID NO	Protein Accession Number	Protein SEQ ID NO
ABC transporter	NM_000033	SEQ ID NO:3	NP_000024	SEQ ID NO:4
PCB1	NM_006196	SEQ ID NO:32	NP_006187	SEQ ID NO:33
SLC1A5	NM_005628	SEQ ID NO:43	NP_005619	SEQ ID NO:44
Chromobox homolog 6	NM_014292	SEQ ID NO:57	NP_055107	SEQ ID NO:58
Cytochrome C	NC_001807	SEQ ID NO:63	NP_536845	SEQ ID NO:64

Name	Nucleic Acid Accession Number	Nucleic Acid SEQ ID NO	Protein Accession Number	Protein SEQ ID NO
oxidase subunit 1				
Δ -5 fatty acid desaturase	NM_013402	SEQ ID NO:68	NP_037534	SEQ ID NO:69
dynactin p27 subunit protein	NC_006571	SEQ ID NO:70	NP_006562.1	SEQ ID NO:71
Elongation factor 1 alpha	NC_001402	SEQ ID NO:76	NP_001393	SEQ ID NO:77
Elongation factor 4 gamma	NM_001418	SEQ ID NO:81	NP_001409	SEQ ID NO:82
filamin A protein	NM_001456	SEQ ID NO:86	NP_001447	SEQ ID NO:87
Gal3 protein	NM_006572	SEQ ID NO:89	NP_006563.1	SEQ ID NO:90
HOXB2 protein	NM_002145	SEQ ID NO:120	NP_002136	SEQ ID NO:121
HSPA5	NM_005347	SEQ ID NO:128	NP_005338	SEQ ID NO:129
Interferon gamma receptor 1	NM_000416	SEQ ID NO:139	NP_000407	SEQ ID NO:140
Importin α 4	NM_002267	SEQ ID NO:153	NP_002258.1	SEQ ID NO:154
lysosomal pepstatin- insensitive protease (CLN2)	NM_000391	SEQ ID NO:163	NP_000382	SEQ ID NO:164
novel protein disulfide isomerase		SEQ ID NO:165		
Microtubule- associated protein 4 (MAP4)	NM_002375	SEQ ID NO:169	NP_002366	SEQ ID NO:170
	NM_030884	SEQ ID NO:171	NP_112146	SEQ ID NO:172
	NM_030885	SEQ ID NO:173	NP_112147	SEQ ID NO:174
	NM_030883	SEQ ID NO:175	NP_112245	SEQ ID NO:176

Name	Nucleic Acid Accession Number	Nucleic Acid SEQ ID NO	Protein Accession Number	Protein SEQ ID NO
Nedd5	NM_004404	SEQ ID NO:183	NM_004395	SEQ ID NO:184
novel tyr/ser/thr kinase	NM_044379	SEQ ID NO:202	XP_044379	SEQ ID NO:203
human chromosome 1 protein		SEQ ID NO:210		
human chromosome 3 protein		SEQ ID NO:218		
human chromosome 17 protein		SEQ ID NO:227		
human chromosome 8 protein		SEQ ID NO:232		
human chromosome 9 protein		SEQ ID NO:248		
1/226		SEQ ID NO:274		
FLJ10688	NM_018179	SEQ ID NO:286	NP_060649	SEQ ID NO:287
KIAA0217	XM_040265	SEQ ID NO:297	NP_040265	SEQ ID NO:298
KIAA1583	AB046803	SEQ ID NO:308	BAB13409	SEQ ID NO:309
KIAA1814	XM_046822	SEQ ID NO:318	XP_046822	SEQ ID NO:319
human chromosome 4 protein		SEQ ID NO:320		
peroxidasin- melanoma antigen related protein	XM_056455	SEQ ID NO:324	XP_056455	SEQ ID NO:325

Name	Nucleic Acid Accession Number	Nucleic Acid SEQ ID NO	Protein Accession Number	Protein SEQ ID NO
WD40/SOCS box protein	NM_018639	SEQ ID NO:330	NP_061109	SEQ ID NO:331
Numb-like protein	NM_004756	SEQ ID NO:340	NP_004747	SEQ ID NO:341
p130CAS	NM_014567	SEQ ID NO:351	NP_055382	SEQ ID NO:352
Perlecan	NM_005529	SEQ ID NO:365	NP_005520	SEQ ID NO:366
PGR-1	NM_033296	SEQ ID NO:377	NP_150638	SEQ ID NO:378
PRPSAP1	NM_002766	SEQ ID NO:384	NP_002757	SEQ ID NO:385
Plakoglobin	NM_002230, NM_021991	SEQ ID NO:406 SEQ ID NO:408	NP_002221 NP_068831	SEQ ID NO:407 SEQ ID NO:409
SERPINE1 or PAI-1	NM_000602	SEQ ID NO:419	NP_000593	SEQ ID NO:420
Proteosomal subunit Y		SEQ ID NO:421		
Rap2B	XM_003032	SEQ ID NO:428	XP_003032	SEQ ID NO:429
Semaphorin 3F	U38276	SEQ ID NO:437	AAB18276	SEQ ID NO:438
SPARC	NM_003118	SEQ ID NO:439	NP_003109	SEQ ID NO:440
ssDNA binding protein-1	NM_018070	SEQ ID NO:445	NP_060540	SEQ ID NO:446
SUSP-1	NM_015571	SEQ ID NO:456	NP_056386	SEQ ID NO:457
Pantophysin	NM_0003246	SEQ ID NO:481	NP_003237	SEQ ID NO:482
Transgelin 2	NM_003564	SEQ ID NO:484	NP_003555	SEQ ID NO:485
Vigilin	NM_005336	SEQ ID NO:493	NP_005327	SEQ ID NO:494
Vimentin	NM_003380 XM_167414	SEQ ID NO:496 SEQ ID NO:498	NP_003371 XP_167414	SEQ ID NO:497 SEQ ID NO:499
Vinexin (SCAM-1)	NM_005775	SEQ ID NO:519	NP_005766	SEQ ID NO:520
Δ -6 fatty acid desaturase	NM_004265 AF134404	SEQ ID NO 521 SEQ ID NO:523	NP_004256 AAD31282	SEQ ID NO:522 SEQ ID NO:524

The terms "angiogenesis regulatory protein or nucleic acid" or a nucleic acid encoding "angiogenesis regulatory protein" refer to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino acid sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to a polypeptide encoded by a nucleic acid of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, and SEQ ID NO:519, or an amino acid sequence of SEQ ID NO:4, SEQ ID NO:33, SEQ ID NO:44, SEQ ID NO:58, SEQ ID NO:64, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:77, SEQ ID NO:82, SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:121, SEQ ID NO:129, SEQ ID NO:140, SEQ ID NO:154, SEQ ID NO:164, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:203, SEQ ID NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, SEQ ID NO:331, SEQ ID NO:341, SEQ ID NO:352, SEQ ID NO:366, SEQ ID NO:378, SEQ ID NO:385, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:420, SEQ ID NO:429, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:457, SEQ ID NO:463, SEQ ID NO:482, SEQ ID NO:485, SEQ ID NO:494, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:520, SEQ ID NO:522, and SEQ ID NO:524 or other sequences listed herein; (2) specifically bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence of SEQ ID NO:4, SEQ ID NO:33, SEQ ID NO:44, SEQ ID NO:58, SEQ ID NO:64, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:77, SEQ ID NO:82, SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:121, SEQ ID NO:129, SEQ ID NO:140, SEQ ID NO:154, SEQ

ID NO:164, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:203, SEQ ID NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, SEQ ID NO:331, SEQ ID NO:341, SEQ ID NO:352, SEQ ID NO:366, SEQ ID NO:378, SEQ ID NO:385, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:420, SEQ ID NO:429, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:457, SEQ ID NO:463, SEQ ID NO:482, SEQ ID NO:485, SEQ ID NO:494, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:520, SEQ ID NO:522, and SEQ ID NO:524, immunogenic fragments thereof, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid encoding

10 SEQ ID NO:4, SEQ ID NO:33, SEQ ID NO:44, SEQ ID NO:58, SEQ ID NO:64, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:77, SEQ ID NO:82, SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:121, SEQ ID NO:129, SEQ ID NO:140, SEQ ID NO:154, SEQ ID NO:164, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:203, SEQ ID NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, 15 SEQ ID NO:325, SEQ ID NO:331, SEQ ID NO:341, SEQ ID NO:352, SEQ ID NO:366, SEQ ID NO:378, SEQ ID NO:385, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:420, SEQ ID NO:429, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:457, SEQ ID NO:463, SEQ ID NO:482, SEQ ID NO:485, SEQ ID NO:494, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:520, SEQ ID NO:522, and SEQ ID NO:524, e.g., a nucleic 20 acid sequence of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID 25 NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID 30 NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ ID NO:523; or its complement, and conservatively modified variants thereof; (4) have a nucleic acid sequence that has greater than about 95%, preferably greater than about 96%, 97%, 98%, 99%, or higher nucleotide

sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ ID NO:523, or the complement of any of those sequences. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or any mammal. The nucleic acids and proteins of the invention include both naturally occurring or recombinant molecules. When available, accession numbers for the human angiogenesis regulatory proteins and genes are provided.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of an angiogenesis regulatory proteins includes the determination of a parameter that is indirectly or directly under the influence of an angiogenesis regulatory protein polypeptide, e.g., a chemical or phenotypic effect such as loss-of angiogenesis phenotype represented by a change in expression of a cell surface marker, such as $\alpha v \beta 3$ integrin, or changes in cellular proliferation, especially endothelial cell proliferation; or enzymatic activity, or, e.g., a physical effect such as ligand binding or inhibition of ligand binding. A functional effect therefore includes ligand binding activity, the ability of cells to proliferate, expression in cells undergoing angiogenesis, and other characteristics of angiogenic cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities. Angiogenesis assays are described, e.g., in *Angiogenesis Protocols* (Murray, ed., 2001).

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an angiogenesis regulatory proteins, e.g., measuring physical and chemical or phenotypic effects. Such functional effects can be measured by any means known to those skilled in the

art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index); hydrodynamic (e.g., shape), chromatographic; or solubility properties for the protein; measuring inducible markers or transcriptional activation of the angiogenesis protein; measuring changes in cell surface markers, e.g., $\alpha v \beta 3$ integrin; and measuring cellular proliferation, particularly endothelial cell proliferation. Functional effects can be measured using ligand binding assays, e.g., binding to antibodies or other molecules. Functional effects can be determined by measuring changes in enzymatic activity. Examples of enzymatic activities include, but are not limited to protein translation, electron transfer, fatty acid desaturase activity, protein disulfide isomerase activity, transcriptional activation activity, peroxidase activity, kinase activity, and proteolytic activity.

Determination of the functional effect of a compound on angiogenesis can also be performed using angiogenesis assays known to those of skill in the art such as $\alpha v \beta 3$ downregulation, VEGF-2 upregulation, endothelial cell tube formation assays; chemotaxis assays, haptotaxis assays; differentiation assays using matrigel or co-culture with smooth muscle cells, the chick CAM assay; the mouse corneal assay; and assays that assess vascularization of an implanted tumor. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, e.g., tube or blood vessel formation, measurement of changes in RNA or protein levels for angiogenesis-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, etc.

“Ligand” refers to a molecule that is specifically bound by a protein. An antibody is one example of a ligand. Other examples of ligands include RNA, cytochrome C, O_2 , NADP or NADPH, heme, MHC molecules, an amino acid sequence comprising a nuclear localization signal, tubulin or other cytoskeletal proteins, the thrombin receptor, transcription factor 7, cadherins, and ssDNA.

“Substrate” refers to a molecule that binds to an enzyme and is part of a specific chemical reaction catalyzed by the enzyme. Substrates of angiogenesis regulatory proteins include ATP, fatty acids, GTP, O_2 , arachadonic acids or its precursors, collagen, and protein molecules or peptides.

“Inhibitors,” “activators,” and “modulators” of angiogenesis regulatory protein polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules identified using *in vitro* and *in vivo* assays of angiogenesis regulatory

protein polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of angiogenesis regulatory proteins, e.g., antagonists. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate angiogenesis regulatory proteins activity, e.g., agonists. Inhibitors, activators, or modulators also include genetically modified versions of angiogenesis regulatory proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, peptides, cyclic peptides, nucleic acids, antisense molecules, ribozymes, RNAi, small organic molecules and the like. Such assays for inhibitors and activators include, e.g., expressing angiogenesis regulatory proteins *in vitro*, in cells, or cell extracts, applying putative modulator compounds, and then determining the functional effects on activity, as described above.

Samples or assays comprising angiogenesis regulatory proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of angiogenesis regulatory protein is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of angiogenesis regulatory protein is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, either naturally occurring or synthetic, e.g., protein, oligopeptide (e.g., from about 5 to about 25 amino acids in length, preferably from about 10 to 20 or 12 to 18 amino acids in length, preferably 12, 15, or 18 amino acids in length), small organic molecule, polysaccharide, lipid, fatty acid, polynucleotide, oligonucleotide, etc., to be tested for the capacity to directly or indirectly modulate angiogenesis. The test compound can be in the form of a library of test compounds, such as a combinatorial or randomized library that provides a sufficient range of diversity. Test compounds are optionally linked to a fusion partner, e.g., targeting compounds, rescue compounds, dimerization compounds, stabilizing compounds, addressable compounds, and other functional moieties. Conventionally, new chemical entities with useful properties are generated by identifying a test compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and

evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

A "small organic molecule" refers to an organic molecule, either naturally occurring or synthetic, that has a molecular weight of more than about 50 daltons and less than about 2500 daltons, preferably less than about 2000 daltons, preferably between about 100 to about 1000 daltons, more preferably between about 200 to about 500 daltons.

"RNAi molecule" or an "siRNA" refers to a nucleic acid that forms a double stranded RNA, which double stranded RNA has the ability to reduce or inhibit expression of a gene or target gene when the siRNA expressed in the same cell as the gene or target gene.

"siRNA" thus refers to the double stranded RNA formed by the complementary strands. The complementary portions of the siRNA that hybridize to form the double stranded molecule typically have substantial or complete identity. In one embodiment, an siRNA refers to a nucleic acid that has substantial or complete identity to a target gene and forms a double stranded siRNA. The sequence of the siRNA can correspond to the full length target gene, or a subsequence thereof. Typically, the siRNA is at least about 15-50 nucleotides in length (e.g., each complementary sequence of the double stranded siRNA is 15-50 nucleotides in length, and the double stranded siRNA is about 15-50 base pairs in length, preferable about 20-30 base nucleotides, preferably about 20-25 nucleotides in length, e.g., 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides in length.

"Biological sample" include sections of tissues such as biopsy and autopsy samples, and frozen sections taken for histologic purposes. Such samples include blood, sputum, tissue, cultured cells, e.g., primary cultures, explants, and transformed cells, stool, urine, etc. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region (e.g., SEQ ID NO:1 or 2), when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (*see, e.g.,* NCBI web site or the like). Such sequences are then said to be

“substantially identical.” This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A “comparison window”, as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990), respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>).

This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*).

5 These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino
10 acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T , and X determine the
15 sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, $M=5$, $N=-4$ and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of
20 50, expectation (E) of 10, $M=5$, $N=-4$, and a comparison of both strands.

“Nucleic acid” refers to deoxyribonucleotides or ribonucleotides and polymers thereof in single- or double-stranded form, or complements thereof. The term encompasses nucleic acids containing known nucleotide analogs or modified backbone residues or linkages, which are synthetic, naturally occurring, and non-naturally occurring, which have
25 similar binding properties as the reference nucleic acid, and which are metabolized in a manner similar to the reference nucleotides. Examples of such analogs include, without limitation, phosphorothioates, phosphoramidates, methyl phosphonates, chiral-methyl phosphonates, 2-O-methyl ribonucleotides, peptide-nucleic acids (PNAs). Nucleic acids also include complementary nucleic acids.

30 Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or

deoxyinosine residues (Batzer *et al.*, *Nucleic Acid Res.* 19:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.* 260:2605-2608 (1985); Rossolini *et al.*, *Mol. Cell. Probes* 8:91-98 (1994)). The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

5 A particular nucleic acid sequence also implicitly encompasses "splice variants." Similarly, a particular protein encoded by a nucleic acid implicitly encompasses any protein encoded by a splice variant of that nucleic acid. "Splice variants," as the name suggests, are products of alternative splicing of a gene. After transcription, an initial nucleic acid transcript may be spliced such that different (alternate) nucleic acid splice products
10 encode different polypeptides. Mechanisms for the production of splice variants vary, but include alternate splicing of exons. Alternate polypeptides derived from the same nucleic acid by read-through transcription are also encompassed by this definition. Any products of a splicing reaction, including recombinant forms of the splice products, are included in this definition.

15 The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

20 The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have
25 the same basic chemical structure as a naturally occurring amino acid, i.e., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical
30 compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid.

 Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical

Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

“Conservatively modified variants” applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are “silent variations,” which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence with respect to the expression product, but not with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a “conservatively modified variant” where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.

The following eight groups each contain amino acids that are conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (*see, e.g., Creighton, Proteins* (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, *see, e.g., Alberts et al., Molecular Biology of the Cell* (3rd ed., 1994) and Cantor and Schimmel, *Biophysical Chemistry Part I: The Conformation of Biological Macromolecules* (1980).

5 “Primary structure” refers to the amino acid sequence of a particular peptide. “Secondary structure” refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains, e.g., transmembrane domains, pore domains, and cytoplasmic tail domains. Domains are portions of a polypeptide that form a compact unit of the polypeptide and are typically 15 to 350 amino acids long. Exemplary domains
10 include domains with enzymatic activity, e.g., phosphatase domains, ligand binding domains, etc. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. “Tertiary structure” refers to the complete three dimensional structure of a polypeptide monomer. “Quaternary structure” refers to the three dimensional structure formed by the noncovalent association of independent tertiary units. Anisotropic terms are
15 also known as energy terms.

A “label” or a “detectable moiety” is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ³²P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins
20 which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

The term “recombinant” when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a
25 native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all.

The term “heterologous” when used with reference to portions of a nucleic
30 acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises

two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1% SDS at 65°C.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, for example, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1X SSC at 45°C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., and *Current Protocols in Molecular Biology*, ed. Ausubel, *et al.*

For PCR, a temperature of about 36°C is typical for low stringency amplification, although annealing temperatures may vary between about 32°C and 48°C

depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C to about 65°C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90°C - 95°C for 30 sec - 2 min., an annealing phase lasting 30 sec. - 2 min., and an extension phase of about 72°C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis *et al.* (1990) *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc. N.Y.).

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody will be most critical in specificity and affinity of binding.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one “light” (about 25 kD) and one “heavy” chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, for example, pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (*see Fundamental Immunology* (Paul ed., 3d ed. 1993)). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole

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antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (*see, e.g., McCafferty et al., Nature* 348:552-554 (1990))

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal

5 antibodies, many techniques known in the art can be used (*see, e.g., Kohler & Milstein, Nature* 256:495-497 (1975); Kozbor *et al., Immunology Today* 4: 72 (1983); Cole *et al.*, pp. 77-96 in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. (1985); Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *Antibodies, A Laboratory Manual* (1988); and Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986)). The

10 genes encoding the heavy and light chains of an antibody of interest can be cloned from a cell, e.g., the genes encoding a monoclonal antibody can be cloned from a hybridoma and used to produce a recombinant monoclonal antibody. Gene libraries encoding heavy and light chains of monoclonal antibodies can also be made from hybridoma or plasma cells. Random combinations of the heavy and light chain gene products generate a large pool of

15 antibodies with different antigenic specificity (*see, e.g., Kuby, Immunology* (3rd ed. 1997)). Techniques for the production of single chain antibodies or recombinant antibodies (U.S. Patent 4,946,778, U.S. Patent No. 4,816,567) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized or human antibodies (*see, e.g., U.S. Patent*

20 Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, Marks *et al., Bio/Technology* 10:779-783 (1992); Lonberg *et al., Nature* 368:856-859 (1994); Morrison, *Nature* 368:812-13 (1994); Fishwild *et al., Nature Biotechnology* 14:845-51 (1996); Neuberger, *Nature Biotechnology* 14:826 (1996); and Lonberg & Huszar, *Intern. Rev. Immunol.* 13:65-93 (1995)). Alternatively, phage display technology can be used to identify

25 antibodies and heteromeric Fab fragments that specifically bind to selected antigens (*see, e.g., McCafferty et al., Nature* 348:552-554 (1990); Marks *et al., Biotechnology* 10:779-783 (1992)). Antibodies can also be made bispecific, i.e., able to recognize two different antigens (*see, e.g., WO 93/08829, Traunecker et al., EMBO J.* 10:3655-3659 (1991); and Suresh *et al., Methods in Enzymology* 121:210 (1986)). Antibodies can also be heteroconjugates, e.g., two

30 covalently joined antibodies, or immunotoxins (*see, e.g., U.S. Patent No. 4,676,980, WO 91/00360; WO 92/200373; and EP 03089*).

Methods for humanizing or primatizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues

are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers (*see, e.g., Jones et al., Nature* 321:522-525 (1986); Riechmann *et al., Nature* 332:323-327 (1988); Verhoeyen *et al., Science* 239:1534-1536 (1988) and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g., an enzyme, toxin, hormone, growth factor, drug, etc.*; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

In one embodiment, the antibody is conjugated to an "effector" moiety. The effector moiety can be any number of molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the antibody modulates the activity of the protein.

The phrase "specifically (or selectively) binds" to an antibody or "specifically (or selectively) immunoreactive with," when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein, often in a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and more typically more than 10 to 100 times background. Specific binding to an antibody under such conditions requires an antibody that is selected for its specificity for a particular protein. For example, polyclonal antibodies raised to angiogenesis regulatory proteins, polymorphic variants, alleles, orthologs, and conservatively modified variants, or splice variants, or portions thereof, can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with angiogenesis regulatory proteins and not with other proteins. This selection may be achieved by subtracting out antibodies that cross-react with

other molecules. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (*see, e.g., Harlow & Lane, Antibodies, A Laboratory Manual* (1988) for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity).

Assays for proteins that modulate angiogenesis

High throughput functional genomics assays can be used to identify modulators of angiogenesis. Such assays can monitor changes in cell surface marker expression, $\alpha v \beta 3$ integrin production, proliferation, and differentiation using either cell lines or primary cells, e.g., endothelial cells such as HUVEC cells. Typically, early passage or primary endothelial cells are contacted with a cDNA or a random peptide library (encoded by nucleic acids). Often the libraries are retroviral libraries. The cDNA library can comprise sense, antisense, full length, and truncated cDNAs. The cDNAs are often from endothelial cells, e.g., HUVEC cells, either differentiated on matrigel or 3-d collagen, or undifferentiated. The peptide library is encoded by nucleic acids. The cDNAs are optionally fused to markers such as GFP. The effect of the cDNA or peptide library on the endothelial cells is then monitored, using an assay such as cell surface marker expression (e.g., $\alpha v \beta 3$ integrin or VEGF2-R2) or a phenotypic assay for angiogenesis such as migration towards an ECM (extracellular matrix) component (*see, e.g., Klenke et al., J. Cell Biol.* 4:961-972 (1998)) or endothelial cell tube formation assays, as well as other bioassays such as the chick CAM assay, the mouse corneal assay, haptotaxis assays, and assays measuring the effect of administering potential modulators on implanted tumors. The effect of the cDNA or peptide can be validated and distinguished from somatic mutations, using, e.g., regulatable expression of the nucleic acid such as expression from a tetracycline promoter. cDNAs and nucleic acids encoding peptides can be rescued using techniques known to those of skill in the art, e.g., using a sequence tags.

Proteins interacting with the peptide or with the protein encoded by the cDNA (e.g., angiogenesis regulatory protein) can be isolated using a yeast two-hybrid system, mammalian two hybrid system, immunoprecipitation and proteomics, phage display screen, etc. Targets so identified can be further used as bait in these assays to identify additional members of the angiogenesis pathway, which members are also targets for drug development (*see, e.g., Fields et al., Nature* 340:245 (1989); Vasavada et al., *Proc. Nat'l Acad. Sci. USA*

88:10686 (1991); Fearon *et al.*, *Proc. Nat'l Acad. Sci. USA* 89:7958 (1992); Dang *et al.*, *Mol. Cell. Biol.* 11:954 (1991); Chien *et al.*, *Proc. Nat'l Acad. Sci. USA* 9578 (1991); and U.S. Patent Nos. 5,283,173, 5,667,973, 5,468,614, 5,525,490, and 5,637,463).

Suitable endothelial cell lines include human umbilical vein cells (*see, e.g.*,
5 Jaffe *et al.*, *J. Clin. Invest.* 52:2745-2754 (1973)); human adult dermal capillary-derived cells (*see, e.g.*, Davison *et al.*, *In Vitro* 19:937-945 (1983)); human adipose capillary derived cells (*see, e.g.*, Kern *et al.*, *J. Clin. Invest.* 71:1822-1829 (1983); bovine aorta (*see, e.g.*, Booyse *et al.*, *Thromb. Diathes. Aemorrh.* 34:825-839 (1975); and rat brain capillary derived cells (*see, e.g.*, Bowman *et al.*, *In Vitro* 17:353-362 (1981)). For culture of endothelial cell lines,
10 explants, and primary cells, *see* Freshney *et al.*, *Culture of Animal Cells* (3rd ed. 1994). Suitable angiogenesis cell surface markers include $\alpha v \beta 3$ integrin (*see, e.g.*, Elicerir & Cheresch, *Cancer J. Sci. Am.* 6 Supp. 3:S245-249 (2000), Maeshima *et al.*, *J. Biol. Chem.* (June 8, 2001)).

Cell surface markers such as $\alpha v \beta 3$ can be assayed using fluorescently labeled
15 antibodies and FACS. Cell proliferation can be measured using ³H-thymidine or dye inclusion. Angiogenesis phenotype is measured by loss of phenotype observation.

cDNA libraries are made from any suitable source, preferably from endothelial cells. Libraries encoding random peptides are made according to techniques well known to those of skill in the art (*see, e.g.*, U.S. Patent No. 6,153,380, 6,114,111, and
20 6,180,343). Any suitable vector can be used for the cDNA and peptide libraries, including, *e.g.*, retroviral vectors.

In a preferred embodiment, target proteins that modulate angiogenesis or nucleic acids that encode the target proteins are identified using a high throughput cell based assay (using a microtiter plate format) and FACS screening for $\alpha v \beta 3$ cell surface expression.
25 cDNA libraries are made which include, *e.g.*, sense, antisense, full length, and truncated cDNAs. The cDNAs are cloned into a retroviral vector. Endothelial cells are infected with the library, cultured for a short effector phase and then the cells with reduced $\alpha v \beta 3$ surface levels are enriched by antibody staining and magnetic cell sorting. The enriched cell population is then sorted into microtiter plates using fluorescent antibodies and FACS.
30 Resultant cell colonies are analyzed by immunofluorescence for reduced $\alpha v \beta 3$ surface levels. Selected colonies are infected with wild type MMLV virus to rescue the proviral vector. The infectious supernatant is used to infect endothelial cells, which are subsequently analyzed for $\alpha v \beta 3$ levels by FACS. The cDNA is isolated and sequenced to determined if it represents a wild type or mutated cDNA, *e.g.*, whether the cDNA represents a negative transdominant

mutant. Optionally, a marker such as GFP can be used to select for retrovirally infected cells. Using this system, cDNA molecules encoding angiogenesis regulatory protein were identified as a targets for anti-angiogenic drug therapy. Some of the cDNAs were fused in frame to a GFP marker. Some cDNA molecules were expressed as inhibitory antisense molecules.

5 Finally, some cDNAs were expressed in the antisense orientation and expression of the translated protein or peptide resulted in an angiogenesis phenotype.

Isolation of nucleic acids encoding angiogenesis regulatory proteins

This invention relies on routine techniques in the field of recombinant
10 genetics. Basic texts disclosing the general methods of use in this invention include Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd ed. 1989); Kriegler, *Gene Transfer and Expression: A Laboratory Manual* (1990); and *Current Protocols in Molecular Biology* (Ausubel *et al.*, eds., 1994)).

Nucleic acids encoding angiogenesis regulatory proteins and their
15 polymorphic variants, orthologs, and alleles that are substantially identical to the amino acid sequence of SEQ ID NO:4, SEQ ID NO:33, SEQ ID NO:44, SEQ ID NO:58, SEQ ID NO:64, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:77, SEQ ID NO:82, SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:121, SEQ ID NO:129, SEQ ID NO:140, SEQ ID NO:154, SEQ ID NO:164, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID
20 NO:184, SEQ ID NO:203, SEQ ID NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, SEQ ID NO:331, SEQ ID NO:341, SEQ ID NO:352, SEQ ID NO:366, SEQ ID NO:378, SEQ ID NO:385, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:420, SEQ ID NO:429, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:457, SEQ ID NO:463, SEQ ID NO:482, SEQ ID NO:485, SEQ ID NO:494, SEQ ID
25 NO:497, SEQ ID NO:499, and SEQ ID NO:520 can be isolated using nucleic acid probes and oligonucleotides under stringent hybridization conditions, by screening libraries.

Alternatively, expression libraries can be used to clone angiogenesis regulatory proteins, polymorphic variants, orthologs, and alleles by detecting expressed homologs immunologically with antisera or purified antibodies made against a human angiogenesis
30 regulatory protein or portions thereof.

To make a cDNA library, one should choose a source that is rich in angiogenesis regulatory protein RNA, e.g., endothelial cells. The mRNA is then made into cDNA using reverse transcriptase, ligated into a recombinant vector, and transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening

cDNA libraries are well known (*see, e.g.,* Gubler & Hoffman, *Gene* 25:263-269 (1983); Sambrook *et al., supra*; Ausubel *et al., supra*).

For a genomic library, the DNA is extracted from the tissue and either mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro*. Recombinant phage are analyzed by plaque hybridization as described in Benton & Davis, *Science* 196:180-182 (1977). Colony hybridization is carried out as generally described in Grunstein *et al., Proc. Natl. Acad. Sci. USA.*, 72:3961-3965 (1975).

An alternative method of isolating angiogenesis regulatory protein nucleic acid and its orthologs, alleles, mutants, polymorphic variants, and conservatively modified variants combines the use of synthetic oligonucleotide primers and amplification of an RNA or DNA template (*see* U.S. Patents 4,683,195 and 4,683,202; *PCR Protocols: A Guide to Methods and Applications* (Innis *et al., eds*, 1990)). Methods such as polymerase chain reaction (PCR) and ligase chain reaction (LCR) can be used to amplify nucleic acid sequences encoding human angiogenesis regulatory proteins directly from mRNA, from cDNA, from genomic libraries or cDNA libraries. Degenerate oligonucleotides can be designed to amplify angiogenesis regulatory protein homologs using the sequences provided herein. Restriction endonuclease sites can be incorporated into the primers. Polymerase chain reaction or other *in vitro* amplification methods may also be useful, for example, to clone nucleic acid sequences that code for proteins to be expressed, to make nucleic acids to use as probes for detecting the presence of angiogenesis regulatory protein encoding mRNA in physiological samples, for nucleic acid sequencing, or for other purposes. Genes amplified by the PCR reaction can be purified from agarose gels and cloned into an appropriate vector.

Gene expression of angiogenesis regulatory proteins can also be analyzed by techniques known in the art, e.g., reverse transcription and amplification of mRNA, isolation of total RNA or poly A⁺ RNA, northern blotting, dot blotting, *in situ* hybridization, RNase protection, high density polynucleotide array technology, e.g., and the like.

Nucleic acids encoding angiogenesis regulatory proteins can be used with high density oligonucleotide array technology (e.g., GeneChipTM) to identify angiogenesis regulatory proteins, orthologs, alleles, conservatively modified variants, and polymorphic variants in this invention. In the case where the homologs being identified are linked to a condition such as neovascularization or angiogenic insufficiency, they can be used with GeneChipTM as a diagnostic tool in detecting the disease in a biological sample, *see, e.g.,*

Gunthand *et al.*, *AIDS Res. Hum. Retroviruses* 14: 869-876 (1998); Kozal *et al.*, *Nat. Med.* 2:753-759 (1996); Matson *et al.*, *Anal. Biochem.* 224:110-106 (1995); Lockhart *et al.*, *Nat. Biotechnol.* 14:1675-1680 (1996); Gingeras *et al.*, *Genome Res.* 8:435-448 (1998); Hacia *et al.*, *Nucleic Acids Res.* 26:3865-3866 (1998).

5 The gene for an angiogenesis regulatory protein is typically cloned into intermediate vectors before transformation into prokaryotic or eukaryotic cells for replication and/or expression. These intermediate vectors are typically prokaryote vectors, e.g., plasmids, or shuttle vectors.

10 **Expression in prokaryotes and eukaryotes**

To obtain high level expression of a cloned gene, such as those cDNAs encoding an angiogenesis regulatory protein, one typically subclones a gene encoding an angiogenesis regulatory protein into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable bacterial promoters are well known in the art and described, e.g., in Sambrook *et al.*, and Ausubel *et al.*, *supra*. Bacterial expression systems for expressing angiogenesis regulatory proteins are available in, e.g., *E. coli*, *Bacillus sp.*, and *Salmonella* (Palva *et al.*, *Gene* 22:229-235 (1983); Mosbach *et al.*, *Nature* 302:543-545 (1983). Kits for such expression systems are commercially available. Eukaryotic expression systems for mammalian cells, yeast, and insect cells are well known in the art and are also commercially available.

Selection of the promoter used to direct expression of a heterologous nucleic acid depends on the particular application. The promoter is preferably positioned about the same distance from the heterologous transcription start site as it is from the transcription start site in its natural setting. As is known in the art, however, some variation in this distance can be accommodated without loss of promoter function.

In addition to the promoter, the expression vector typically contains a transcription unit or expression cassette that contains all the additional elements required for the expression of the angiogenesis regulatory protein encoding nucleic acid in host cells. A typical expression cassette thus contains a promoter operably linked to the nucleic acid sequence encoding an angiogenesis regulatory protein and signals required for efficient polyadenylation of the transcript, ribosome binding sites, and translation termination. Additional elements of the cassette may include enhancers and, if genomic DNA is used as the structural gene, introns with functional splice donor and acceptor sites.

In addition to a promoter sequence, the expression cassette should also contain a transcription termination region downstream of the structural gene to provide for efficient termination. The termination region may be obtained from the same gene as the promoter sequence or may be obtained from different genes.

5 The particular expression vector used to transport the genetic information into the cell is not particularly critical. Any of the conventional vectors used for expression in eukaryotic or prokaryotic cells may be used. Standard bacterial expression vectors include plasmids such as pBR322 based plasmids, pSKF, pET23D, and fusion expression systems such as MBP, GST, and LacZ. Epitope tags can also be added to recombinant proteins to
10 provide convenient methods of isolation, e.g., c-myc.

Expression vectors containing regulatory elements from eukaryotic viruses are typically used in eukaryotic expression vectors, e.g., SV40 vectors, papilloma virus vectors, retroviral vectors, and vectors derived from Epstein-Barr virus. Other exemplary eukaryotic vectors include pMSG, pAV009/A⁺, pMTO10/A⁺, pMAMneo-5, baculovirus pDSVE, and
15 any other vector allowing expression of proteins under the direction of the CMV promoter, SV40 early promoter, SV40 later promoter, metallothionein promoter, murine mammary tumor virus promoter, Rous sarcoma virus promoter, polyhedrin promoter, or other promoters shown effective for expression in eukaryotic cells.

Expression of proteins from eukaryotic vectors can be also be regulated using
20 inducible promoters. With inducible promoters, expression levels are tied to the concentration of inducing agents, such as tetracycline or ecdysone, by the incorporation of response elements for these agents into the promoter. Generally, high level expression is obtained from inducible promoters only in the presence of the inducing agent; basal expression levels are minimal. Inducible expression vectors are often chosen if expression of
25 the protein of interest is detrimental to eukaryotic cells.

In one embodiment, the vectors of the invention have a regulatable promoter, e.g., tet-regulated systems and the RU-486 system (*see, e.g., Gossen & Bujard, Proc. Nat'l Acad. Sci. USA* 89:5547 (1992); Oligino *et al., Gene Ther.* 5:491-496 (1998); Wang *et al., Gene Ther.* 4:432-441 (1997); Neering *et al., Blood* 88:1147-1155 (1996); and Rendahl *et al., Nat. Biotechnol.* 16:757-761 (1998)). These impart small molecule control on the expression
30 of the candidate target nucleic acids. This beneficial feature can be used to determine that a desired phenotype is caused by a transfected cDNA rather than a somatic mutation.

Some expression systems have markers that provide gene amplification such as thymidine kinase and dihydrofolate reductase. Alternatively, high yield expression

systems not involving gene amplification are also suitable, such as using a baculovirus vector in insect cells, with an angiogenesis regulatory protein encoding sequence under the direction of the polyhedrin promoter or other strong baculovirus promoters.

The elements that are typically included in expression vectors also include a replicon that functions in *E. coli*, a gene encoding antibiotic resistance to permit selection of bacteria that harbor recombinant plasmids, and unique restriction sites in nonessential regions of the plasmid to allow insertion of eukaryotic sequences. The particular antibiotic resistance gene chosen is not critical, any of the many resistance genes known in the art are suitable. The prokaryotic sequences are preferably chosen such that they do not interfere with the replication of the DNA in eukaryotic cells, if necessary.

Standard transfection methods are used to produce bacterial, mammalian, yeast or insect cell lines that express large quantities of angiogenesis regulatory proteins, which are then purified using standard techniques (*see, e.g., Colley et al., J. Biol. Chem.* 264:17619-17622 (1989); *Guide to Protein Purification*, in *Methods in Enzymology*, vol. 182 (Deutscher, ed., 1990)). Transformation of eukaryotic and prokaryotic cells are performed according to standard techniques (*see, e.g., Morrison, J. Bact.* 132:349-351 (1977); Clark-Curtiss & Curtiss, *Methods in Enzymology* 101:347-362 (Wu *et al.*, eds, 1983).

Any of the well-known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, biolistics, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g., Sambrook et al., supra*). It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing angiogenesis regulatory protein.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of angiogenesis regulatory protein, which is recovered from the culture using standard techniques identified below.

Purification of angiogenesis regulatory proteins

Either naturally occurring or recombinant angiogenesis regulatory proteins can be purified for use in functional assays. Naturally occurring angiogenesis regulatory protein can be purified, e.g., from human tissue. Recombinant angiogenesis regulatory protein can be purified from any suitable expression system.

The angiogenesis regulatory proteins may be purified to substantial purity by standard techniques, including selective precipitation with such substances as ammonium sulfate; column chromatography, immunopurification methods, and others (*see, e.g., Scopes, Protein Purification: Principles and Practice* (1982); U.S. Patent No. 4,673,641; Ausubel *et al., supra*; and Sambrook *et al., supra*).

A number of procedures can be employed when recombinant angiogenesis regulatory proteins are being purified. For example, proteins having established molecular adhesion properties can be reversibly fused to the angiogenesis regulatory proteins. With the appropriate ligand, the angiogenesis regulatory proteins can be selectively adsorbed to a purification column and then freed from the column in a relatively pure form. The fused protein is then removed by enzymatic activity. Finally, the angiogenesis regulatory proteins could be purified using immunoaffinity columns.

A. Purification of angiogenesis regulatory proteins from recombinant bacteria

Recombinant proteins are expressed by transformed bacteria in large amounts, typically after promoter induction; but expression can be constitutive. Promoter induction with IPTG is one example of an inducible promoter system. Bacteria are grown according to standard procedures in the art. Fresh or frozen bacteria cells are used for isolation of protein.

Proteins expressed in bacteria may form insoluble aggregates ("inclusion bodies"). Several protocols are suitable for purification of inclusion bodies containing angiogenesis regulatory proteins. For example, purification of inclusion bodies typically involves the extraction, separation and/or purification of inclusion bodies by disruption of bacterial cells, e.g., by incubation in a buffer of 50 mM TRIS/HCL pH 7.5, 50 mM NaCl, 5 mM MgCl₂, 1 mM DTT, 0.1 mM ATP, and 1 mM PMSF. The cell suspension can be lysed using 2-3 passages through a French Press, homogenized using a Polytron (Brinkman Instruments) or sonicated on ice. Alternate methods of lysing bacteria are apparent to those of skill in the art (*see, e.g., Sambrook et al., supra; Ausubel et al., supra*).

If necessary, the inclusion bodies are solubilized, and the lysed cell suspension is typically centrifuged to remove unwanted insoluble matter. Proteins that formed the inclusion bodies may be renatured by dilution or dialysis with a compatible buffer. Suitable solvents include, but are not limited to urea (from about 4 M to about 8 M), formamide (at least about 80%, volume/volume basis), and guanidine hydrochloride (from about 4 M to about 8 M). Some solvents which are capable of solubilizing aggregate-forming proteins, for example SDS (sodium dodecyl sulfate), 70% formic acid, are inappropriate for use in this

procedure due to the possibility of irreversible denaturation of the proteins, accompanied by a lack of immunogenicity and/or activity. Although guanidine hydrochloride and similar agents are denaturants, this denaturation is not irreversible and renaturation may occur upon removal (by dialysis, for example) or dilution of the denaturant, allowing re-formation of immunologically and/or biologically active protein. Other suitable buffers are known to those skilled in the art. Human angiogenesis regulatory proteins are separated from other bacterial proteins by standard separation techniques, e.g., with Ni-NTA agarose resin.

Alternatively, it is possible to purify angiogenesis regulatory proteins from bacteria periplasm. After lysis of the bacteria, when the angiogenesis regulatory proteins are exported into the periplasm of the bacteria, the periplasmic fraction of the bacteria can be isolated by cold osmotic shock in addition to other methods known to skill in the art. To isolate recombinant proteins from the periplasm, the bacterial cells are centrifuged to form a pellet. The pellet is resuspended in a buffer containing 20% sucrose. To lyse the cells, the bacteria are centrifuged and the pellet is resuspended in ice-cold 5 mM MgSO_4 and kept in an ice bath for approximately 10 minutes. The cell suspension is centrifuged and the supernatant decanted and saved. The recombinant proteins present in the supernatant can be separated from the host proteins by standard separation techniques well known to those of skill in the art.

B. Standard protein separation techniques for purifying angiogenesis regulatory proteins

Solubility fractionation

Often as an initial step, particularly if the protein mixture is complex, an initial salt fractionation can separate many of the unwanted host cell proteins (or proteins derived from the cell culture media) from the recombinant protein of interest. The preferred salt is ammonium sulfate. Ammonium sulfate precipitates proteins by effectively reducing the amount of water in the protein mixture. Proteins then precipitate on the basis of their solubility. The more hydrophobic a protein is, the more likely it is to precipitate at lower ammonium sulfate concentrations. A typical protocol includes adding saturated ammonium sulfate to a protein solution so that the resultant ammonium sulfate concentration is between 20-30%. This concentration will precipitate the most hydrophobic of proteins. The precipitate is then discarded (unless the protein of interest is hydrophobic) and ammonium sulfate is added to the supernatant to a concentration known to precipitate the protein of interest. The precipitate is then solubilized in buffer and the excess salt removed if

necessary, either through dialysis or diafiltration. Other methods that rely on solubility of proteins, such as cold ethanol precipitation, are well known to those of skill in the art and can be used to fractionate complex protein mixtures.

Size differential filtration

The molecular weight of the angiogenesis regulatory proteins can be used to isolate it from proteins of greater and lesser size using ultrafiltration through membranes of different pore size (for example, Amicon or Millipore membranes). As a first step, the protein mixture is ultrafiltered through a membrane with a pore size that has a lower molecular weight cut-off than the molecular weight of the protein of interest. The retentate of the ultrafiltration is then ultrafiltered against a membrane with a molecular cut off greater than the molecular weight of the protein of interest. The recombinant protein will pass through the membrane into the filtrate. The filtrate can then be chromatographed as described below.

Column chromatography

The angiogenesis regulatory proteins can also be separated from other proteins on the basis of its size, net surface charge, hydrophobicity, and affinity for ligands. In addition, antibodies raised against proteins can be conjugated to column matrices and the proteins immunopurified. All of these methods are well known in the art. It will be apparent to one of skill that chromatographic techniques can be performed at any scale and using equipment from many different manufacturers (e.g., Pharmacia Biotech).

Assays for modulators of angiogenesis regulatory proteins and angiogenesis

A. Assays

Modulation of a angiogenesis regulatory proteins, and corresponding modulation of angiogenesis, can be assessed using a variety of *in vitro* and *in vivo* assays, including high throughput ligand binding and cell based assays, as described herein. Such assays can be used to test for inhibitors and activators of angiogenesis regulatory proteins, and, consequently, inhibitors and activators of angiogenesis. Such modulators of angiogenesis regulatory proteins are useful for treating angiogenesis disorders. Modulators of angiogenesis regulatory proteins are tested using either recombinant or naturally occurring angiogenesis regulatory protein, preferably human angiogenesis regulatory protein.

Preferably, the angiogenesis regulatory proteins will have the sequence displayed in SEQ ID NO:4, SEQ ID NO:33, SEQ ID NO:44, SEQ ID NO:58, SEQ ID NO:64, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:77, SEQ ID NO:82, SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:121, SEQ ID NO:129, SEQ ID NO:140, SEQ ID NO:154, SEQ ID NO:164, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:203, SEQ ID NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, SEQ ID NO:331, SEQ ID NO:341, SEQ ID NO:352, SEQ ID NO:366, SEQ ID NO:378, SEQ ID NO:385, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:420, SEQ ID NO:429, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:457, SEQ ID NO:463, SEQ ID NO:482, SEQ ID NO:485, SEQ ID NO:494, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:520, SEQ ID NO:522, and SEQ ID NO:524 or a conservatively modified variant thereof. Alternatively, the angiogenesis regulatory proteins of the assay will be derived from a eukaryote and include an amino acid subsequence having substantial amino acid sequence identity to SEQ ID NO:4, SEQ ID NO:33, SEQ ID NO:44, SEQ ID NO:58, SEQ ID NO:64, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:77, SEQ ID NO:82, SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:121, SEQ ID NO:129, SEQ ID NO:140, SEQ ID NO:154, SEQ ID NO:164, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:203, SEQ ID NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, SEQ ID NO:331, SEQ ID NO:341, SEQ ID NO:352, SEQ ID NO:366, SEQ ID NO:378, SEQ ID NO:385, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:420, SEQ ID NO:429, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:457, SEQ ID NO:463, SEQ ID NO:482, SEQ ID NO:485, SEQ ID NO:494, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:520, SEQ ID NO:522, and SEQ ID NO:524. Generally, the amino acid sequence identity will be at least 60%, preferably at least 65%, 70%, 75%, 80%, 85%, or 90%, most preferably at least 95%.

Measurement of an angiogenic or loss-of-angiogenesis phenotype in angiogenesis regulatory proteins or cells expressing angiogenesis regulatory proteins, either recombinant or naturally occurring, can be performed using a variety of assays, *in vitro*, *in vivo*, and *ex vivo*. For example, recombinant or naturally occurring angiogenesis regulatory protein can be used *in vitro*, in a ligand binding or enzymatic function assay. Angiogenesis regulatory proteins present in a cellular extract can also be used in *in vitro* assays. Cell- and animal-based *in vivo* assays can also be used to assay for angiogenesis regulatory protein modulators. Any suitable physical, chemical, or phenotypic change that affects activity or binding can be used to assess the influence of a test compound on the polypeptide of this

invention. When the functional effects are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of angiogenesis associated with tumors, tumor growth, neovascularization, cell surface markers such as $\alpha v \beta 3$, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In one embodiment, measurement of $\alpha v \beta 3$ integrin cell surface expression and FACS sorting is used to identify modulators of angiogenesis.

In vitro assays

Assays to identify compounds with angiogenesis regulatory protein modulating activity, e.g., anti-angiogenic activity, can be performed *in vitro*, e.g., binding assays. Such assays can use full length angiogenesis regulatory proteins or a variant thereof (see, e.g., SEQ ID NO:2), or a fragment of an angiogenesis regulatory proteins having a desired activity. Purified recombinant or naturally occurring angiogenesis regulatory proteins can be used in the *in vitro* methods of the invention. In addition to purified angiogenesis regulatory proteins, the recombinant or naturally occurring angiogenesis regulatory proteins can be part of a cellular lysate. As described below, the assay can be either solid state or soluble. Preferably, the protein is bound to a solid support, either covalently or non-covalently. Often, the *in vitro* assays of the invention are ligand binding or ligand affinity assays, either non-competitive or competitive. Other *in vitro* assays include measuring changes in spectroscopic (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein.

In one embodiment, a high throughput binding assay is performed in which the angiogenesis regulatory proteins or chimera comprising a fragment thereof is contacted with a potential modulator and incubated for a suitable amount of time. In one embodiment, the potential modulator is bound to a solid support, and the angiogenesis regulatory proteins is added. In another embodiment, the angiogenesis regulatory proteins is bound to a solid support. A wide variety of modulators can be used, as described below, including small organic molecules, peptides, and antibodies. A wide variety of assays can be used to identify angiogenesis regulatory protein -modulator binding or enzymatic activity, including labeled protein-protein binding assays, electrophoretic mobility shifts, immunoassays, and the like. In some cases, the binding of the candidate modulator is determined through the use of competitive binding assays, where interference with binding of a known ligand is measured

in the presence of a potential modulator. Often, either the potential modulator or the known ligand is labeled. Binding of the candidate modulator can also be assessed by determining its effect on the enzymatic activity of an angiogenesis regulatory protein.

Cell-based *in vivo* assays

In another embodiment, an angiogenesis regulatory proteins is expressed in a cell, and functional, e.g., physical and chemical or phenotypic, changes are assayed to identify angiogenesis modulators, preferably anti-angiogenesis compounds. Cells expressing angiogenesis regulatory proteins can also be used in binding assays or enzymatic assays.

Any suitable functional effect can be measured, as described herein. For example, ligand binding, cell surface marker expression, cellular proliferation, cellular differentiation assays and cell migration assays are all suitable assays to identify potential modulators using a cell based system. Suitable cells for such cell based assays include both primary endothelial cells and cell lines, as described herein. The angiogenesis regulatory proteins can be naturally occurring or recombinant. Also, as described above, a fragment of an angiogenesis regulatory protein with a desired activity can be used in cell based assays.

As described above, in one embodiment, loss-of angiogenesis phenotype is measured by contacting endothelial cells comprising an angiogenesis regulatory protein target with a potential modulator. Modulation of angiogenesis is identified by screening for cell surface marker expression, e.g., $\alpha v\beta 3$ integrin expression levels, using fluorescent antibodies and FACS sorting.

In another embodiment, cellular angiogenesis regulatory protein levels are determined by measuring the level of protein or mRNA. The level of angiogenesis regulatory protein or proteins are measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the angiogenesis regulatory protein polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, angiogenesis regulatory protein expression can be measured using a reporter gene system. Such a system can be devised using a angiogenesis regulatory proteins promoter operably linked to a reporter gene such as chloramphenicol

acetyltransferase, firefly luciferase, bacterial luciferase, β -galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as red or green fluorescent protein (*see, e.g.,* Mistili & Spector, *Nature Biotechnology* 15:961-964 (1997)). The reporter construct is typically
5 transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In another embodiment, angiogenesis regulatory protein enzymatic activity can be measured, using, e.g., labeled substrate proteins, gel electrophoresis, and ELISA
10 assays, and other appropriate enzymatic activities.

A variety of phenotypic angiogenesis assays are known to those of skill in the art. Various models have been employed to evaluate angiogenesis (e.g., Croix *et al.*, *Science* 289:1197-1202 (2000) and Kahn *et al.*, *Amer. J. Pathol.* 156:1887-1900). Assessment of angiogenesis in the presence of a potential modulator of angiogenesis can be performed using
15 cell-culture-based angiogenesis assays, e.g., endothelial cell tube formation assays, cellular differentiation assays using matrigel matrix or by co-culture with smooth muscle cells, chemotaxis assays using VEGF or FGF, and haptotaxis assays, as well as other animal based bioassays such as the chick CAM assay, the mouse corneal assay, and assays measuring the effect of administering potential modulators on implanted tumors.

Animal models

A number of animal based assays for angiogenesis phenotypes are known to those of skill in the art and can be used to assay for modulators of angiogenesis. For example, the chick CAM assay is described by O'Reilly, *et al.* *Cell* 79: 315-328 (1994).
25 Briefly, 3 day old chicken embryos with intact yolks are separated from the egg and placed in a petri dish. After 3 days of incubation, a methylcellulose disc containing the protein to be tested is applied to the CAM of individual embryos. After about 48 hours of incubation, the embryos and CAMs are observed to determine whether endothelial growth has been inhibited.

The mouse corneal assay involves implanting a growth factor-containing pellet, along with another pellet containing the suspected endothelial growth inhibitor, in the cornea of a mouse and observing the pattern of capillaries that are elaborated in the cornea.
30

Angiogenesis can also be measured by determining the extent of neovascularization of a tumor. For example, carcinoma cells can be subcutaneously inoculated into athymic nude mice and tumor growth then monitored. Immunoassays using endothelial cell-specific antibodies are typically used to stain for vascularization of tumor and the number of vessels in the tumor.

As described above, animal models of angiogenesis find use in screening for modulators of angiogenesis. Similarly, transgenic animal technology including gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, or gene overexpression, will result in the absence or increased expression of the angiogenesis regulatory proteins. The same technology can also be applied to make knock-out cells. When desired, tissue-specific expression or knockout of the gene encoding an angiogenesis regulatory protein may be necessary. Transgenic animals generated by such methods find use as animal models of angiogenesis and are additionally useful in screening for modulators of angiogenesis.

Knock-out cells and transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous gene site encoding an angiogenesis regulatory protein in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous angiogenesis regulatory protein with a mutated version of angiogenesis regulatory protein, or by mutating the endogenous angiogenesis regulatory protein, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (*see, e.g., Capecchi et al., Science* 244:1288 (1989)). Chimeric targeted mice can be derived according to Hogan *et al., Manipulating the Mouse Embryo: A Laboratory Manual*, Cold Spring Harbor Laboratory (1988) and *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, ed., IRL Press, Washington, D.C., (1987).

B. Modulators

The compounds tested as modulators of angiogenesis regulatory proteins can be any small organic molecule, or a biological entity, such as a protein, e.g., an antibody or peptide, a sugar, a nucleic acid, e.g., an antisense oligonucleotide, RNAi, or a ribozyme, or a

lipid. Alternatively, modulators can be genetically altered versions of an angiogenesis regulatory proteins. Typically, test compounds will be small organic molecules, peptides, lipids, and lipid analogs.

Essentially any chemical compound can be used as a potential modulator or
5 ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to screen large chemical libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of
10 chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka Chemika-Biochemica Analytika (Buchs Switzerland) and the like.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial small organic molecule or peptide library containing a large
15 number of potential therapeutic compounds (potential modulator or ligand compounds). Such "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential
20 or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical
25 building blocks (amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.,* U.S. Patent 5,010,175, Furka, *Int. J. Pept. Prot. Res.* 37:487-493 (1991) and Houghton *et al., Nature* 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (e.g., PCT Publication No. WO 91/19735), encoded peptides (e.g., PCT Publication No. WO 93/20242), random bio-oligomers (e.g., PCT Publication No. WO 92/00091),

benzodiazepines (e.g., U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci. USA* 90:6909-6913 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568 (1992)), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.* 114:9217-9218 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.* 116:2661 (1994)), oligocarbamates (Cho *et al.*, *Science* 261:1303 (1993)), and/or peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.* 59:658 (1994)), nucleic acid libraries (*see* Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (*see, e.g.*, U.S. Patent 5,539,083), antibody libraries (*see, e.g.*, Vaughn *et al.*, *Nature Biotechnology*, 14(3):309-314 (1996) and PCT/US96/10287), carbohydrate libraries (*see, e.g.*, Liang *et al.*, *Science*, 274:1520-1522 (1996) and U.S. Patent 5,593,853), small organic molecule libraries (*see, e.g.*, benzodiazepines, Baum C&EN, Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337; benzodiazepines, 5,288,514, and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA). In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

C. Solid State and soluble high throughput assays

In one embodiment the invention provides soluble assays using angiogenesis regulatory proteins, or a cell or tissue expressing angiogenesis regulatory proteins, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based *in vitro* assays in a high throughput format, where the angiogenesis regulatory protein is attached to a solid phase substrate. Any one of the assays described herein can be adapted for high throughput screening, e.g., ligand binding, cellular proliferation, cell surface marker flux, e.g., $\alpha\beta 3$ integrin, enzymatic activity, etc.. In one preferred embodiment, the cell-based system using $\alpha\beta 3$ integrin modulation and FACS assays is used in a high throughput format for identifying modulators of angiogenesis regulatory proteins, and therefore modulators of T cell angiogenesis.

In the high throughput assays of the invention, either soluble or solid state, it is possible to screen up to several thousand different modulators or ligands in a single day. This methodology can be used for angiogenesis regulatory proteins *in vitro*, or for cell-based assays comprising an angiogenesis regulatory proteins. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate can assay about 100 (e.g., 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 100- about 1500 different compounds. It is possible to assay many plates per day; assay screens for up to about 6,000, 20,000, 50,000, or more than 100,000 different compounds are possible using the integrated systems of the invention.

For a solid state reaction, the protein of interest or a fragment thereof, e.g., an extracellular domain, or a cell comprising the protein of interest or a fragment thereof as part of a fusion protein can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage e.g., via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, etc.) Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders; *see*, SIGMA Immunochemicals 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (e.g., cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors, immunoglobulin receptors and antibodies, the cadherein

family, the integrin family, the selectin family, and the like; *see, e.g.,* Pigott & Power, *The Adhesion Molecule Facts Book I* (1993). Similarly, toxins and venoms, viral epitopes, hormones (e.g., opiates, steroids, etc.), intracellular receptors (e.g. which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D; peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes, polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about 5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethylene glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent which fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups which are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. *See, e.g.,* Merrifield, *J. Am. Chem. Soc.* 85:2149-2154 (1963) (describing solid phase synthesis of, e.g., peptides); Geysen *et al.*, *J. Immun. Meth.* 102:259-274 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron* 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al.*, *Science*, 251:767-777 (1991); Sheldon *et al.*, *Clinical Chemistry* 39(4):718-719 (1993); and Kozal *et al.*, *Nature Medicine* 2(7):753759 (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

Antibodies to angiogenesis regulatory proteins

In addition to the detection of genes encoding angiogenesis regulatory proteins and gene expression using nucleic acid hybridization technology, one can also use

immunoassays to detect angiogenesis regulatory proteins of the invention. Such assays are useful for screening for modulators of angiogenesis regulatory proteins and angiogenesis, as well as for therapeutic and diagnostic applications. Immunoassays can be used qualitatively or quantitatively to analyze angiogenesis regulatory proteins. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

A. Production of antibodies

Methods of producing polyclonal and monoclonal antibodies that react specifically with the angiogenesis regulatory proteins are known to those of skill in the art (see, e.g., Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *supra*; Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986); and Kohler & Milstein, *Nature* 256:495-497 (1975). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by immunizing rabbits or mice (see, e.g., Huse *et al.*, *Science* 246:1275-1281 (1989); Ward *et al.*, *Nature* 341:544-546 (1989)).

A number of immunogens comprising portions of angiogenesis regulatory proteins may be used to produce antibodies specifically reactive with angiogenesis regulatory proteins. For example, recombinant angiogenesis regulatory proteins or an antigenic fragment thereof, can be isolated as described herein. Recombinant protein can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used as an immunogen. Naturally occurring protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in the art. An inbred strain of mice (e.g., BALB/C mice) or rabbits is immunized with the protein using a standard adjuvant, such as Freund's adjuvant, and a standard immunization

protocol. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the beta subunits. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (*see*, Harlow & Lane, *supra*).

Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen are immortalized, commonly by fusion with a myeloma cell (*see*, Kohler & Milstein, *Eur. J. Immunol.* 6:511-519 (1976)). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a vertebrate host. Alternatively, one may isolate DNA sequences which encode a monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse, *et al.*, *Science* 246:1275-1281 (1989).

Monoclonal antibodies and polyclonal sera are collected and titered against the immunogen protein in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Typically, polyclonal antisera with a titer of 10^4 or greater are selected and tested for their cross reactivity against non-angiogenesis regulatory proteins, using a competitive binding immunoassay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Antibodies specific only for a particular angiogenesis regulatory protein ortholog, such as human angiogenesis regulatory protein, can also be made, by subtracting out other cross-reacting orthologs from a species such as a non-human mammal. In this manner, antibodies that bind only to angiogenesis regulatory proteins may be obtained.

Once the specific antibodies against specific angiogenesis regulatory proteins are available, the proteins can be detected by a variety of immunoassay methods. In addition, the antibodies can be used therapeutically as a angiogenesis regulatory protein modulators. For a review of immunological and immunoassay procedures, see *Basic and Clinical Immunology* (Stites & Terr eds., 7th ed. 1991). Moreover, the immunoassays of the present

invention can be performed in any of several configurations, which are reviewed extensively in Enzyme Immunoassay (Maggio, ed., 1980); and Harlow & Lane, *supra*.

B. Immunological binding assays

5 Angiogenesis regulatory proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (*see, e.g.*, U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, see also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993); *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed. 1991). Immunological binding
10 assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case the angiogenesis regulatory proteins or antigenic subsequence thereof). The antibody (e.g., anti- angiogenesis regulatory protein) may be produced by any of a number of means well known to those of skill in the art and as described above.

 Immunoassays also often use a labeling agent to specifically bind to and label
15 the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent may be a labeled angiogenesis regulatory protein or a labeled anti-angiogenesis regulatory protein antibody. Alternatively, the labeling agent may be a third moiety, such a secondary antibody, that specifically binds to the antibody/angiogenesis regulatory protein complex (a secondary
20 antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see, e.g.*, Kronval *et al.*, *J. Immunol.* 111:1401-1406 (1973); Akerstrom *et al.*, *J.*
25 *Immunol.* 135:2589-2542 (1985)). The labeling agent can be modified with a detectable moiety, such as biotin, to which another molecule can specifically bind, such as streptavidin. A variety of detectable moieties are well known to those skilled in the art.

 Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several
30 hours, optionally from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

Non-competitive assay formats

Immunoassays for detecting angiogenesis regulatory proteins in samples may be either competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of antigen is directly measured. In one preferred "sandwich" assay, for example, the anti-angiogenesis regulatory protein antibodies can be bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture angiogenesis regulatory protein present in the test sample. Angiogenesis regulatory proteins thus immobilized are then bound by a labeling agent, such as a second angiogenesis regulatory protein-antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, e.g., streptavidin, to provide a detectable moiety.

Competitive assay formats

In competitive assays, the amount of angiogenesis regulatory proteins present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) angiogenesis regulatory proteins displaced (competed away) from an anti-angiogenesis regulatory protein antibody by the unknown angiogenesis regulatory proteins present in a sample. In one competitive assay, a known amount of angiogenesis regulatory proteins is added to a sample and the sample is then contacted with an antibody that specifically binds to angiogenesis regulatory proteins. The amount of exogenous angiogenesis regulatory proteins bound to the antibody is inversely proportional to the concentration of angiogenesis regulatory proteins present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of angiogenesis regulatory proteins bound to the antibody may be determined either by measuring the amount of angiogenesis regulatory protein present in angiogenesis regulatory proteins/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of angiogenesis regulatory proteins may be detected by providing a labeled angiogenesis regulatory protein molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known angiogenesis regulatory proteins is immobilized on a solid substrate. A known amount of anti-angiogenesis regulatory protein antibody is added to the sample, and the

sample is then contacted with the immobilized angiogenesis regulatory protein. The amount of anti-angiogenesis regulatory protein antibody bound to the known immobilized angiogenesis regulatory protein is inversely proportional to the amount of angiogenesis regulatory proteins present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for crossreactivity determinations. For example, angiogenesis regulatory proteins can be immobilized to a solid support. Proteins (e.g., angiogenesis regulatory protein and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the angiogenesis regulatory protein to compete with itself. The percent crossreactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% crossreactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, e.g., distantly related homologs.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a angiogenesis regulatory proteins, to the immunogen protein. In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the angiogenesis regulatory proteins that is required to inhibit 50% of binding, then the second protein is said to specifically bind to the polyclonal antibodies generated to angiogenesis regulatory protein immunogen.

Other assay formats

Western blot (immunoblot) analysis is used to detect and quantify the presence of an angiogenesis regulatory protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind angiogenesis regulatory protein. The anti-angiogenesis regulatory protein antibodies specifically bind to the angiogenesis regulatory protein on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (e.g., labeled sheep anti-mouse antibodies) that specifically bind to the anti-angiogenesis regulatory protein antibodies.

Other assay formats include liposome immunoassays (LIA), which use liposomes designed to bind specific molecules (e.g., antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (see Monroe *et al.*, *Amer. Clin. Prod. Rev.* 5:34-41 (1986)).

Reduction of non-specific binding

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

Labels

The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, most any label useful in such methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical

means. Useful labels in the present invention include magnetic beads (e.g., DYNABEADSTM), fluorescent dyes (e.g., fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (e.g., ³H, ¹²⁵I, ³⁵S, ¹⁴C, or ³²P), enzymes (e.g., horse radish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric
5 labels such as colloidal gold or colored glass or plastic beads (e.g., polystyrene, polypropylene, latex, etc.).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety of labels may be used, with the choice of label depending on sensitivity required, ease of
10 conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (e.g., biotin) is covalently bound to the molecule. The ligand then binds to another molecules (e.g., streptavidin) molecule, which is either inherently detectable or
15 covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize angiogenesis regulatory proteins, or secondary antibodies that recognize anti-angiogenesis regulatory protein.

The molecules can also be conjugated directly to signal generating
20 compounds, e.g., by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, etc. Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, e.g., luminol. For a review
25 of various labeling or signal producing systems that may be used, see U.S. Patent No. 4,391,904.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it
30 may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, or by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally simple colorimetric labels

may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

10 Gene therapy

The present invention provides the nucleic acids of angiogenesis regulatory protein for the transfection of cells *in vitro* and *in vivo*. These nucleic acids can be inserted into any of a number of well-known vectors for the transfection of target cells and organisms as described below. The nucleic acids are transfected into cells, *ex vivo* or *in vivo*, through the interaction of the vector and the target cell. The nucleic acid, under the control of a promoter, then expresses the angiogenesis regulatory proteins of the present invention, thereby mitigating the effects of absent, partial inactivation, or abnormal expression of the angiogenesis regulatory protein gene, particularly as it relates to angiogenesis. The compositions are administered to a patient in an amount sufficient to elicit a therapeutic response in the patient. An amount adequate to accomplish this is defined as "therapeutically effective dose or amount."

Such gene therapy procedures have been used to correct acquired and inherited genetic defects, cancer, and other diseases in a number of contexts. The ability to express artificial genes in humans facilitates the prevention and/or cure of many important human diseases, including many diseases which are not amenable to treatment by other therapies (for a review of gene therapy procedures, *see* Anderson, *Science* 256:808-813 (1992); Nabel & Felgner, *TIBTECH* 11:211-217 (1993); Mitani & Caskey, *TIBTECH* 11:162-166 (1993); Mulligan, *Science* 926-932 (1993); Dillon, *TIBTECH* 11:167-175 (1993); Miller, *Nature* 357:455-460 (1992); Van Brunt, *Biotechnology* 6(10):1149-1154 (1998); Vigne, *Restorative Neurology and Neuroscience* 8:35-36 (1995); Kremer & Perricaudet, *British Medical Bulletin* 51(1):31-44 (1995); Haddada *et al.*, in *Current Topics in Microbiology and Immunology* (Doerfler & Böhm eds., 1995); and Yu *et al.*, *Gene Therapy* 1:13-26 (1994)).

The nucleic acids of the invention can also be used to make transgenic animals, such as transgenic mice, either by knock-out or overexpression. Such animals are useful, e.g., for testing modulators of angiogenesis.

5 **Pharmaceutical compositions and administration**

Pharmaceutically acceptable carriers are determined in part by the particular composition being administered (e.g., nucleic acid, protein, modulatory compounds or transduced cell), as well as by the particular method used to administer the composition. Accordingly, there are a wide variety of suitable formulations of pharmaceutical compositions of the present invention (*see, e.g., Remington's Pharmaceutical Sciences*, 17th ed., 1989). Administration can be in any convenient manner, e.g., by injection, oral administration, inhalation, transdermal application, or rectal administration.

Formulations suitable for oral administration can consist of (a) liquid solutions, such as an effective amount of the packaged nucleic acid suspended in diluents, such as water, saline or PEG 400; (b) capsules, sachets or tablets, each containing a predetermined amount of the active ingredient, as liquids, solids, granules or gelatin; (c) suspensions in an appropriate liquid; and (d) suitable emulsions. Tablet forms can include one or more of lactose, sucrose, mannitol, sorbitol, calcium phosphates, corn starch, potato starch, microcrystalline cellulose, gelatin, colloidal silicon dioxide, talc, magnesium stearate, stearic acid, and other excipients, colorants, fillers, binders, diluents, buffering agents, moistening agents, preservatives, flavoring agents, dyes, disintegrating agents, and pharmaceutically compatible carriers. Lozenge forms can comprise the active ingredient in a flavor, e.g., sucrose, as well as pastilles comprising the active ingredient in an inert base, such as gelatin and glycerin or sucrose and acacia emulsions, gels, and the like containing, in addition to the active ingredient, carriers known in the art.

The compound of choice, alone or in combination with other suitable components, can be made into aerosol formulations (i.e., they can be "nebulized") to be administered via inhalation. Aerosol formulations can be placed into pressurized acceptable propellants, such as dichlorodifluoromethane, propane, nitrogen, and the like.

Formulations suitable for parenteral administration, such as, for example, by intraarticular (in the joints), intravenous, intramuscular, intradermal, intraperitoneal, and subcutaneous routes, include aqueous and non-aqueous, isotonic sterile injection solutions, which can contain antioxidants, buffers, bacteriostats, and solutes that render the formulation isotonic with the blood of the intended recipient, and aqueous and non-aqueous sterile

suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives. In the practice of this invention, compositions can be administered, for example, by intravenous infusion, orally, topically, intraperitoneally, intravesically or intrathecally. Parenteral administration and intravenous administration are the preferred methods of administration. The formulations of compositions can be presented in unit-dose or multi-dose sealed containers, such as ampules and vials.

Injection solutions and suspensions can be prepared from sterile powders, granules, and tablets of the kind previously described. Cells transduced by nucleic acids for *ex vivo* therapy can also be administered intravenously or parenterally as described above.

The dose administered to a patient, in the context of the present invention should be sufficient to effect a beneficial therapeutic response in the patient over time. The dose will be determined by the efficacy of the particular vector employed and the condition of the patient, as well as the body weight or surface area of the patient to be treated. The size of the dose also will be determined by the existence, nature, and extent of any adverse side-effects that accompany the administration of a particular vector, or transduced cell type in a particular patient.

In determining the effective amount of the vector to be administered in the treatment or prophylaxis of conditions owing to diminished or aberrant expression of the angiogenesis regulatory proteins, the physician evaluates circulating plasma levels of the vector, vector toxicities, progression of the disease, and the production of anti-vector antibodies. In general, the dose equivalent of a naked nucleic acid from a vector is from about 1 μg to 100 μg for a typical 70 kilogram patient, and doses of vectors which include a retroviral particle are calculated to yield an equivalent amount of therapeutic nucleic acid.

For administration, compounds and transduced cells of the present invention can be administered at a rate determined by the LD-50 of the inhibitor, vector, or transduced cell type, and the side-effects of the inhibitor, vector or cell type at various concentrations, as applied to the mass and overall health of the patient. Administration can be accomplished via single or divided doses.

EXAMPLES

Using a functional assay described herein (see also Figure 1), angiogenesis regulatory proteins and nucleic acids have been identified and cloned from a green fluorescent protein (GFP) fusion cDNA retroviral library. The cDNAs can be in-frame, out of frame, sense, or antisense. Primary endothelial cells were transduced with retroviral

cDNA/GFP fusion libraries. Transduced cells were selected and assayed for alterations consistent with modulation of angiogenesis, *e.g.* downregulation of cell surface expression of $\alpha v \beta 3$ or downregulation of haptotaxis.

5 Example 1: Identification of plakoglobin angiogenesis regulatory protein.

Using the functional assay described above, expression of a plakoglobin-GFP fusion protein (*i.e.*, GFP- Δ N-plakoglobin) was found to decrease levels of the cell surface marker $\alpha v \beta 3$. (*See, e.g.*, Figures 2 and 3.) The plakoglobin functional hit was an N-terminal deletion, fused in frame to the GFP protein that contained armadillo repeats. (*See, e.g.*,
10 Figure 3). GFP- Δ N-Plakoglobin expression downregulated vitronectin receptors ($\alpha v \beta 3$ and $\alpha v \beta 5$) but not the fibronectin receptor ($\alpha 5 \beta 1$). (*See, e.g.*, Figure 4.)

The angiogenesis phenotype of GFP- Δ N-Plakoglobin was confirmed by co-culturing HUVECs on smooth muscle cells and using a tubule formation assay. Briefly, on day 1 a Collagen solution (Collagen type I solution, Sigma C8919) was diluted 1 to 10 with
15 PBS and used to coat each well of 24 well plate (250ul). Plates were incubated at 37°C for 4-5 hrs. Wells were then aspirated and allowed to dry overnight. On day 2, stock flask(s) of PASCs (Clonetics Pulmonary Artery SMCs CC-2581, fewer than 5 passages) were trypsinized to provide enough cells to plate 60,000 cells per well. Cells were cultured in Smooth muscle cell growth medium (Clonetics SmGM-2 bullet kit CC-3182) and stock
20 cultures were maintained according to Clonetics protocols.

PASCs were nearly confluent on day 3. Trypsinize Stock flask(s) of HUVECs were trypsinized to generate enough cells to plate 12,000 cells per well (trypsin, Clonetics ReagentPack CC-5034). The SmGM-2 medium was removed and HUVECS were plated onto the PASCs in EGM-2 (Endothelial cell growth medium, Clonetics EGM-2
25 bullet kit CC-3162) at 1ml per well.

Medium was exchanged every 2-3 days and tubule formation was assessed. Using the tubule formation assay, GFP- Δ N-Plakoglobin expression was found to inhibit branch formation. (Data not shown.)

Expression of GFP- Δ N-Plakoglobin downregulated endogenous β -catenin
30 levels, as well as expression of endogenous plakoglobin and VE-cadherin. (*See, e.g.*, Figure 5.) β -catenin was shown to be required to maintain $\alpha v \beta 3$ expression. (Data not shown.)

In addition, GFP- Δ N-Plakoglobin expression upregulated surface levels of the laminin receptor, $\alpha 6 \beta 4$. (*See, e.g.*, Figure 6.)

Example 2: Identification of HoxB2 angiogenesis regulatory protein.

Using the functional assay described above, expression of a HoxB2-GFP fusion protein (*i.e.*, Δ N-HoxB2) was found to decrease levels of the cell surface marker α v β 3. Cells transfected with the Δ N-HoxB2-GFP fusion protein construct exhibit lower α v β 3 expression levels than control cells. The HoxB2 functional screen hit is an N-terminal deletion that contains the HoxB2 homeodomain. (See, *e.g.*, Figure 7.)

Δ N-HoxB2 downregulated both α v and β 3 integrin subunit surface expression, as well as α v β 5 surface expression. (See, *e.g.*, Figure 8.) Δ N-HoxB2 also downregulated β 3 transcript expression. (Data not shown.) Δ N-HoxB2 inhibited proliferation in HUVECs, a primary cell line. (See, *e.g.*, Figure 9.) In addition, full length HoxB2 phenocopied Δ N-HoxB2 and downregulated surface expression of α v β 3. (See, *e.g.*, Figure 10.)

Cells expressing full length HoxB2 or Δ N-HoxB2 were isolated by cell sorting and assayed for tube formation using the co-culture assay described above. Both full length HoxB2 and Δ N-HoxB2 increased branch formation in the co-culture assay. (Data not shown.) α v β 3 expression was directly downregulated using β 3 siRNA. Downregulation of α v β 3 expression did not affect branch formation in the co-culture assay.

Example 3: Identification of SUSP-1 angiogenesis regulatory protein.

Using the functional assay described above, expression of a SUSP-1 GFP fusion protein (*i.e.*, GFP-SUSP-1) was found to decrease levels of the cell surface marker α v β 3. (See, *e.g.*, Figure 11.) Cells transfected with the GFP-SUSP-1 fusion protein construct exhibit lower α v β 3 expression levels than control cells. The SUSP-1 functional screen hit is an N-terminal fusion in the sense orientation and that has an additional encoded cDNA insert before the wild-type start codon. (See, *e.g.*, Figure 11.)

The GFP-SUSP-1 screening hit did not affect proliferation when expressed in HUVEC (human umbilical vein endothelial cells), PASMC (pulmonary artery smooth muscle cells), and NHDF (normal human dermal fibroblasts). (See, *e.g.*, Figure 12.) SUSP-1 mRNA was found to be expressed in a variety of cell lines. (See, *e.g.*, Figure 13.)

GFP-SUSP-1 expression inhibited tube formation in the co-culture assay described above. (Data not shown.) Two SUSP-1 siRNAs were synthesized and found to inhibit SUSP-1 expression. (See, *e.g.*, Figure 14.) The SUSP-1 siRNAs also inhibited tube formation in the co-culture assay. (Data not shown.)

Example 4: Identification of $\Delta 5$ FADS angiogenesis regulatory protein.

Using the functional assay described above, expression of a $\Delta 5$ FADS antisense nucleic acid (*i.e.*, GFP- $\Delta 5$ FADS) was found to decrease levels of the cell surface marker $\alpha v \beta 3$. (*See, e.g.*, Figure 30.) Cells transfected with the GFP- $\Delta 5$ FADS construct exhibit lower $\alpha v \beta 3$ expression levels than control cells. The $\Delta 5$ FADS functional screen hit is a 300bp antisense nucleic acid. (*See, e.g.*, Figure 30.)

The GFP- $\Delta 5$ FADS screening hit did not affect proliferation when expressed in HUVEC (human umbilical vein endothelial cells), PASMC (pulmonary artery smooth muscle cells), and NHDF (normal human dermal fibroblasts). (*See, e.g.*, Figure 31.) $\Delta 5$ FADS mRNA was found to be expressed in a variety of cell lines, and appeared to be highly expressed in endothelial cells, hepatocytes, and mammary epithelial cells. (Data not shown.)

Antisense $\Delta 5$ FADS nucleic acids inhibited tube formation in the co-culture assay described above. (Data not shown.) Two $\Delta 5$ FADS siRNAs were synthesized and found to inhibit $\Delta 5$ FADS expression. (*See, e.g.*, Figure 32.) The $\Delta 5$ FADS siRNAs inhibited tube formation in the co-culture assay. (Data not shown.) The $\Delta 5$ FADS siRNAs inhibited vitronectin haptotaxis and reduced SDF-1 induced chemotaxis in Jurkat cells. (*See, e.g.*, Figures 33-34.)

Example 5: Identification of $\Delta 6$ FADS angiogenesis regulatory protein.

Using the functional assay described above, expression of a KIAA1583 antisense nucleic acid (*i.e.*, GFP-KIAA1583) was found to decrease levels of the cell surface marker $\alpha v \beta 3$. (Data not shown.) KIAA1583 and $\Delta 6$ FADS genomic sequences are both located on chromosome 11q12, and transcripts of the two genes are spiced together. (*See, e.g.*, Figure 35.) $\Delta 6$ FADS mRNA is reduced in cells expressing GFP-KIAA1583, the antisense screening hit. (*See, e.g.*, Figure 36.) $\Delta 6$ FADS also interacts with C1 phosphatase, another $\alpha v \beta 3$ screening hit. (Data not shown.) $\Delta 6$ FADS is highly expressed in endothelial cells, hepatocytes and skeletal muscle cells. (Data not shown.)

$\Delta 6$ FADS siRNAs were synthesized and found to inhibit $\Delta 5$ FADS expression. (*See, e.g.*, Figure 37.) The $\Delta 6$ FADS siRNAs inhibited tube formation in the co-culture assay described above. (Data not shown.) Expression of the $\Delta 6$ FADS siRNAs also downregulated $\alpha v \beta 3$ surface expression levels. (*See, e.g.*, Figure 37.)

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

5 Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to one of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

WHAT IS CLAIMED IS:

- 1 1. A method for identifying a compound that modulates angiogenesis,
2 the method comprising the steps of:
- 3 (i) contacting the compound with a nucleic acid, or a polypeptide or a
4 fragment thereof encoded by a nucleic acid, wherein the nucleic acid hybridizes under
5 stringent conditions to a second nucleic acid comprising a nucleotide sequence selected
6 from the group consisting of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID
7 NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID
8 NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID
9 NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID
10 NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID
11 NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID
12 NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID
13 NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID
14 NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID
15 NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID
16 NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID
17 NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID
18 NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ
19 ID NO:523 ; and
- 20 (ii) determining the functional effect of the compound upon the nucleic
21 acid or polypeptide.
- 1 2. The method of claim 1, wherein the functional effect is determined
2 *in vitro*.
- 1 3. The method of claim 2, wherein the functional effect is a physical
2 effect.
- 1 4. The method of claim 2, wherein the functional effect is determined
2 by measuring ligand or substrate binding to the polypeptide.
- 1 5. The method of claim 2, wherein the functional effect is a chemical
2 effect.

1 6. The method of claim 2, wherein the functional effect is determined
2 by measuring an enzymatic activity.

1 7. The method of claim 1, wherein the polypeptide is expressed in a
2 eukaryotic host cell.

1 8. The method of claim 7, wherein the functional effect is a physical
2 effect.

1 9. The method of claim 8, wherein the functional effect is determined
2 by measuring ligand or substrate binding to the polypeptide.

1 10. The method of claim 7, wherein the functional effect is a chemical
2 or phenotypic effect.

1 11. The method of claim 10, wherein the functional effect is
2 determined by measuring an enzymatic activity.

1 12. The method of claim 7, wherein the host cell is an endothelial cell.

1 13. The method of claim 12, wherein the functional effect is
2 determined by measuring $\alpha v\beta 3$ expression.

1 14. The method of claim 12, wherein the functional effect is
2 determined by measuring a member selected from $\alpha v\beta 3$ expression, haptotaxis, and
3 chemotaxis.

1 15. The method of claim 14, wherein the functional effect is
2 determined by measuring $\alpha v\beta 3$ expression.

1 16. The method of claim 1, wherein modulation is inhibition of
2 angiogenesis.

1 17. The method of claim 1 wherein the polypeptide is recombinant.

1 18. The method of claim 1, wherein the nucleic acid comprises a
2 nucleotide sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:32,
3 SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ

4 ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID
5 NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID
6 NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID
7 NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID
8 NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID
9 NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID
10 NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID
11 NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID
12 NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID
13 NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID
14 NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID
15 NO:521, and SEQ ID NO:523.

1 19. The method of claim 1, wherein the polypeptide comprises a
2 sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:33, SEQ ID
3 NO:44, SEQ ID NO:58, SEQ ID NO:64, SEQ ID NO:69, SEQ ID NO:71, SEQ ID
4 NO:77, SEQ ID NO:82, SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:121, SEQ ID
5 NO:129, SEQ ID NO:140, SEQ ID NO:154, SEQ ID NO:164, SEQ ID NO:170, SEQ ID
6 NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:203, SEQ ID
7 NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, SEQ ID
8 NO:331, SEQ ID NO:341, SEQ ID NO:352, SEQ ID NO:366, SEQ ID NO:378, SEQ ID
9 NO:385, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:420, SEQ ID NO:429, SEQ ID
10 NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:457, SEQ ID NO:463, SEQ ID
11 NO:482, SEQ ID NO:485, SEQ ID NO:494, SEQ ID NO:497, SEQ ID NO:499, SEQ ID
12 NO:520, SEQ ID NO:522, and SEQ ID NO:524.

1 20. The method of claim 1, wherein the compound is an antibody.

1 21. The method of claim 1, wherein the compound is an antisense
2 molecule.

1 22. The method of claim 1, wherein the compound is a small organic
2 molecule.

1 23. The method of claim 1, wherein the compound is a peptide.

1 24. A method for identifying a compound that modulates angiogenesis,
2 the method comprising the steps of:

3 (i) contacting the compound with a nucleic acid, or a polypeptide or a
4 fragment thereof encoded by a nucleic acid, wherein the nucleic acid hybridizes under
5 stringent conditions to a second nucleic acid comprising a nucleotide sequence selected
6 from the group consisting of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID
7 NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID
8 NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID
9 NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID
10 NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID
11 NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID
12 NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID
13 NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID
14 NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID
15 NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID
16 NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439 SEQ ID
17 NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID
18 NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ
19 ID NO:523;

20 (ii) determining the functional effect of the compound upon the nucleic
21 acid or polypeptide; and

22 (iii) expressing the nucleic acid or polypeptide in a cell, contacting the
23 nucleic acid or polypeptide with the compound, and determining the phenotypic or
24 chemical effect upon the cell.

1 25. A method of modulating angiogenesis in a subject, the method
2 comprising the step of administering to the subject a therapeutically effective amount of a
3 compound identified using the method of claim 1.

1 26. The method of claim 25, wherein the subject is a human.

1 27. The method of claim 25, wherein the compound is an antibody.

1 28. The method of claim 25, wherein the compound is an antisense
2 molecule.

1 29. The method of claim 25, wherein the compound is a small organic
2 molecule.

1 30. The method of claim 25, wherein the compound is a peptide.

1 31. The method of claim 25, wherein the compound is an RNAi
2 molecule.

1 32. The method of claim 25, wherein the compound inhibits
2 angiogenesis

1 33. A method of modulating angiogenesis in a subject, the method
2 comprising the step of administering to the subject a therapeutically effective amount of a
3 polypeptide, the polypeptide encoded by a nucleic acid that hybridizes under stringent
4 conditions to a second nucleic acid comprising a nucleotide sequence selected from the
5 group consisting of SEQ ID NO:63, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86,
6 SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:165, SEQ ID NO:183,
7 SEQ ID NO:202, SEQ ID NO:218, SEQ ID NO:232, SEQ ID NO:274, SEQ ID NO:285,
8 SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320,
9 SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:340, SEQ ID NO:377, SEQ ID NO:384,
10 SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:439 SEQ ID NO:445, SEQ ID NO:456,
11 SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, and SEQ ID
12 NO:498.

1 34. A method of modulating angiogenesis in a subject, the method
2 comprising the step of administering to the subject a therapeutically effective amount of a
3 nucleic acid that hybridizes under stringent conditions to a second nucleic acid
4 comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:3,
5 SEQ ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ
6 ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID
7 NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID
8 NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID
9 NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID
10 NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID
11 NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID

12 NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID
13 NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID
14 NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID
15 NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID
16 NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID
17 NO:519, SEQ ID NO:521, and SEQ ID NO:523.

1 35. An isolated nucleic acid, wherein the nucleic acid hybridizes
2 under stringent conditions to a polynucleotide comprising a nucleotide sequence selected
3 from the group consisting of SEQ ID NO:165, SEQ ID NO:202, SEQ ID NO:210, SEQ
4 ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ
5 ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ
6 ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ
7 ID:329, and SEQ ID:330.

1 36. The isolated nucleic acid of claim 35, wherein the nucleic acid
2 comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:165,
3 SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232,
4 SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297,
5 SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320,
6 SEQ ID NO:323, SEQ ID NO:324, SEQ ID:329, and SEQ ID:330.

1 37. An isolated polypeptide comprising an amino acid sequence
2 selected from the group consisting of SEQ ID NO:287, SEQ ID NO:298, SEQ ID
3 NO:309, SEQ ID NO:319, SEQ ID NO:325, and SEQ ID NO:331.

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Anti-Angiogenesis Screening: Target Angiogenic-Endothelial Cell Functions

WO 2004/019893

10/525573

PCT/US2003/027523

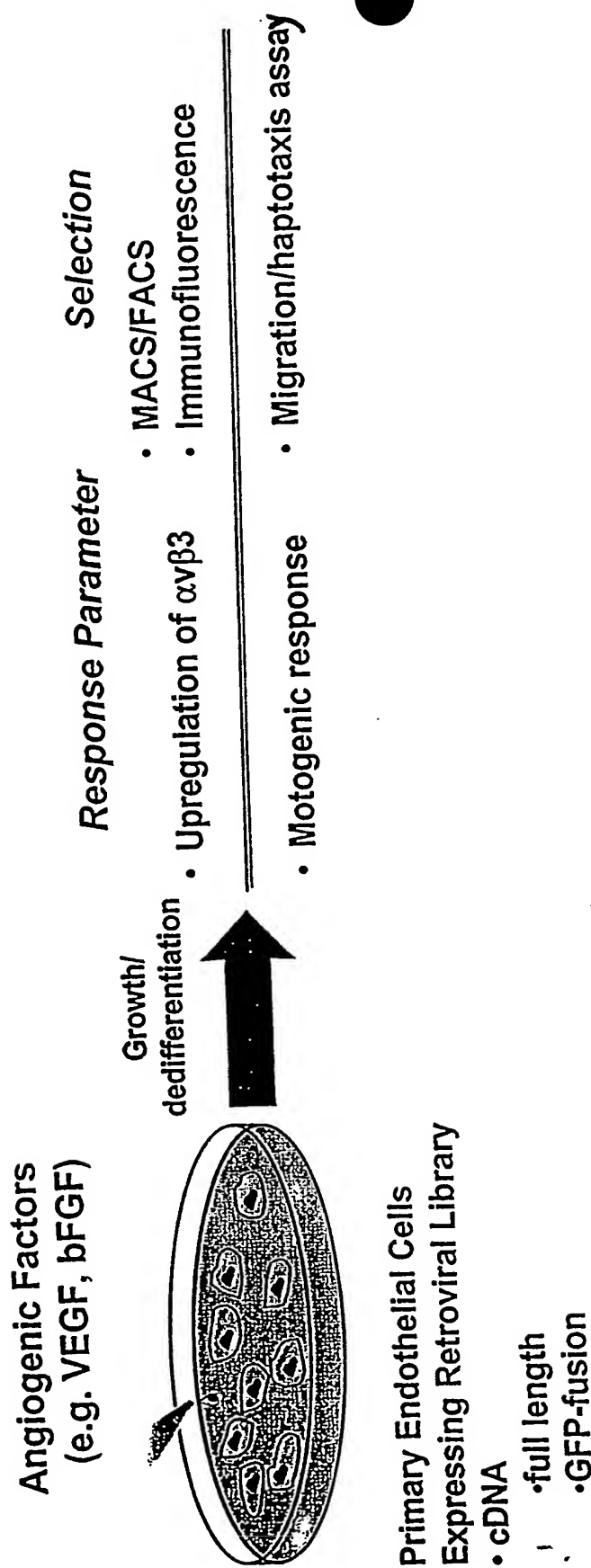
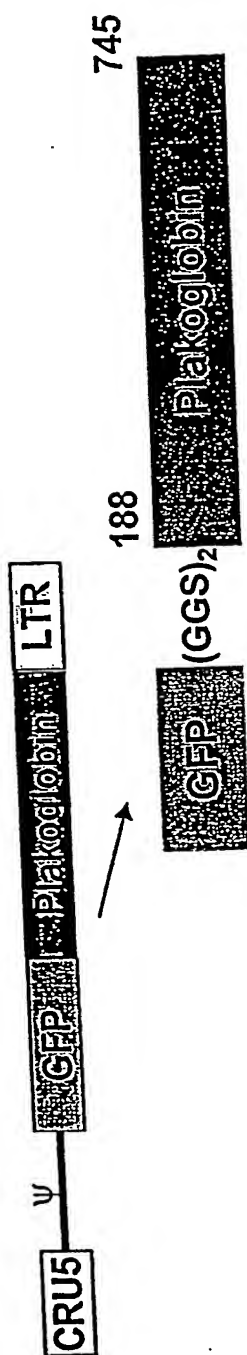


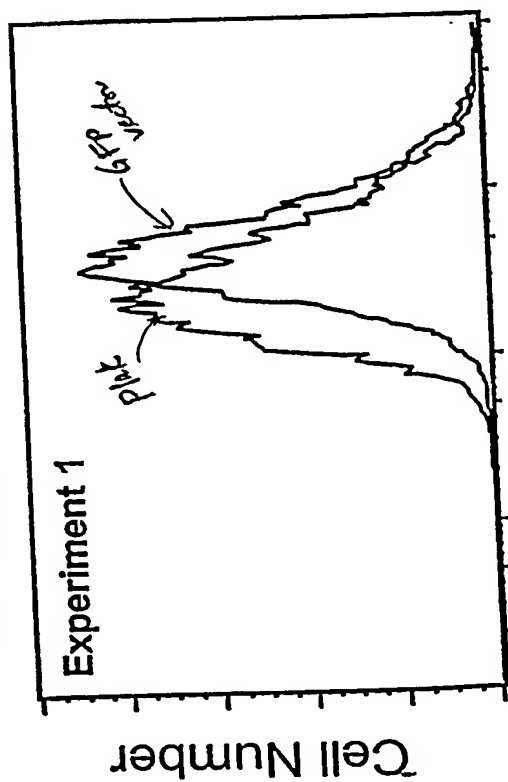
FIG. 1

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Clone 19B5 Encodes a GFP-Plakoglobin Fusion Protein



— GFP-Plakoglobin
— GFP-vector



$\alpha v \beta 3$

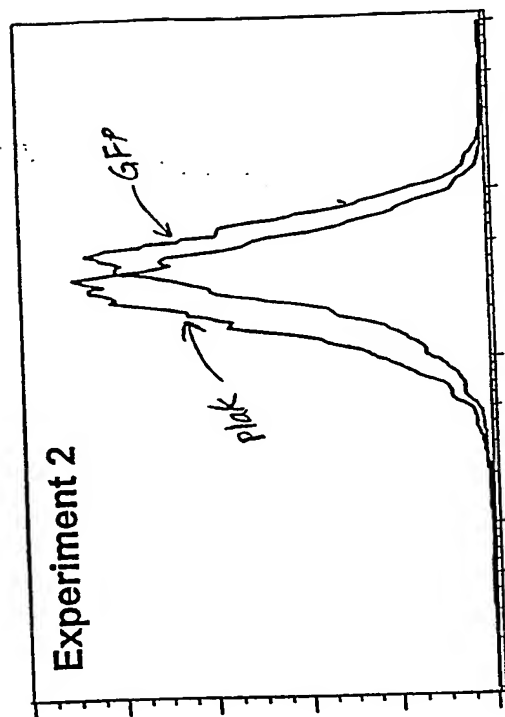


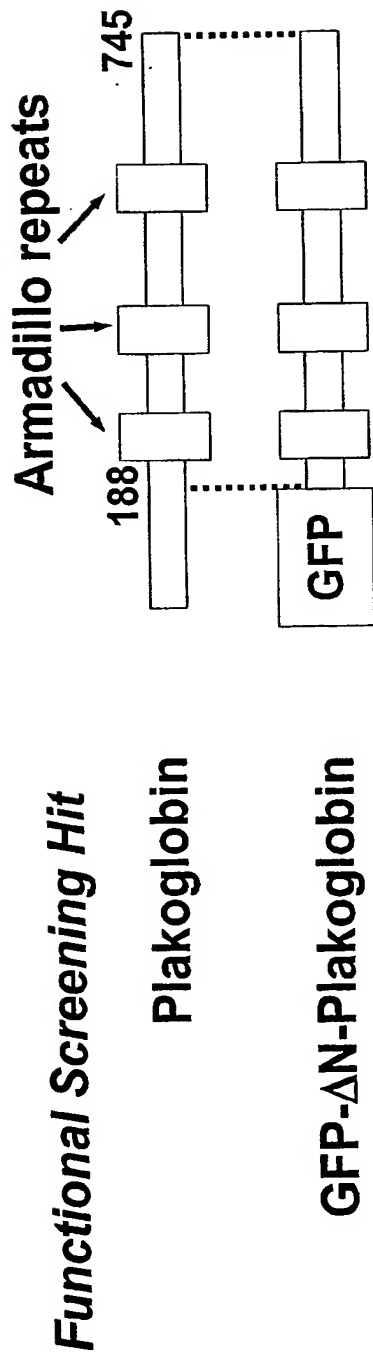
FIG. 2

24010001 23 FEB 2005

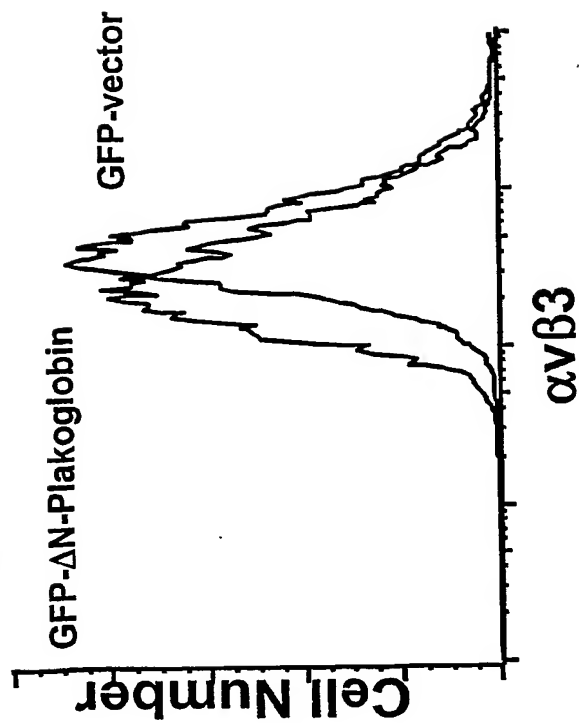
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GFP-ΔN-Plakoglobin Expression in Endothelial Cells Downregulates α v β 3 Surface Levels

Figure 3



FACS Analysis



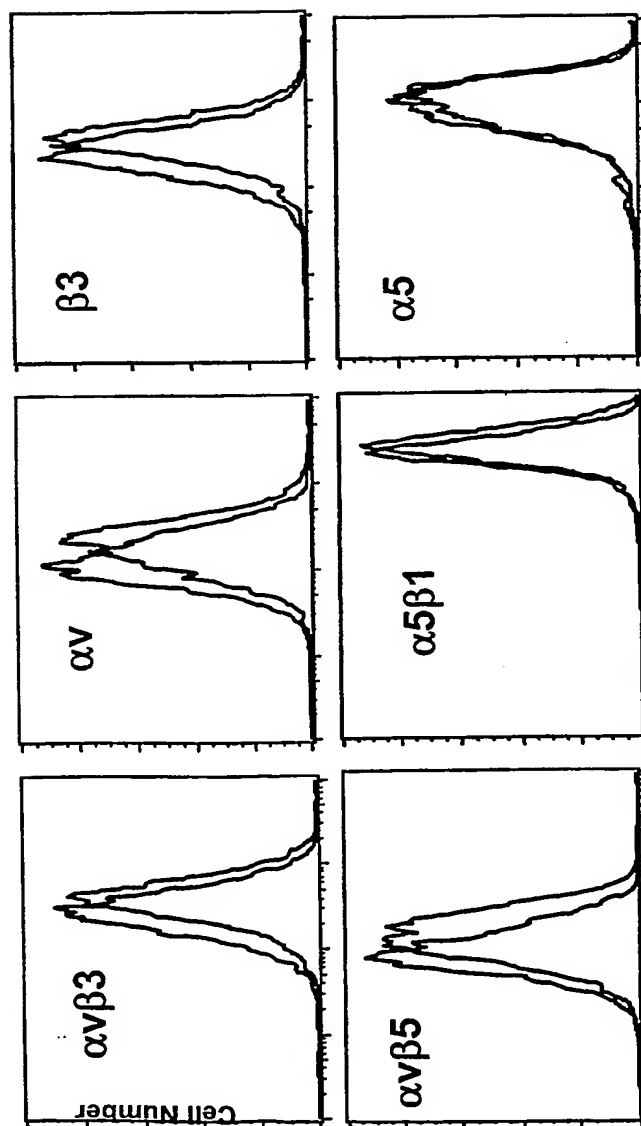
DT15 Rec [REDACTED] 23 FEB 2005

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Figure 4

GFP- Δ N-Plako Expression Downregulates Vitronectin Receptors (α v β 3 and α v β 5) But Not the Fibronectin Receptor (α 5 β 1)

FACS Analysis

GFP- Δ N-Plako

GFP

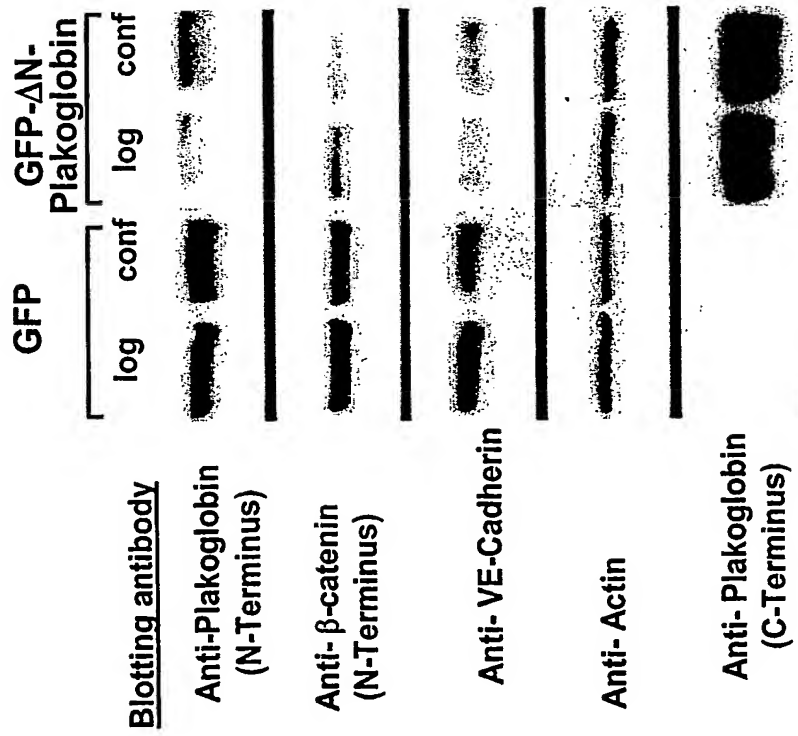
DT15 Rec'd USPTO 23 FEB 2005

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Expression of GFP-ΔN-Plakoglobin Downregulates Endogenous Catenin Levels

Figure 5

Western blot

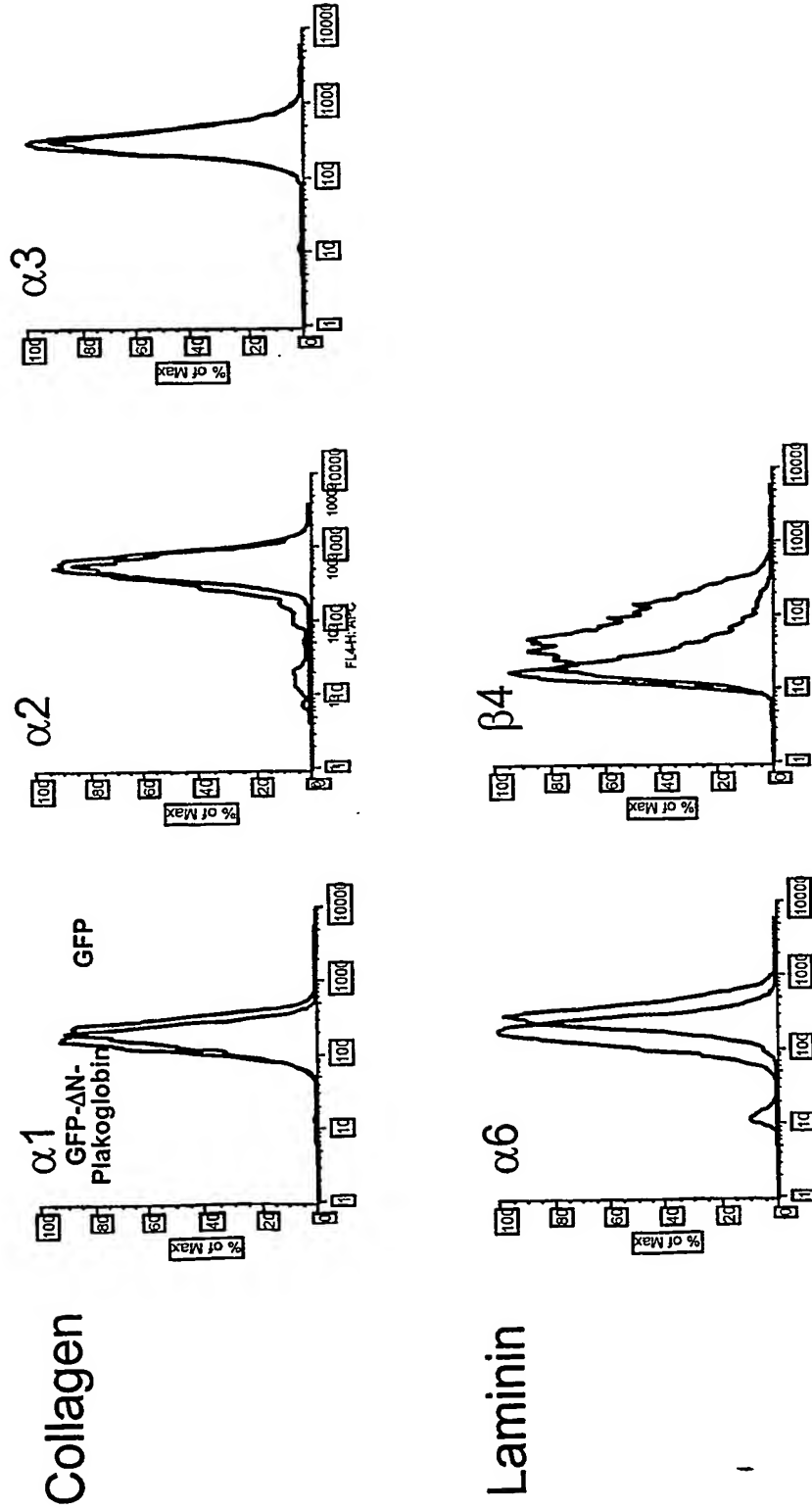


(Transduced HUVEC)

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GFP-ΔN-Plakoglobin Expression Upregulates Surface Levels of the Laminin Receptor, α6β4

Figure 6



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10/525573

αvβ3 Screen Clone Encodes an N-terminally Truncated Splice Variant of HoxB2

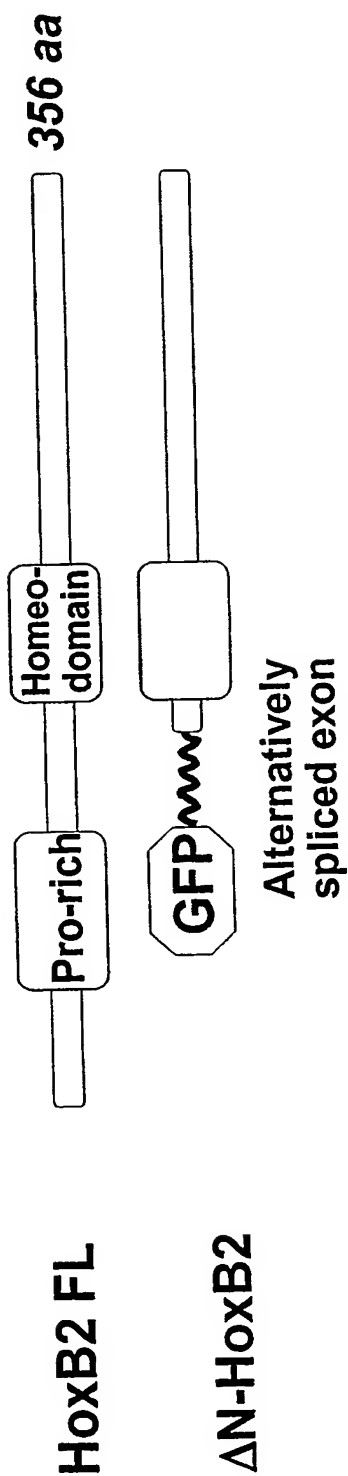
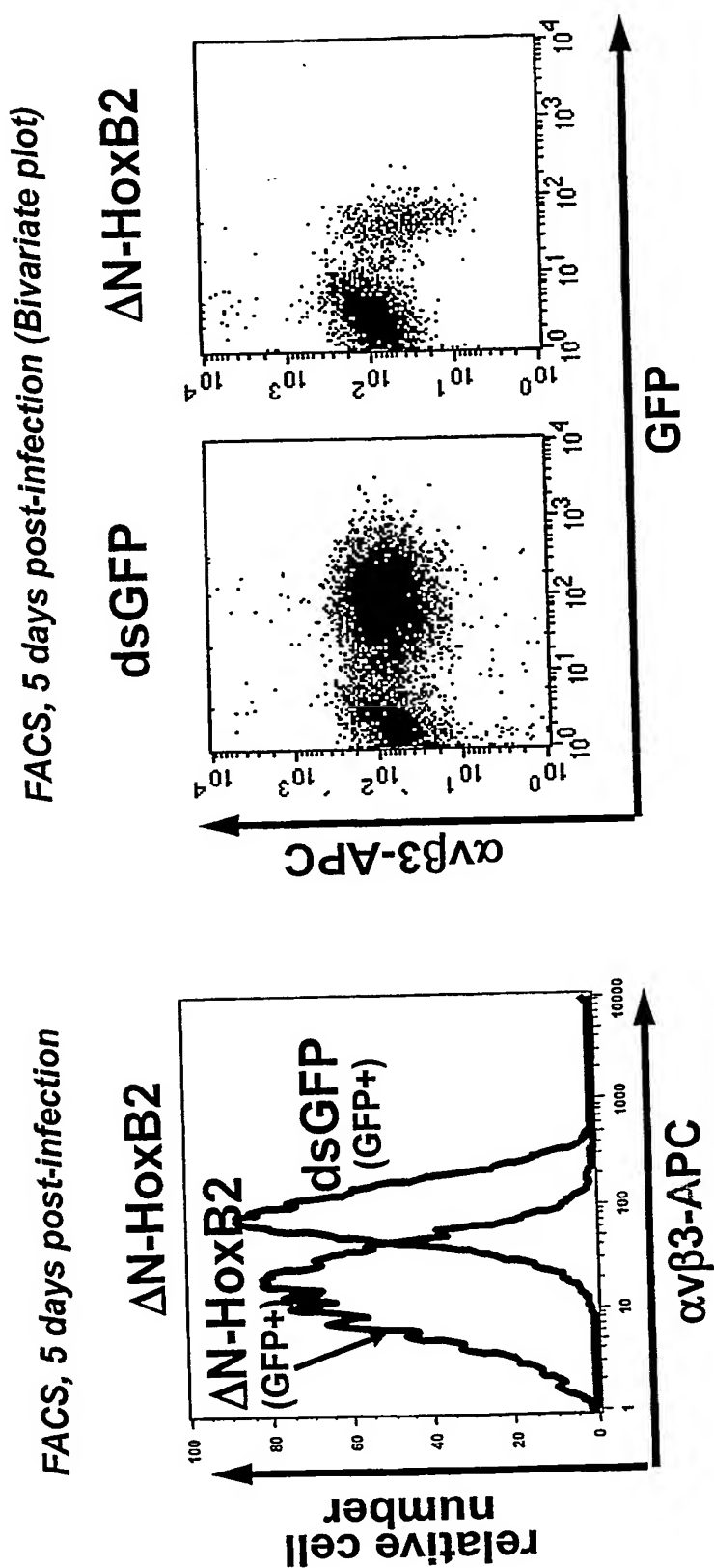


Figure 7



23 FEB 2005

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Δ N-HoxB2 Downregulates Both α v and β 3 Integrin Subunit Surface Expression

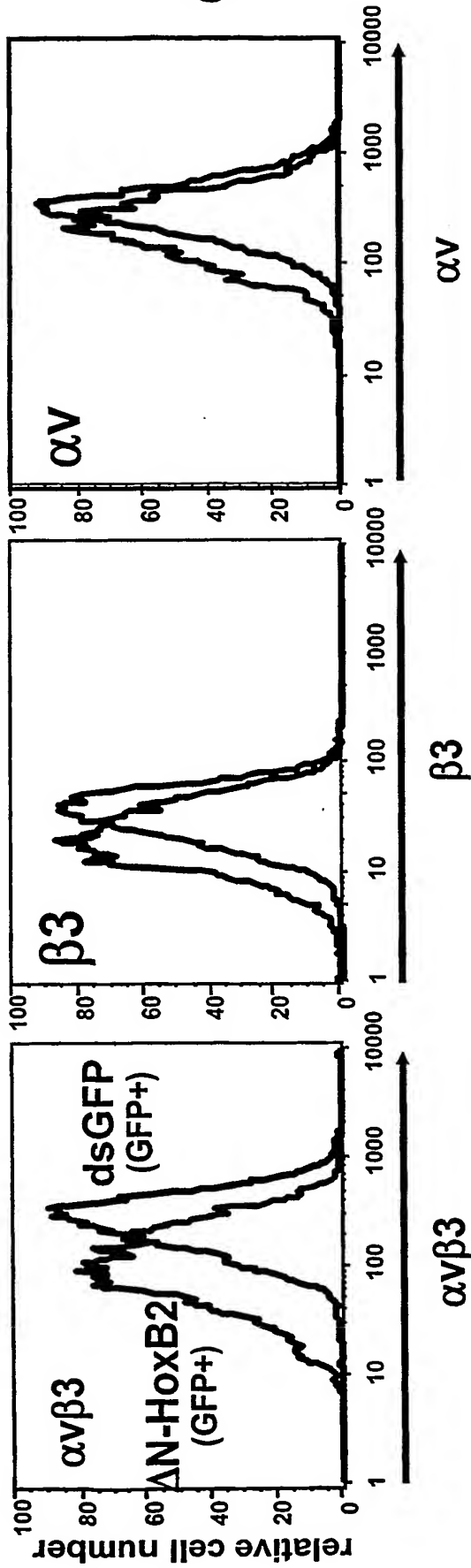
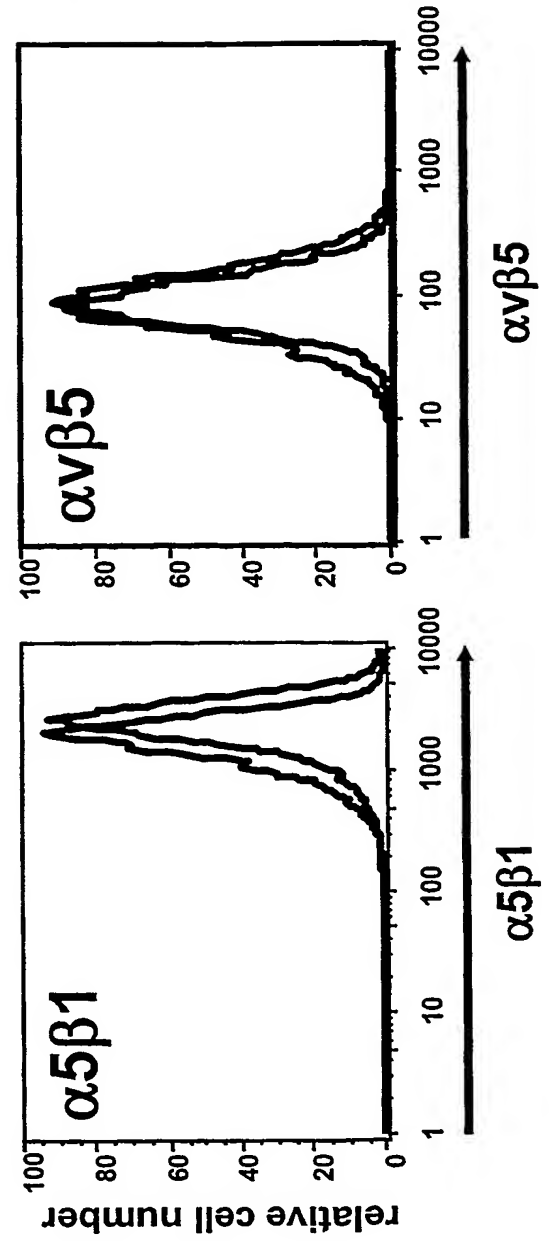


Figure 8

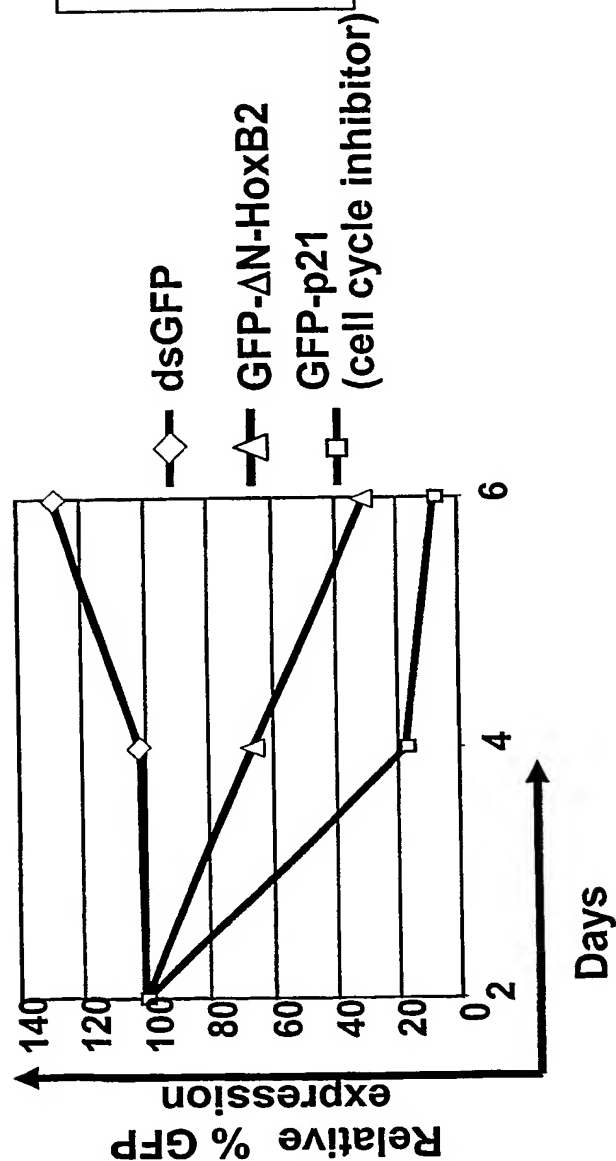
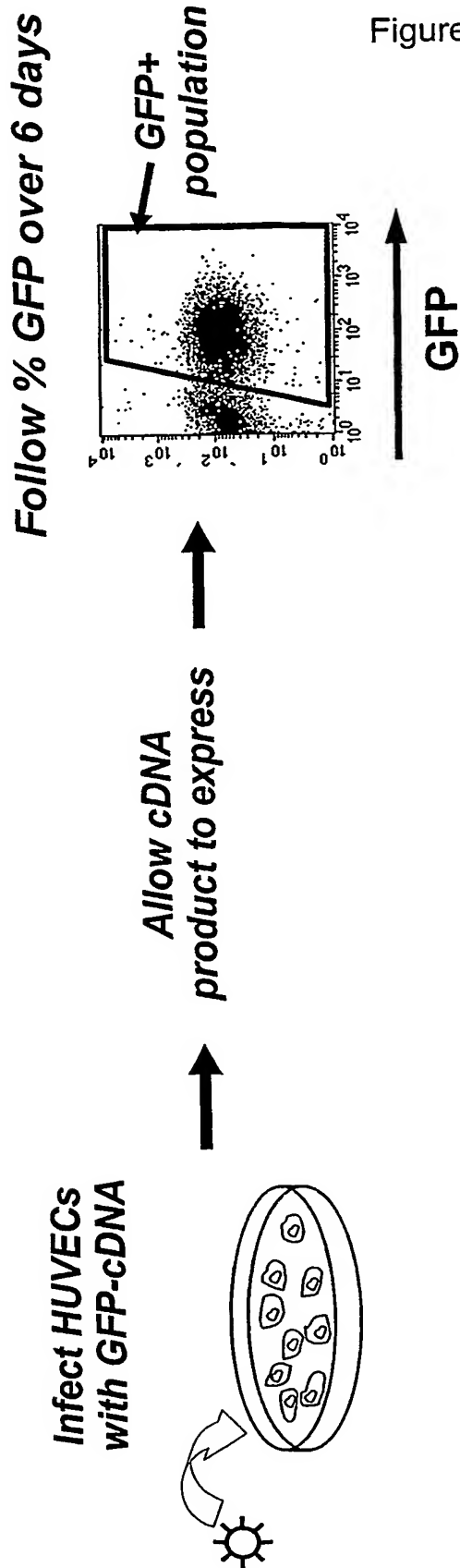
Δ N-HoxB2 also Downregulates α 5 β 1 Surface Expression



DT15 Rep DTG 23 FEB 2005

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Δ N-HoxB2 Inhibits Proliferation in HUVECs



% GFP+ Δ N-HoxB2-expressing cells decreases over time compared to dsGFP vector, indicative of decreased proliferation (or increased apoptosis)

DT15 Rec'd PCT/PTO 23 FEB 2005

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Full Length HoxB2 Phenocopies Δ N-HoxB2 in the Downregulation of α v β 3

WO 2004/019893

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PCT/US2003/027523

FACS, 5 days post-infection

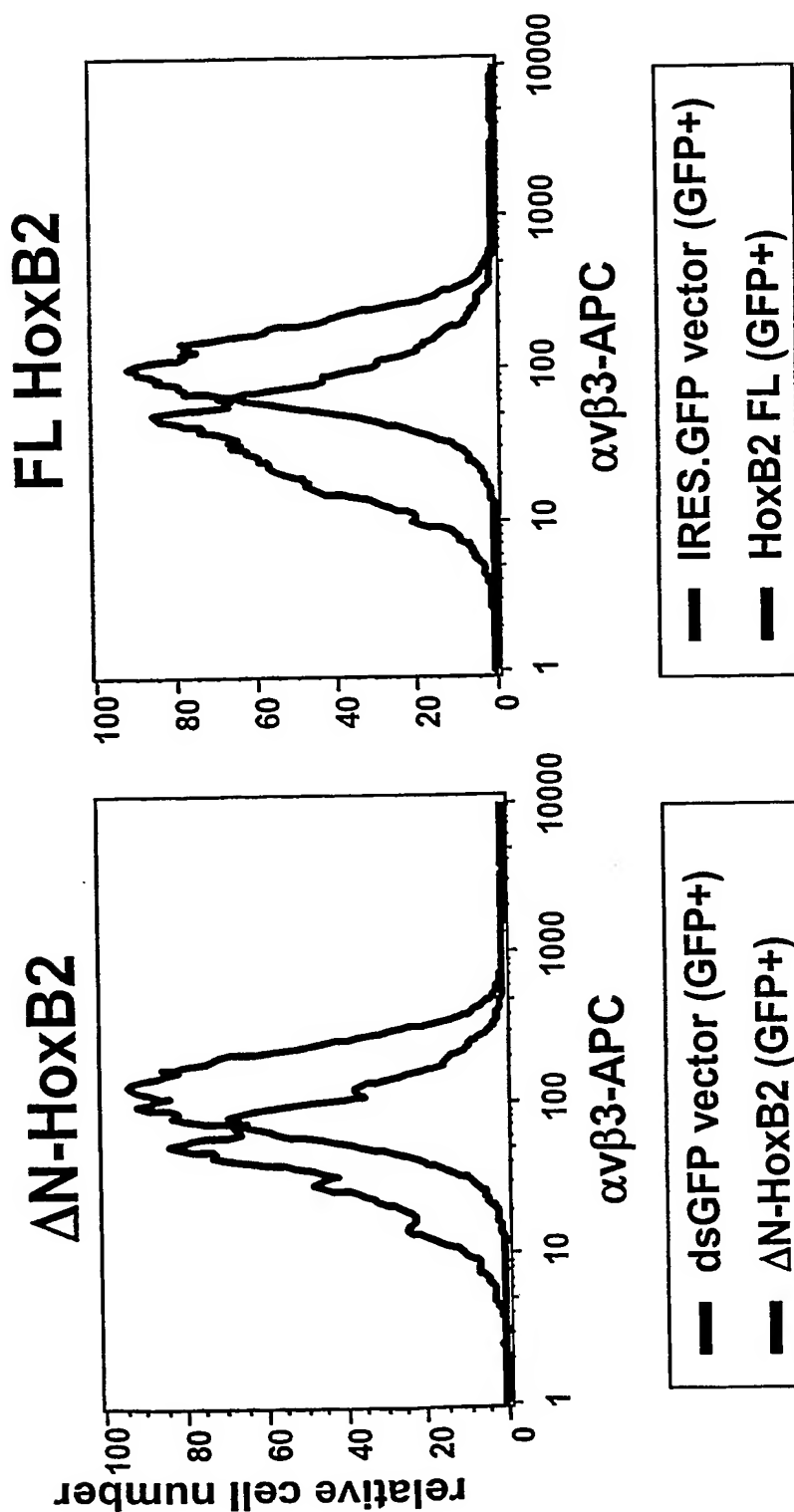


Figure 10

23 SEP 2008

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SUSP-1

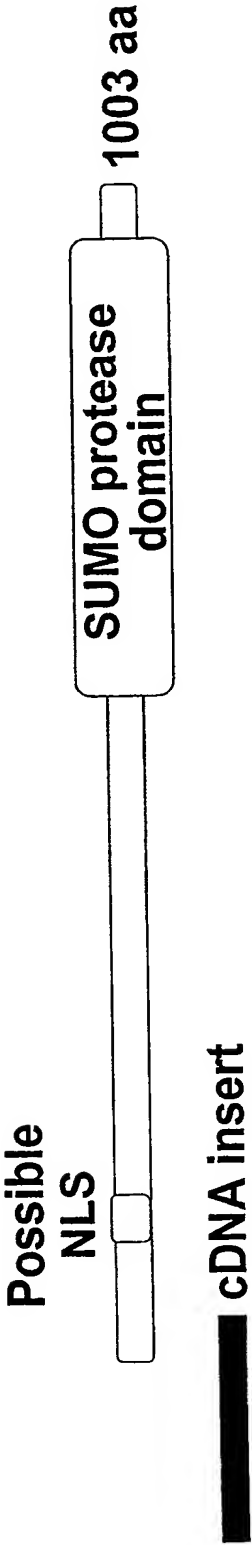
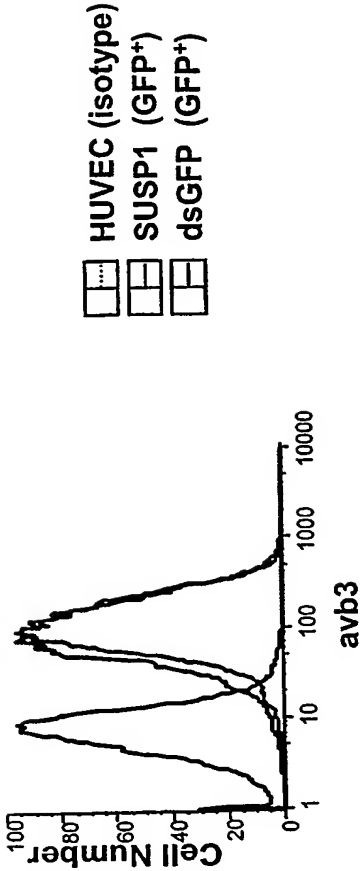


Figure 11



Sense orientation, N-terminal fusion

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10/525575

GFP-SUSP-1 Screening Hit Does Not Affect Proliferation

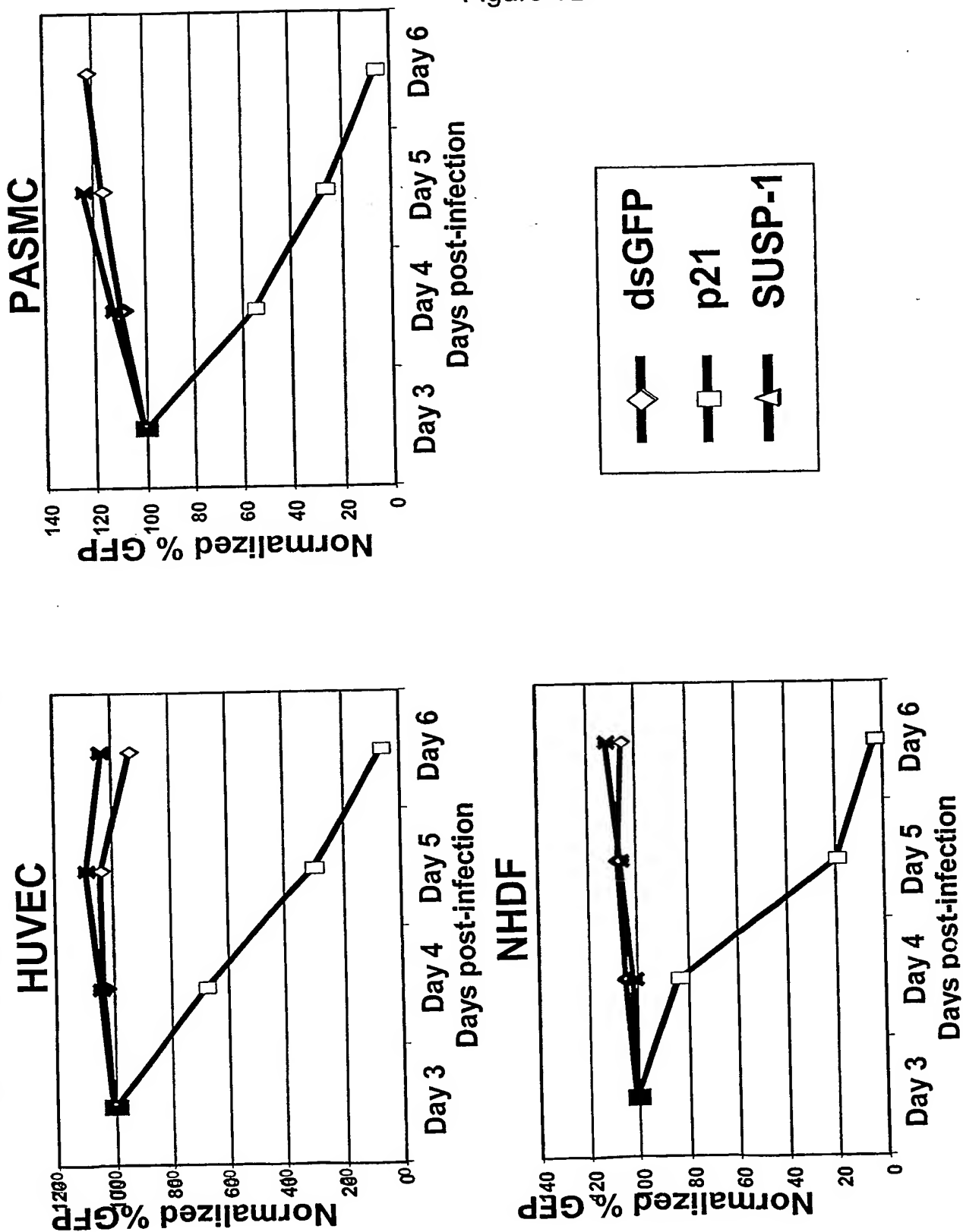


Figure 12

0115 Rec 07/PTO 2 3 FEB 2005

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Expression Analysis of SUSP-1

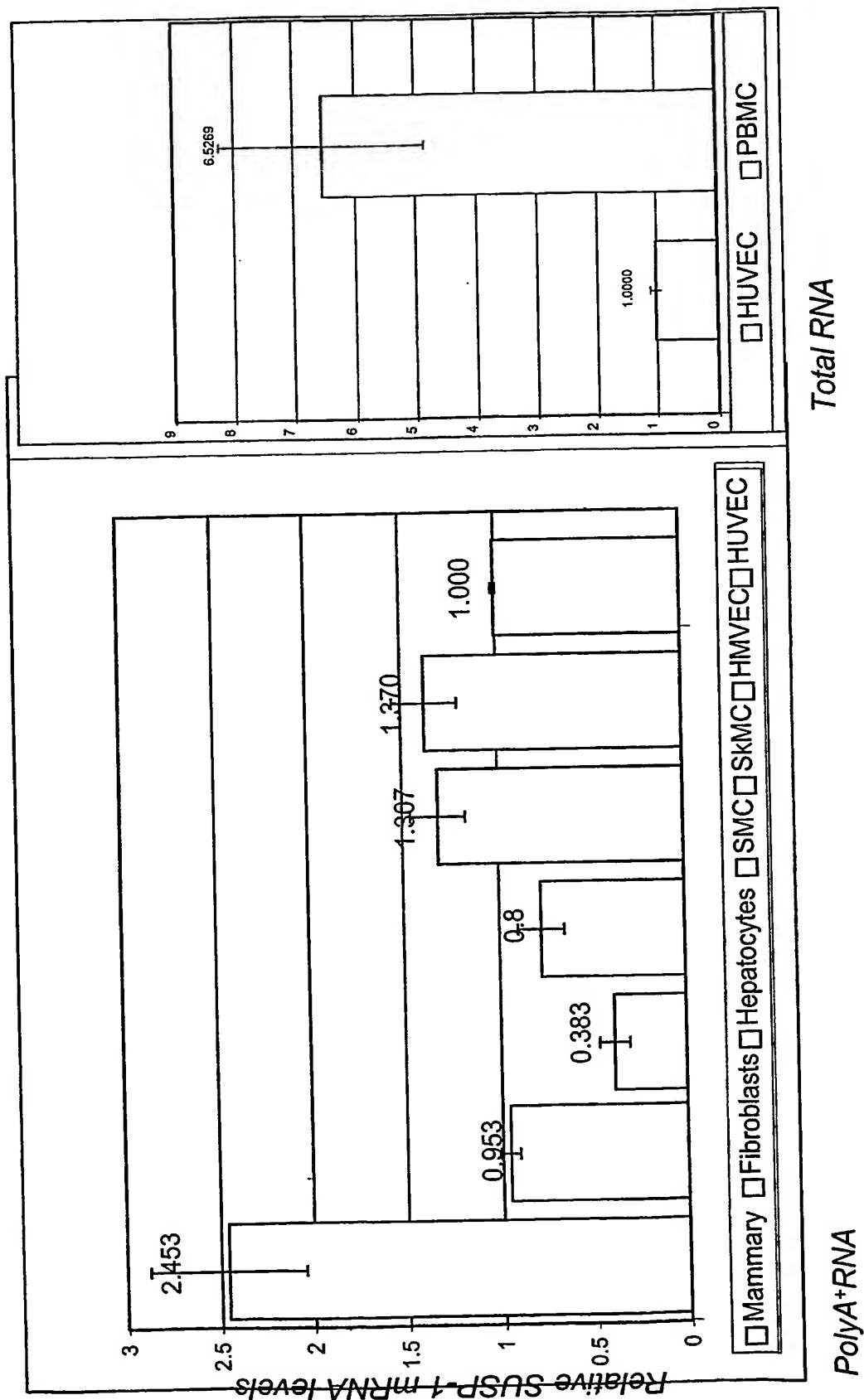


Figure 13

DT15 Rec/ST/PTO 23 FEB 2005

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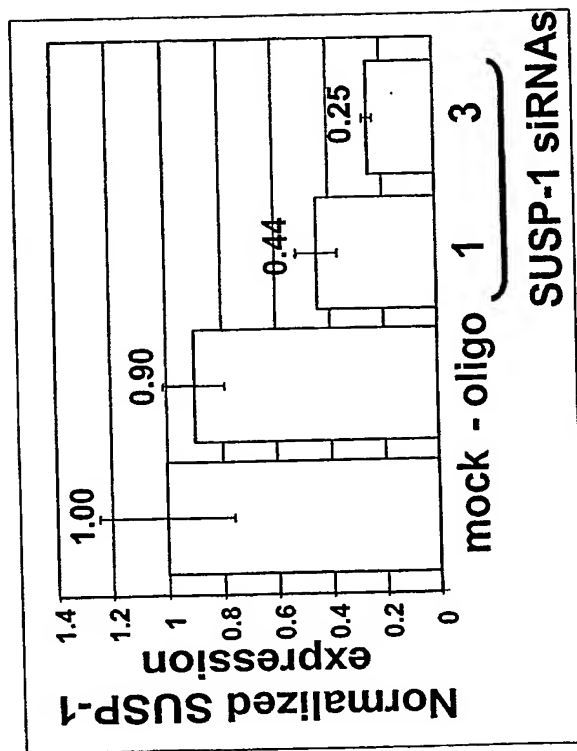
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Figure 14

SUSP-1 siRNA inhibits SUSP-1 expression

Taqman



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Figure 15

A new sequence determination for the ABC transporter gene, SEQ ID NO:2.

ABC transporter>

GGACGCGCCTGGTGCCCCGGGGAGGGGCGCCACCGGGGAGGAGGAGGAG
GAGAAGGTGGAGAGGAAGAGACGCCCCCTCTGCCCCGAGACCTCTCAAGGC
CCTGACCTCAGGGGCCAGGGCACTGACAGGACAGGAGAGCAAGTTCTCTC
CACTTGGGCTGCCCCAAGAGGCCGCGACCCCTGGAGGGCCCTGAGCCCACC
GCACCAGGGGCCCCAGCACCACCCCGGGGGCCTAAAGCGACAGTCTCAGG
GGCCATCGCAAGGTTTCCAGTTGCCTAGACAACAGGCCCAGGGTCAGAGC
AACAAATCCTTCCAGCCACCTGCCTCAACTGCTGCCCCAGGCACCAGCCCC
AGTCCCTACGCGGCAGCCAGCCAGGTGACATGCCGGTGCTCTCCAGGCC
CCGGCCCTGGCGGGGGAACACGCTGAAGCGCACGGCCGTGCTCCTGGCCC
TCGCGGCCTATGGAGCCACAAAGTCTACCCCTTGGTGCGCCAGTGCTG
GCCCCGGCCAGGGGTCTTCAGGCGCCCGCGGGGAGCCACGCAGGAGGC
CTCCGGGGTTCGCGCGGCCAAAGCTGGCATGAACCGGGTATTCTTGCCAGC
GGCTCCTGTGGCTCCTGCGGCTGCTGTTCCCCCGGGTCTGTGCCGGGAG
ACGGGGCTGCTGGCCCTGCACTCGGCCCGCTTGGTGAGCCGCACCTTCCT
GTGGGTGTATGTGGCCCGCCTGGACGGAAGGCTGGCCCGCTGCATCGTCC
GCAAGGACCCGCGGGCTTTTGGCTGGCAGCTGCTGCAGTGGCTCCTCATC
GCCCTCCCTGTACTCTCGTCAACAGTGCCATCCGTTACCTGGAGGGCCA
ACTGGCCCTGTCTGTTCCGCGAGCCGTCTGGTGGCCACGCCTACCGCCTCT
ACTTCTCCAGCAGACCTACTACCGGGTCAGCAACATGGACGGGCGGCTT
CGCAACCCTGACCAGTCTCTGACGGAGGACGTGGTGGCCTTTGCGGCCTC
TGTGGCCACCTCTACTCAACCTGACCAAGCCACTCCTGGACGTGGCTG
TGACTTCTACACCCTGCTTCGGGCGGCCCGCTCCCGTGGAGCCGGCACA
GCCTGGCCCTCGGCCATCGCCGGCCTCGTGGTGTTCCTACGGCCAACGT
GCTGCGGGCCTTCTCGCCCAAGTTCGGGGAGCTGGTGGCAGAGGAGGCGC
GGCGGAAGGGGGAGCTGCGCTACATGCACTCGCGTGTGGTGGCCAACCTCG
GAGGAGATCGCCTTCTATGGGGGCCATGAGGTGGAGCTGGCCCTGCTACA
GCGCTCCTACAGGACCTGGCCTCGCAGATCAACCTCATCCTTCTGGAAC
GCCTGTGGTATGTTATGCTGGAGCAGTTCCTCATGAAGTATGTGTGGAGC
GCCTCGGGCCTGCTCATGGTGGCTGTCCCATCATCACTGCCACTGGCTA
CTCAGAGTCAGATGCAAGGCCGTGAAGAAGGCAGCCTTGGAAAAGAAGG
AGGAGGAGCTGGTGAGCGAGCGCACAGAAGCCTTCACTATTGCCCGCAAC
CTCCTGACAGCGCTGCAAGATGCCATTGAGCGGATCATGTCTGTGTAACA
GGAGGTGACGGAGCTGGCTGGCTACACAGCCCGGGTGACAGAGATGTTCC
AGGTATTGGAAGATGTTACGCGCTGTCACTTCAAGAGGCCAGGGAGCTA
GAGGACGCTCAGGCGGGGTCTGGGACCATAGGCCGTGCTGGTGTCCGTGT
GGAGGGCCCCCTGAAGATCCGAGGCCAGGTGGTGGATGTGGAACAGGGGA
TCATCTGCGAGAACATCCCCATCGTCACGCCCTCAGGAGAGGTGGTGGT
GCCAGCCTCAACATCAGGGTGGAGGAAGGCATGCATCTGCTCATCACAGG
CCCCAATGGCTGCGGCAAGAGCTCCCTGTTCGGGATCCTGGGTGGGCTCT
GGCCACGTACGGTGGTGTGCTCTACAAGCCCCCAGCCAGCATGTTT
TACATCCCGCAGAGGCCCTACATGTCTGTGGGCTCCCTGCGTGACCAGGT
GATCTACCCGGACTCAGTGGAGGACATGCAAAGGAAGGGCTACTCGGAGC
AGGACCTGGAAGCCATCCTGGACGTCGTGCACCTGCACCACATCCTGCAG
CGGGAGGGAGGTTGGGAGGCTATGTGTGACTGGAAGGACGTCCTGTCTGGG
TGGCGAGAAGCAGAGAATCGGCATGGCCCGCATGTTCTACCACAGGCCCCA
AGTACGCCCTCCTGGATGAATGCACCAGCGCCGTGAGCATCGACGTGGAA
GGCAAGATCTTCCAGGCGGCCAAGGACGCGGGCATTGCCCTGCTCTCCAT
CACCCACCGGCCCTCCCTGTGGAAATACCACACACACTTGCTACAGTTTCG
ATGGGGAGGGCGGCTGGAAGTTCGAGAAGCTGGACTCAGCTGCCCGCCTG
AGCCTGACGGAGGAGAAGCAGCGGCTGGAGCAGCAGCTGGCGGGCATTCC
CAAGATGCAGCGGCGCCTCCAGGAGCTCTGCCAGATCCTGGGCGAGGCCG

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50/525573

TGGCCCCAGCGCATGTGCCGGCACCTAGCCCGCAAGGCCCTGGTGGCCTC
CAGGGTGCCCTCCACCTGACACAACCGTCCCCGGCCCCCTGCCCCGCCCCCA
AGCTCGGATCACATGAAGGAGACAGCAGCACCCACCCATGCACGCACCCC
GCCCCTGCAATGCCCTGGCCCCCTCCTCCTAGAAAACCCCTCCCGCCCTCGGG
AAAGTAGATGTGGAGGGTGGCGCCCTGCGTAACCCCTCGCCCTGTCCCTCC
CACTCCCTGGGGGCGCTGTTCACAGTGACTGGGCCCTGTCCAGGGCAGT
GAGTCCCTTACTTTTGCTCCGTGGAGGAAGCTGGGGGTACAAGGGGCCCAGT
GCTGGCCACACAGCAGCGCAGCCGAGCCCCAGGAGCCCGTCAGGCCACAG
CCCCTGGCACTGCAGGTGGCCCTCCCTCCAGAGACTCGAGTCCCCATGATT
CCCTCCTCGTCAGTCTCTCAAAGACCCCATGGTCCATCCCCTGAGGGTGG
TCAGCCAAGGCTCCCGTTCCGTGGGATGCCATAAAAGCCGCCAGTGGA
CCCACAGTCACACAGAGCGCCTCACCTGCATCCTCTCCCCACAAGAGCC
CCAAAGATCCCACGGGAGAGGGGAGAGGGACGCACAGCACTGCCTGCCAA
GCGAGAAATGCAGGCCCCGCCCCCTCGGCCCTCACACCTCTTTCTACAG
CCTAATTTATTGGATTCCCTATTTCGTAGCCATCTCCGTGGCCAATGTGAC
TACCGTGCCAGCAGCGGGGGCGGCCAGCCTCTGAGTCCCGTGGGGCCCC
GGCTCCCACCGGTGCCAAACCCAGCCCCCTGCGGCCGTACCCCGCCAGCC
TACACTGCCAGCCGCCACCGGGGCACACGGGCCTCTGCTTGCCAGCCAGG
AGTGCGGACACCATGTTCCAGCTCAGTGCCAAAGAGGGGTACCCAGGGG
GAGCTGTCTGCGGAGCCAGCGCCTGCCCGAGAGAGACCCACCGCCACCG
TGTGCCTTTCCCGGGCCCTCAGCCCTCGGGCCGGGCACCAACCCAGTCC
CCCCAGTAAAAGCCTCCACTGGCAAAAAAAAAAAAAAAAAAAAAA

Figure 15 cont.

23 FEB 2005

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Figure 16

A new sequence determination, SEQ ID NO:127 for HSPA5

SEQ ID NO:127

HSP5>

ATGGAGGAGGACAAGAAGGAGGACGTGGGCACGGTGGTTCGGCATCGACCT
GGGGACCACCTACTCCTGCGTCGGCGTGTTCAAGAACGGCCGCGTGGAGA
TCATCGCCAACGATCAGGGCAACCGCATCACGCCGTCCTATGTCGCCTTC
ACTCCTGAAGGGGAACGTCTGATTGGCGATGCCGCCAAGAACCAGCTCAC
CTCCAACCCCGAGAACACGGTCTTTGACGCCAAGCGGCTCATCGGCCGCA
CGTGGAATGACCCGTCTGTGCAGCAGGACATCAAGTTCTTGCCGTTCAAG
GTGGTTGAAAAGAAAATAAACCATAATTCAAGTTGATATTGGAGGTGG
GCAAACAAAGACATTTGCTCCTGAAGAAATTTCTGCCATGGTTCTCACTA
AAATGAAAGAAACCGCTGAGGCTTATTTGGGAAAGAAGGTTACCCATGCA
GTTGTTACTGTACCGCCTATTTTAATGATGCCCAACGCCAAGCAACCAA
AGACGCTGGAATATTGCTGGCCTAAATGTTATGAGGATCATCAACGAGC
CTACGGCAGCTGCTATTGCTTATGGCCTGGATAAGAGGGAGGGGAGAAG
AACATCCTGGTGTGTTGACCTGGGTGGCGGAACCTTCGATGTGTCTCTTCT
CACCATTGACAATGGTGTCTTCAAGTTGTGGCCACTAATGGAGATACTC
ATCTGGGTGGAGAAGACTTTGACCAGCGTGTATGGAACACTTCATCAAA
CTGTACAAAAAGAAGACGGGCAAAGATGTCAGGAAAGACAATAGAGCTGT
GCAGAAACTCCGGCGCGAGGTAGAAAAGGCCAAACGGGGCCCTGTCTTCTC
AGCATCAAGCAAGAATTGAAATTGAGTCCCTTCTATGAAGGAGAAGACTTT
TCTGAGACCCTGACTCGGGCCAAATTTGAAGAGCTCAACATGGATCTGTT
CCGGTCTACTATGAAGCCCGTCCAGAAAGTGTGGAAGATTCTGATTGA
AGAAGTCTGATATTGATGAAATTGTTCTTGTGGTGGCTCGACTCGAATT
CCAAAGATTCAAGCAACTGGTTAAAGAGTTCTTCAATGGCAAGGAACCATC
CCGTGGCATAAACCAGATGAAGCTGTAGCGTATGGTGTCTGTGTCAGG
CTGGTGTGCTCTCTGGTGTATCAAGATACAGGTGACCTGGTACTGCTTGAT
GTATGTCCCCCTTACACTTGGTATTGAAACTGTGGGAGGTGTATGACCAA
ACTGATTTCCAAGGAACACAGTGGTGCCACCAAGAAGTCTCAGATCTTTT
CTACAGCTTCTGATAATCAACCAACTGTTACAATCAAGGTCTATGAAGGT
GAAAGACCCCTGACAAAAGACAATCATCTTCTGGGTACATTTGATCTGAC
TGGAATTCTCTCTGCTCCTCGTGGGGTCCACAGATTGAAGTCACCTTTG
AGATAGATGTGAATGGTATTCTTCGAGTGACAGCTGAAGACAAGGGTACA
GGGAACAAAAATAAGATCACAAATCACCATGACCAGAATCGCCTGACACC
TGAAGAAATCGAAAGGATGGTTAATGATGCTGAGAAGTTTGCTGAGGAAG
ACAAAAAGCTCAAGGAGCGCATTTGATACTAGAAATGAGTTGGAAAGCTAT
GCCTATTCTCTAAAGAATCAGATTGGAGATAAAGAAAAGCTGGGAGGTAA
ACTTTCTCTGAAGATAAGGAGACCATGGAAAAAGCTGTAGAAGAAAAGA
TTGAATGGCTGGAAAGCCACCAAGATGCTGACATTGAAGACTTCAAAGCT
AAGAAGAAGGAAGTGAAGAAATTTGTTCAACCAATTATCAGCAAACCTCTA
TGGAAGTGCAGGCCCTCCCCCAACTGGTGAAGAGGATACAGCAGAAGCTCC
ACCACCACCACCACCAC

DTIC Ref ID: A617710 23 FEB 2005

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Figure 17

Protein disulfide isomerase, SEQ ID NO:165.

SEQ ID NO:165

Novel protein disulfide isomerase

Novel (disulfide isomerase-like)

CGGACCAACACAGTATTGAGTCAACTGTGACCTTAAGATCAGAGGAACGTCAATACTGCCACAAGGCCACCTTTCCA
GAACTCGTGGGCAGGTAAACTATGCTTTGGATGTGCTTTCTTTCACCAAATCACTCAACTCAGGAGCCACAAATAG
TCCAGCAATTTCAATTTCCCTCAACGCTATTTTAGTCTCAAAGGAAACCATGTAAATTTTCATCAAGAGAAGGTCAAAG
GGGATATATCGCCACTGAAAATGTTTACACAGTGACCATGAGTTACACATTTACTTAGAGAACTTAACTTAATAAA
GAATCTGTAGAGTGTGTTGGCTTGGAAAACACACACAAAGAAGATACCTCACGCTTAGTATGTTCTGCTTTCTGA
ACAGCCACCACTGGGAACCCAGTGGCCTCTGTGGGACTGAACTCCTAAACGCAGGGTGCGGGAGCTGGGCAGGAGAG
GTGACCTCCAACGTGTGTTCTAAAGTTTCGTCTTTTCGCTTGGCTCAGGACAAAGCGGTGTAACGAGTCAAAGTCTCTG
CCTCCACTGTGCTCACTGACTTTCTTCCCTCCTCGGAAAAGCAATAACGTGGGGTAGCCTCGT

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Figure 18

Chromosome 1 protein

SEQ ID NO:210

Clone 30 -Novel (Chromosome 1) >

ATCTACATGAGGTCCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGCTA
CCACCTGTTACTTTGACAACTCTAGCTTCAGGGCTACCAGGACCATTTGCAAACTTACACCCACAGAAACTCAAA
GTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCCTTCTCCTTCTAGTAGTACTTTTGGTTTCCA
GGAAAATCATCTCATGCTCGGGCCACAGTCACAGTCCTGACCAGCACCATAGAAAATTTAGCCATTATTCTAGTTGT
ATGGAGTCATTCAAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACCTTTGCTAATTT
TTCCATAAATTGAAAGCCTT

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Figure 19

Chromosome 3 protein

SEQ ID NO:218

Clone 95 -Novel (Chromosome 3/ H41) >

GCCTCGCTCGGCGTTAGCCAAGGCCCCGGGCGGCCACCCTCCGGGGGCACTAGGTCTGGGGCCGCAGTGCCCAGCA
CAGAGCAGCGTTTATCGGGACGAAGATGAATGGAAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCGGCCTCAGGGG
TTCAGGCAATGCAAATAAGCAGTGAAAAGGAAGAAGACGATAATGAAAAG

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Figure 20

Chromosome 17

SEQ ID NO:227

Clone 147 - Novel (Chromosome 17) >

CTGCTTCTCTTCTAGGATAGTTTCCCTCTAGAAATCCATGTTGCTCCTTCTCTCATTAAATGATCAGATATTTATGT
GCCTCCTTAGCTAAGAGGCCTTCCTTATCTACCCCTAACTAAGAGAATCCCCATATCACTCTTATCCTTTTATCCTGA
TTTATTTTTCCATAAACTTGCCACATTACTGGGCATTATCTATCATTTAGTAATGTGTATATTGCTTATTGACAGT
CTTCCCTACTATAATATGAGCTCCATGAGGCAGAGACTTTGTTTTGTTCACTGCTGAATTTCCAGCACCTACAACAA
GCCTACTCACTAAACATTTGTTGAATTAATCTTCAGGATACATCAAATGTAAAATATCCTATCATATATTTATTGAT
GTGATGCATAGGAAAATGTCTGGAAGGGTACATACCAAAATGTTAATTATTTATTTAACCTGGTGGGAGGTGGTTTT
TCTTTCCCTTTTCTTTTCTTTTGGAGACAGAGTTTCGCTCTCGTTGCCAGGCTGGAGTGGAATGGCAAG

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Figure 21

Chromosome 8 protein

SEQ ID NO:232

Novel (chromosome 8) >

GCTTGCAAAGGAGAGGCTGTGACTACCAAGTCGTGTCAACAACCTGAATGGCTGAAATACCCAACTTGCCCATGCAA
ATGGGCTTGGGTCTCTCCTGGCAGCCGCTTTGAAGGCTCTAGACTTATCTGTGAACCTCTTTTGTGAGAGGGTCTT
TCCAAGTAGTGGTTTATTCTTTGACTCTCCTCATACTTTTTTGCCAGAGAGTGAGAGTGAGAAGGGAGGGCTAATG
CCTGAGCTCCTGCCCTTTCTATGCAGTGAGGGTCAAGATCCTCAGCTAGTGTGAGGGAACTGGTGTAACCTGGGT
CTCTCATTTTCTACCATCCAAGTTGCC

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Figure 22

Chromosome 9 protein

SEQ ID NO:248

Clone 49 -Novel (Chromosome 9) >

CTGCAGGAGACCACAGGCAGGTGCCCACCTAAGAGGGACAGCCACAGAAACCCTCTAACCTCAGCACTGCACTCCAC
CACGACCACCCACGCAGGCCCTCAGCACCGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCCAGAAG
CTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGACTCGGAC
CTCCGCCAGGCCCCCAGCGCACAACCATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

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Figure 23

1/226 protein

SEQ ID NO:274

Clone 1/226 - Novel (Clone1/226) >

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCTTC
TTGCTTGTCGTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTCTCCGCCC
CAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACTTCATCCCTTCTACCCA
TCACAACATACAAAGCAACTACACCTGGATTTTTTCAAACAACTTTTATTTCTCAGAGTCTTCCTTAATCCTATGG
AACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATATAAAAATATAG
ACTTTTAAAAAAAAAAAAAAAAAAAAA

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Figure 24

A new sequence determination for FLJ10688

SEQ ID NO:285

Novel (FLJ10688) >

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGAAG
CCACACTTGAAGTTAGCACGCGTTCAGAGTCAAAATGGCATAGTACTGTCATGGAGTGCCTGGAGGTGGATCGAAG
CTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAATGGAAAA
AGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTACCCAGTTTGTATCTGGTAGCAAATACTAC
TTTG

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Figure 25

A new sequence determination for KIAA1583

SEQ ID NO:307

Clone 89 -Novel (KIAA1583)>

ACTGCAGGTGGCAGCCACGGGCGCGCCGCTCGGCCTCATCTGACGCCTCTGCAGCGGGTTCCGCAGGCCTGCAGGGC
GGGGAGGCCGGGACTGGCCGTGACGCTGAACGGGCCAGCCTGCCAGGGCCCAGCTGCTGGAGACCCGCAGCTCGT
CCCCGGCGGCTCCTAATCACCAGCAGCTCCTGTTTCTCAAAACGCAGACATCCGCCCCCTCTTGGGGTCAGGCCCTTC
CACCTTGCAGGCGAGCCGCCCCAGCCCACTCCCGACTGGCGCTATGCCCTCGATCACCGCTCTTGCTCCCAAGTGGAC
CGCAGGGGAGACGCTCTCTTACGGGGACCCTGGGGGCGCTCACTCTCTGAAGGGCCTGGAAGCTAGATTCCAGAGGC
GTGGGCCACCTCTCCCTGGGTTTTGGGGAGCCCCCTCCGAGGGTGTTTCATTTCTGAGCTCTGTGTCATCTTAGGCT
CTGAGGGT

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Figure 26

A new sequence determination for KIAA1814

SEQ ID NO:317

Clone 75 -Novel (KIAA1814) >

CTGGACGGCCTGGCTGGGCTGAAGGGCGAGGACAGCCGAGCAAGGAGGCAGGGGAGGGCGGCCTACCGCTGTGCGG
GCCCACGGACAAGACCCCACTGCTGAGCGGCAAGGCCGCCAAGGCCCGGACCGCGAGGTCGACCTCAAGAATGGCC
ACAACCTCTTCACTCTGCGGCGGCCGTGCCTCCCGGAAGCCTCCTCAGCGGCCCGGCCTGGCCCCGGCGGCCTCCT
CCGACGGCGGCGCGGCGTCCCTCCGCCCAGACGCACCGGTCTCTTCTGGGCCCCCTTCCCGCCGGGACCGCAGTTCGCG
CTCGGCCCCATGTCCCTGCAGGCCAACCTCGGCTCCGTGGCCGGCTCCTCCGTGCTGCAGTCGCTGTTTCAGCTCTGT
GCCGGCCGCGCAGGCCTGGTGCACGTGTCGTCCGCTGCCACCAGACTGACCAACTCGCACGCCATGGGCAG

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Figure 27

Chromosome 4 protein

SEQ ID NO:320

Novel (maps to chromosome 4)

Novel (Chromosome 4)>

GGAATAAAAGAGTGGAAATGGGGATTTCCAGGTGCTCCCCTGGTTCATCTAGGCACCAGAGAGCTGCACTAGCAGGT
CTATCATGAATCTCCTTGGAATGCTCATTTTTAGTCCTACTTGATGTGTCTGTTTCTGGAAATGCAGTATTTTAAAT
GTATCTCAACAAAATATTTTATGATTAGTAAGCTTATTCTTATATAAAGGACAATTTTTTTCCTTTTTCACAGGTTC
TAATAATTTTTTATTTAATAATTAGATCTATTAGATTTTATTCATAACTGTGGTAGTTGAAGTACCTTCTAAGCTGA
GTTTCAATTTGAGAATAAACCTTGGGGTATCATTACAGAAAATTTTGTCTCAATCTGCTTTGTATTTGAAAGATATG
AGATTCTTGAATTATATATCTTACAGACTAGTCCCCAAAAGAATACGTGTTTCCTTACCTTTAATTTCTCATGGTAG
TTAGTCTGTGAAT

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Figure 28

A new sequence determination for peroxidasin/melanoma antigen related protein

SEQ ID NO:323

Novel peroxidasin-like/ melanoma antigen>

CGACCTGGCCAGCCACCGCGGCCTGCTGCGGCAGGGCATCGTGCAGCGGTCCGGGAAGCCGCTGCTCCCCCTTCGCCA
CCGGGCGCGCCACGGAGTGCATGCGGGACGAGAACGAGAGCCCCATCCCCCTGCTTCCTGGCCCGGGACCACCGCGCC
AACGAGCAGCTGGGCCTGACCAGCATGCAACGCTGTGGTTCCGCGAGCACAACCGCATTGCCACGGAGCTGCTCAA
GCTGAACCCGCACTGGGACGGCGACACCATCTACTATGAGACCAGGAAGATCGTGGGTGCGGAGATCCAGCACATCA
CCTACCAGCACTGGCTCCCGAAGATCCTGGGGGAGGTGGGCATGAGGACGCTGGGAGAGTACCACGGCTACGACCCC
GGCATCAATGCTGGCATCTTCAACGCCTTCGCCACCGCGGCCTTCAGGTTTGGCCACACGCTTGTCAACCCACTGCT
TTACCGGCTGGACGAGAACTTCCAGCCCATTGCACAAGATCACCTCCCCCTTCACAAAGCTTTCTTCTCTCCCTTCC
GGATTGTGAATGAGGGCGGCATCGATCCGCTTCTCAGGGGGCTGTTCCGGGGTGGCGGGGAAAATGCGTGTGCCCTCG
CAGCTGCTGAACACGGAGCTCACGGAGCGGCTGTTCTCCATGGCACACACGGTGGCTCTGGACCTGGCGGCCATCAA
CATCCAGCGGGGCGGGACCACGGGATCCCACCCTACCACGACTACAGGGTCTACTGCAATCTATCGGCGGCACACA
CGTTCGAGGACCTGAAAAATGAGATTAAAAACCTTGAGATCCGG

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Figure 29

WD40/SOCS box protein

SEQ ID NO:329

Novel WD40/SOCS box protein>

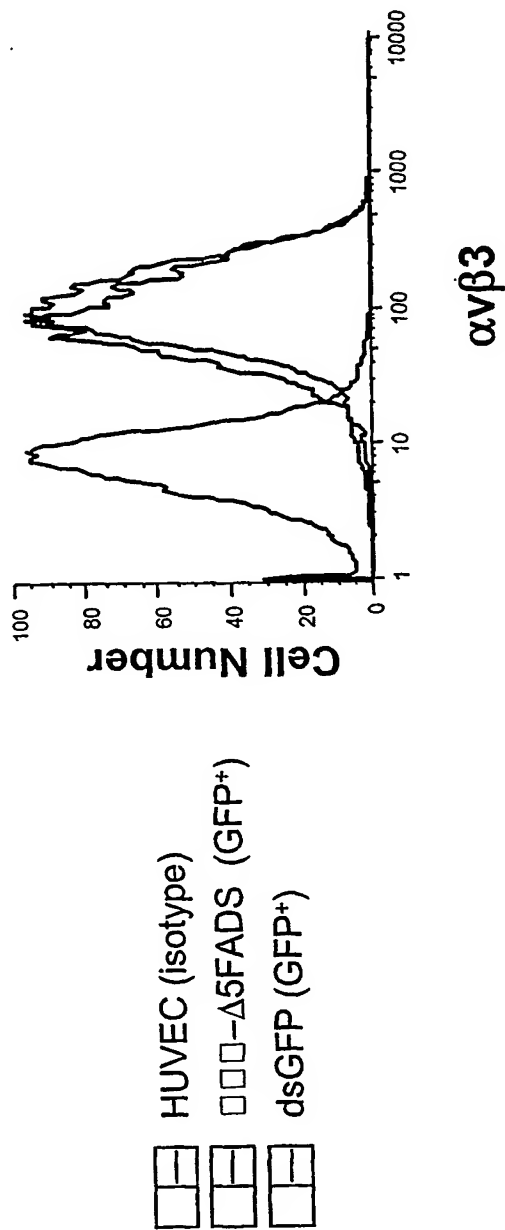
CGGCTCTGTTGCCGTGCAAGTGGAATCATCTTACCTCTAAGACATGACTTTCACATGCCAGGGGAGAGAAAGATCCA
TGACTAGTACACTGGCAATCTGGTTTTGCTACATTCTATTCACAATCCCAAAGAAATGCTATTTCAATGCAAGACCA
GATGTTTGGCCCATTATTCCAGCAACTCCCTTTGACAGGACGATTTACCTTGCTACCAAAGAAGCACAAGATGTGGT
GTTGCTTAAAAAAGTCCTGTATGTGAGGAACTCTTTCATTTCTTGGGGATTGGCAGTGCTAGGACTTGGTAAGTTG
TTAGGAACTTCGAAGGGCTTCCGGCATAAGTGCTTCAGTGAGGACAGGACCCTAGGAGCTGTCCAGAACTGGACG
TGGCCATCTCTTGTCCCTGTGGCAATGACTCCACCATGTGGAAAAAATGTGCAGCAAAGCCCATTGGTCATAGGAGC
AAATGCAATGGGAGTTTTTCAGTTCCAGGGCCCAGATCCTGAGGAGTCTGTCATCTGCCACCGTGGCAAGGTACAAGC
CCCCG

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GFP-Δ5FADS Antisense Screening Hit Downregulates Surface αvβ3 Levels



• GFP- Δ5FADS screening hit: 300 bp antisense



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GFP-Δ5FADS Antisense Screening Hit does not Affect Cell Proliferation

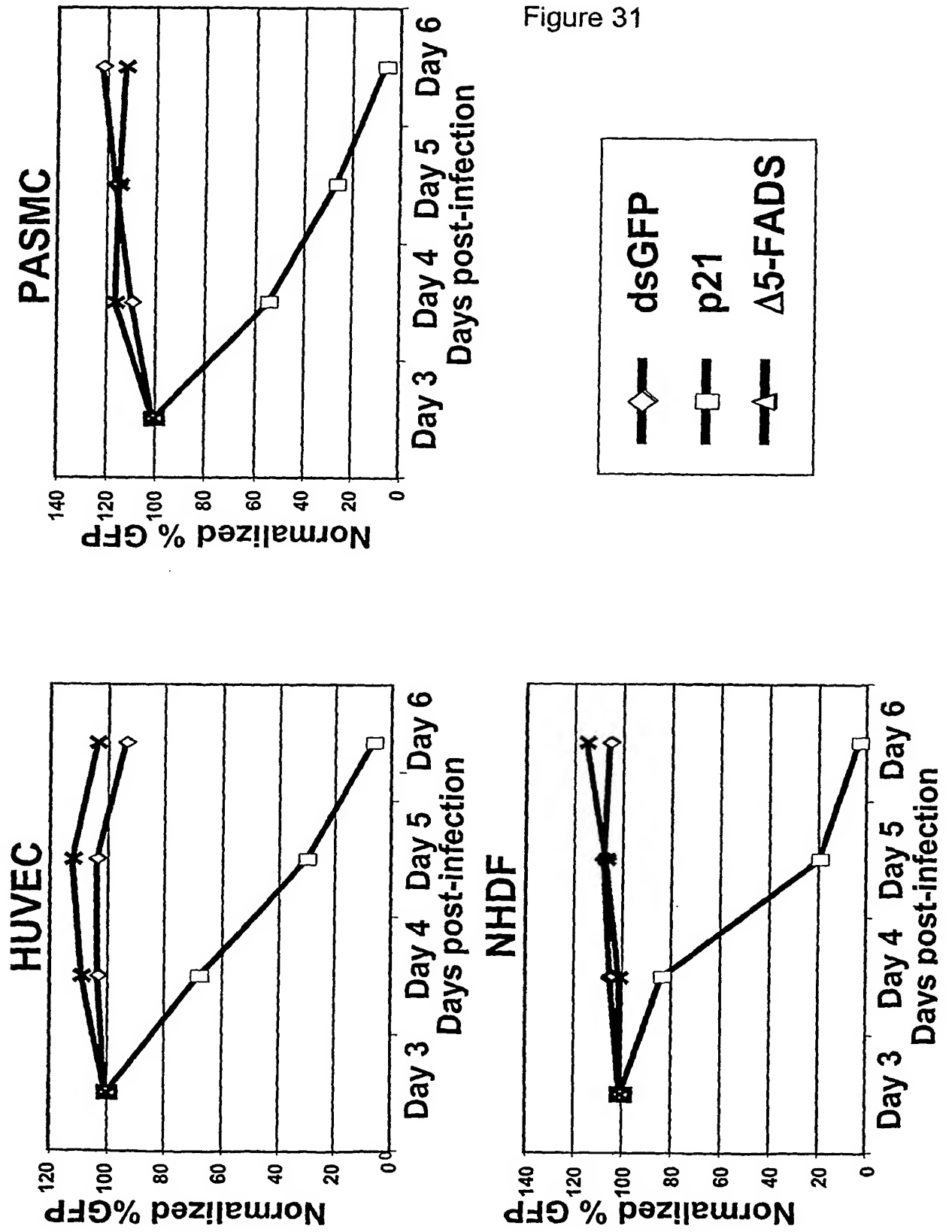


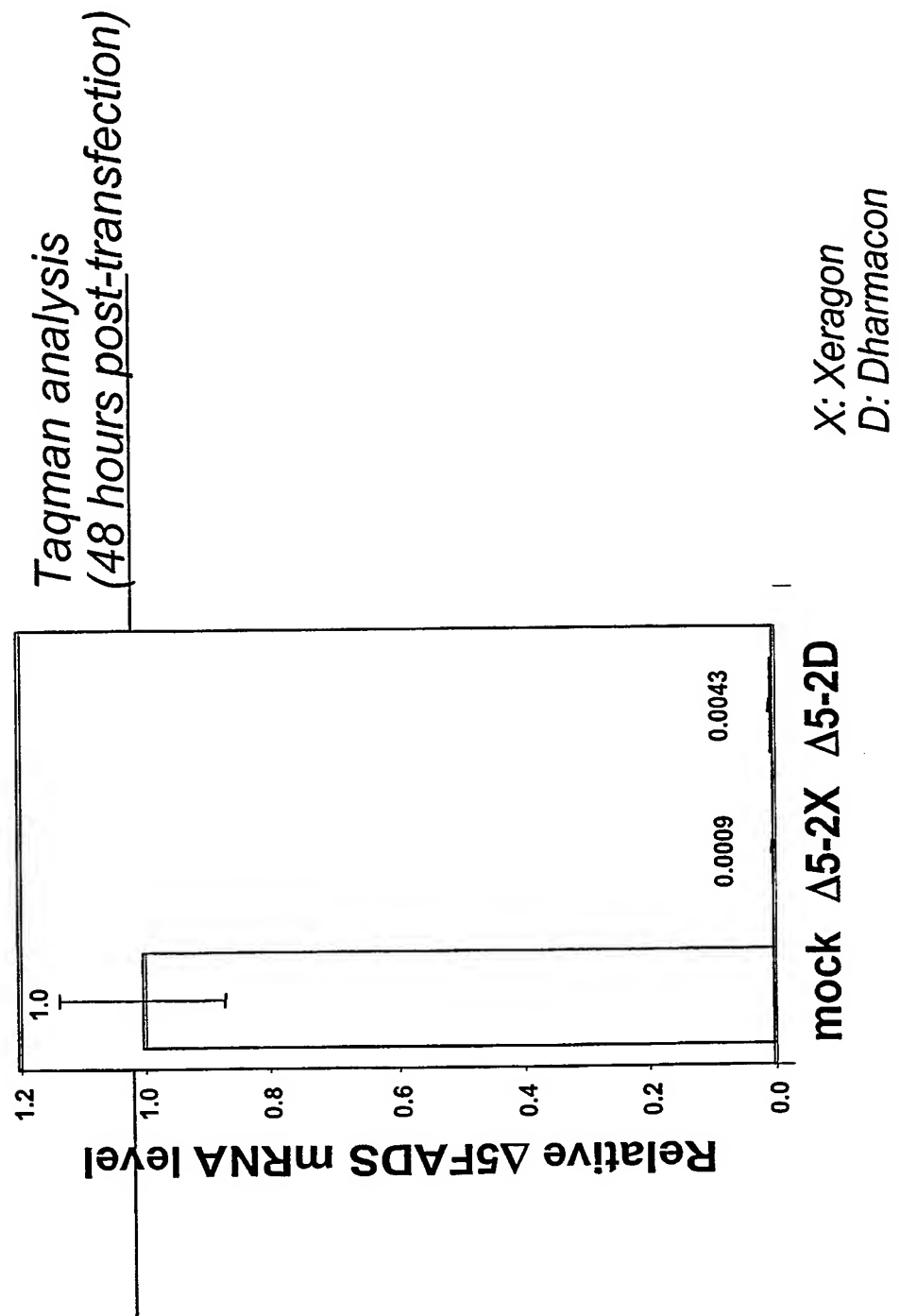
Figure 31

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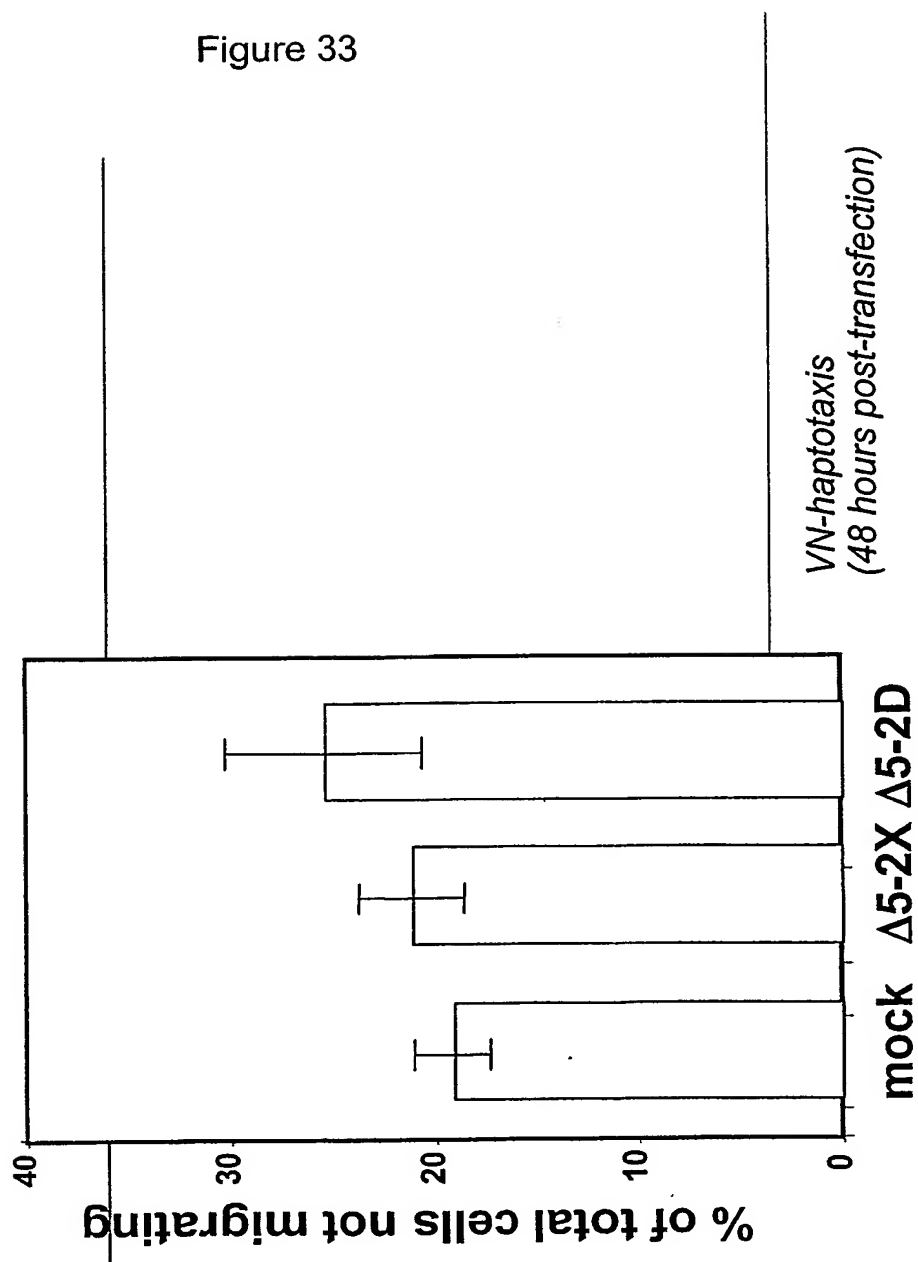
Figure 32

siRNA($\Delta 5-2$) Blocks $\Delta 5$ FADS Expression in HUVEC



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$\Delta 5$ FADS RNAi Inhibits Haptotaxis

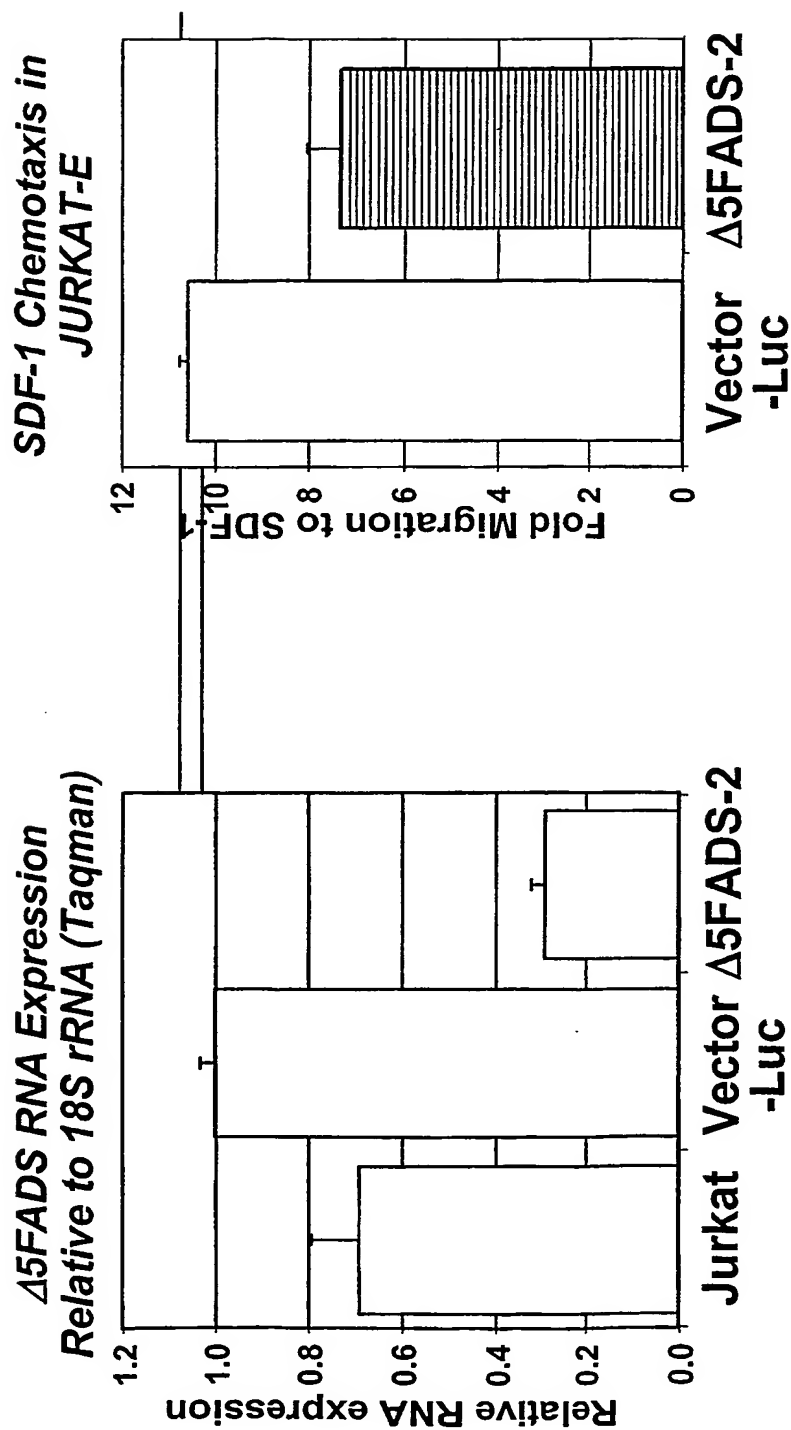


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23 FEB 2003

Figure 34

Δ5-FADS RNAi Vector Reduces SDF-1 Induced Chemotaxis in Jurkat Cells



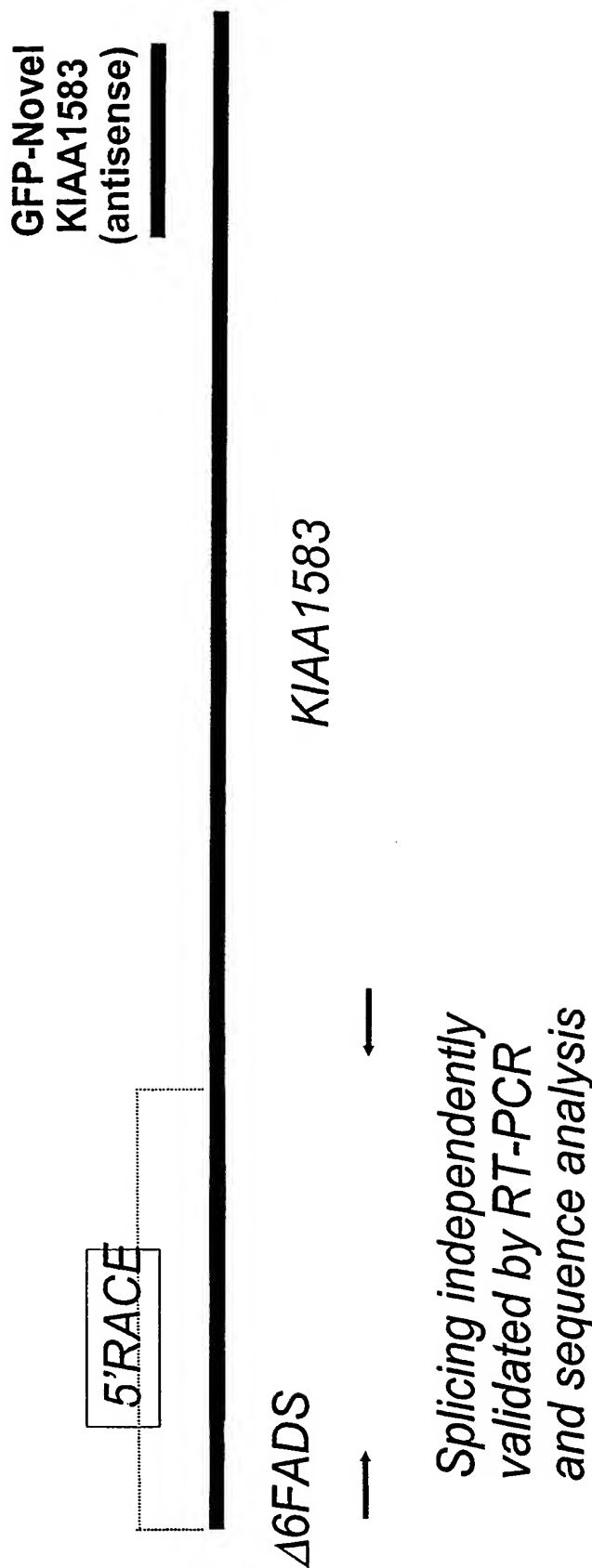
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23 FEB 2003

Figure 35

Δ 6FADS is a Functional Screening Hit

- 5' RACE analysis indicates that the Δ 6FADS transcript is spliced with the Novel (KIAA1583) transcript.
- Δ 6FADS and KIAA1583 sequences are both located on Chromosome 11q12



23 FEB 2005

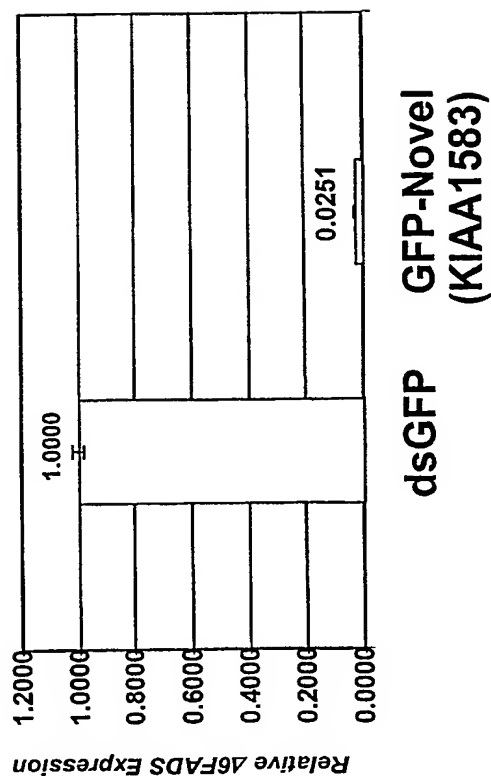
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Figure 36

Δ 6FADS is a Functional Screening Hit

- HUVECs expressing the GFP- Novel (KIAA1583) screening hit have strongly reduced levels of Δ 6FADS mRNA.

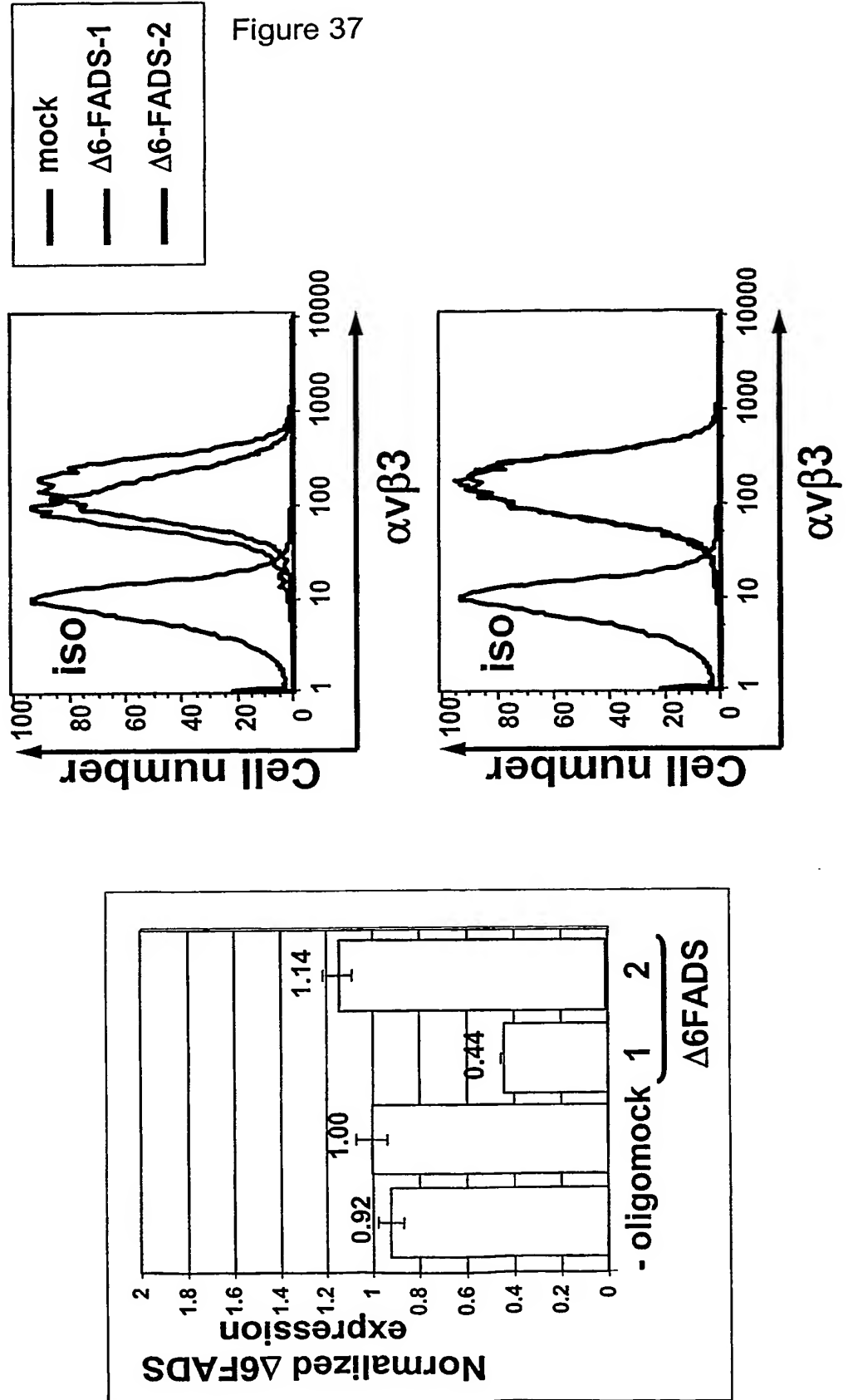
Taqman analysis of Δ 6FADS mRNA levels



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$\Delta 6$ FADS RNAi Reduces $\alpha v\beta 3$ Surface Expression



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BRIEF SUMMARY OF THE INVENTION

The present application identifies, for the first time, a number of proteins and DNA molecules involved in regulation of angiogenesis, *e.g.*, angiogenesis regulatory proteins and DNA molecules. The invention further relates to methods for identifying and using agents, including small organic molecules, antibodies, peptides, cyclic peptides, nucleic acids, antisense nucleic acids, RNAi, and ribozymes, that modulate angiogenesis via modulation of angiogenesis regulatory proteins and DNA molecules; as well as to the use of expression profiles and compositions in diagnosis and therapy of diseases related to insufficient or increased angiogenesis.

In one aspect, the present invention provides a method for identifying a compound that modulates angiogenesis, the method comprising the steps of:

(i) contacting the compound with an angiogenesis regulatory nucleic acid, or an angiogenesis regulatory polypeptide or a fragment thereof encoded by a nucleic acid, wherein the nucleic acid hybridizes under stringent conditions to a second nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ ID NO:523; and (ii) determining the functional effect of the compound upon the nucleic acid or polypeptide.

In one embodiment, the functional effect is determined in vitro. In another embodiment, the functional effect is a physical effect. In another embodiment, the functional effect is determined by measuring ligand or substrate binding to the polypeptide. In another embodiment, the functional effect is a chemical effect. In another embodiment, the functional effect is determined by measuring an enzymatic activity.

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In one embodiment, the polypeptide is expressed in a eukaryotic host cell. In a further embodiment, the functional effect is a physical effect. In another embodiment, the functional effect is determined by measuring ligand or substrate binding to the polypeptide. In a further embodiment, the functional effect is a chemical or phenotypic effect. In another embodiment, the functional effect is determined by measuring an enzymatic activity. In another embodiment, the host cell is an endothelial cell. In a further embodiment, the functional effect is determined by measuring $\alpha v \beta 3$ expression or haptotaxis, or chemotaxis, or co-culture tube formation.

In one embodiment, modulation is inhibition of angiogenesis.

In one embodiment, the polypeptide is recombinant. In another embodiment, the nucleic acid comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ ID NO:523.

In another embodiment, the polypeptide comprises a sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:33, SEQ ID NO:44, SEQ ID NO:58, SEQ ID NO:64, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:77, SEQ ID NO:82, SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:121, SEQ ID NO:129, SEQ ID NO:140, SEQ ID NO:154, SEQ ID NO:164, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:203, SEQ ID NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, SEQ ID NO:331, SEQ ID NO:341, SEQ ID NO:352, SEQ ID NO:366, SEQ ID NO:378, SEQ ID NO:385, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:420, SEQ ID NO:429, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID

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NO:457, SEQ ID NO:463, SEQ ID NO:482, SEQ ID NO:485, SEQ ID NO:494, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:520, SEQ ID NO:522, and SEQ ID NO:524.

In one embodiment, the compound is an antibody, an antisense molecule, a small organic molecule, or a peptide.

5 In another aspect, the present invention provides a method for identifying a compound that modulates angiogenesis, the method comprising the steps of (i) contacting the compound with a nucleic acid, or a polypeptide or a fragment thereof encoded by a nucleic acid, wherein the nucleic acid hybridizes under stringent conditions to a second nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:3, SEQ
10 ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID
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20 NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ ID NO:523; (ii) determining the functional effect of the compound upon the nucleic acid or polypeptide; and (iii) expressing the nucleic acid or polypeptide in a cell, contacting the nucleic acid or polypeptide with the compound, and determining the
25 phenotypic or chemical effect upon the cell.

In another aspect, the present invention provides a method of modulating angiogenesis in a subject, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as a modulator of angiogenesis using the methods described herein. In one embodiment, the subject is a human. In a further
30 embodiment, the compound is an antibody, an antisense molecule, a small organic molecule, a peptide, or an RNAi molecule. In another embodiment, the compound inhibits angiogenesis.

In another aspect, the present invention provides a method of modulating angiogenesis in a subject, the method comprising the step of administering to the subject a

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therapeutically effective amount of a polypeptide, the polypeptide encoded by a nucleic acid that hybridizes under stringent conditions to a second nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:63, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:165, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:218, SEQ ID NO:232, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:340, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, and SEQ ID NO:498.

In another aspect, the present invention provides a method of modulating angiogenesis in a subject, the method comprising the step of administering to the subject a therapeutically effective amount of a nucleic acid that hybridizes under stringent conditions to a second nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ ID NO:523.

In another aspect, the present invention provides the nucleic acid sequences of SEQ ID NO:165, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, and SEQ ID NO:330.

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In another aspect, the present invention provides the amino acid sequences of SEQ ID NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, and SEQ ID NO:331.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 provides a schematic diagram of an assay for modulators of angiogenesis.

Figure 2 provides results of an experiment demonstrating the effect of a plakoglobin-GFP fusion protein expression on levels of the cell surface marker $\alpha\beta3$.

Plakoglobin is an exemplar angiogenesis regulatory protein. Human umbilical vein endothelial (HUVEC) cells were transfected with a vector expressing the plakoglobin-GFP fusion protein ((GGS)₂ = SEQ ID NO:525) or a control vector, expressing GFP only. Cells were incubated with APC-labeled antibodies directed against the cell surface marker $\alpha\beta3$. The X-axis depicts cell number and the Y-axis depicts the amount of $\alpha\beta3$ -APC antibody derived fluorescence. Cells transfected with the plakoglobin-GFP fusion protein construct exhibit lower $\alpha\beta3$ expression levels than control cells.

Figure 3 also provides results of an experiment demonstrating the effect of a plakoglobin-GFP fusion protein (*i.e.*, GFP- Δ N-plakoglobin) expression on levels of the cell surface marker $\alpha\beta3$. The figure also depicts the presence of armadillo repeats in the functional screen hit, GFP- Δ N-plakoglobin.

Figure 4 demonstrates that GFP- Δ N-Plako expression downregulates vitronectin receptors ($\alpha\beta3$ and $\alpha\beta5$) but not the fibronectin receptor ($\alpha5\beta1$).

Figure 5 demonstrates that expression of GFP- Δ N-Plakoglobin downregulates endogenous catenin levels, as well as expression of endogenous plakoglobin and VE-cadherin.

Figure 6 demonstrates that GFP- Δ N-Plakoglobin expression upregulates surface levels of the laminin receptor, $\alpha6\beta4$.

Figure 7 provides results of an experiment demonstrating the effect of a HoxB2-GFP fusion protein expression (*i.e.*, Δ N-HoxB2) on levels of the cell surface marker $\alpha\beta3$. Cells transfected with the Δ N-HoxB2-GFP fusion protein construct exhibit lower $\alpha\beta3$ expression levels than control cells. The figure also provides the structure of the functional screen hit, demonstrating that the homeodomain is present in Δ N-HoxB2.

Figure 8 demonstrates that Δ N-HoxB2 downregulates both $\alpha\gamma$ and $\beta3$ integrin subunit surface expression, as well as $\alpha\beta5$ surface expression.

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Figure 9 demonstrates that Δ N-HoxB2 Inhibits Proliferation in HUVECs, a primary cell line.

Figure 10 demonstrates that full length HoxB2 phenocopies Δ N-HoxB2 in the downregulation of α v β 3.

Figure 11 provides results of an experiment demonstrating the effect of a SUSP-1 GFP fusion protein expression (*i.e.*, GFP-SUSP-1) on levels of the cell surface marker α v β 3. Cells transfected with the GFP-SUSP-1 fusion protein construct exhibit lower α v β 3 expression levels than control cells. The figure also provides the structure of the functional screen hit, demonstrating that GFP-SUSP-1 is an N-terminal fusion in the sense orientation and that a cDNA insert is present before the wild-type start codon.

Figure 12 demonstrates that the GFP-SUSP-1 screening hit does not affect proliferation when expressed in HUVEC (human umbilical vein endothelial cells), PASMC (pulmonary artery smooth muscle cells), and NHDF (normal human dermal fibroblasts).

Figure 13 provides expression analysis of SUSP-1 mRNA in a variety of cell lines.

Figure 14 demonstrates that SUSP-1 siRNAs inhibit SUSP-1 mRNA expression.

Figure 15 provides a new sequence determination for a nucleic acid encoding an ABC transporter protein (SEQ ID NO:2).

Figure 16 provides a new sequence determination for a nucleic acid encoding an HSPA5 protein (SEQ ID NO:127).

Figure 17 provides a new sequence determination for a nucleic acid encoding a protein disulfide isomerase (SEQ ID NO:165).

Figure 18 provides a new sequence determination for a nucleic acid encoding a novel protein from human chromosome 1 (SEQ ID NO:210).

Figure 19 provides a new sequence determination for a nucleic acid encoding a novel protein from human chromosome 3 (SEQ ID NO:218).

Figure 20 provides a new sequence determination for a nucleic acid encoding a novel protein from human chromosome 17 (SEQ ID NO:227).

Figure 21 provides a new sequence determination for a nucleic acid encoding a novel protein from human chromosome 8 (SEQ ID NO:232).

Figure 22 provides a new sequence determination for a nucleic acid encoding a novel protein from human chromosome 9 (SEQ ID NO:248).

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Figure 23 provides a new sequence determination for a nucleic acid encoding a 1/226 protein (SEQ ID NO:274).

Figure 24 provides a new sequence determination for a nucleic acid encoding an FLJ10688 protein (SEQ ID NO:285).

5 Figure 25 provides a new sequence determination for a nucleic acid encoding a KIAA1583 protein (SEQ ID NO:307).

Figure 26 provides a new sequence determination for a nucleic acid encoding a KIAA1814 protein (SEQ ID NO:317).

10 Figure 27 provides a new sequence determination for a nucleic acid encoding a novel protein from human chromosome 4 (SEQ ID NO:320).

Figure 28 provides a new sequence determination for a nucleic acid encoding a peroxidasin/melanoma antigen related protein (SEQ ID NO:323).

Figure 29 provides a new sequence determination for a nucleic acid encoding a WD40/SOCS box protein (SEQ ID NO:329).

15 Figure 30 provides provides results of an experiment demonstrating the effect of a $\Delta 5FADS$ antisense screening hit (*i.e.*, GFP- $\Delta 5FADS$ or D5ADS) on levels of the cell surface marker $\alpha\beta 3$. Cells transfected with the GFP- $\Delta 5FADS$ antisense construct exhibit lower $\alpha\beta 3$ expression levels than control cells. The figure also provides the structure of the functional screen hit, demonstrating that GFP- $\Delta 5FADS$ is in the antisense orientation and
20 that a the anti sense portion of the $\Delta 5FADS$ nucleic acid is about 300 base pairs long.

Figure 31 demonstrates that the GFP-D5FADS antisense screening hit does not affect cell proliferation.

Figure 32 demonstrates that $\Delta 5FADS$ siRNAs inhibit $\Delta 5FADS$ mRNA expression.

25 Figure 33 demonstrates that $\Delta 5FADS$ siRNAs inhibit haptotaxis.

Figure 34 demonstrates that $\Delta 5FADS$ siRNAs inhibit SDF-1 induced chemotaxis in Jurkat cells.

Figure 35 demonstrates that $\Delta 6FADS$ is a functional screening hit. The figure shows that $\Delta 6FADS$ transcript is spliced to the KIAA1583 functional screen hit.

30 Figure 36 demonstrates tha $\Delta 6FADS$ mRNA levels are straongly reduced in cells that express the antisense KIAA1583 functional screen hit.

Figure 37 that $\Delta 6FADS$ siRNAs inhibit $\Delta 6FADS$ mRNA expression and also reduce $\alpha\beta 3$ surface expression.

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DETAILED DESCRIPTION OF THE INVENTION

Introduction

Using a functional assay, angiogenesis regulatory proteins and nucleic acids have been identified and cloned from a green fluorescent protein (GFP) fusion library.

5 Primary endothelial cells were transduced with retroviral cDNA/GFP fusion libraries. Transduced cells were selected and assayed for alterations consistent with inhibition of angiogenesis, e.g. downregulation of cell surface expression of $\alpha v \beta 3$ or downregulation of haptotaxis.

10 Using the screen described above, fifty-two proteins and/or DNA molecules were shown for the first time to regulate angiogenesis. Thirty-four of the proteins and/or DNA molecules are known, while fifteen of the proteins and/or DNA molecules are completely novel. However, this is the first demonstration of a function in regulation of angiogenesis for these molecules.

15 The ABC transporter is involved in peroxisome biogenesis. Relevant sequence data for the protein, nucleic acids encoding the ABC transporter, and related sequences include the nucleic acid accession number NM_000033, SEQ ID NO:3; protein accession number NP_000024, SEQ ID NO:4; a new sequence determination, SEQ ID NO:2; and the functional screen hit, SEQ ID NO:1. The protein has an ATP-binding domain. The gene encoding the ABC transporter is linked to a genetic disease, adrenoleukodystrophy
20 (Mosser *et al.*, *Nature* 361:682-3 (1993)). An antisense version of the ABC transporter gene, e.g., SEQ ID NO:1, was identified as a functional hit in the screen for modulators of angiogenesis.

25 PCB1, a poly (rC) binding protein functions as a translational co-activator and also binds 3' UTRs of RNA, most likely through KH domains, thereby regulating RNA stability. Relevant sequence data for the protein, nucleic acids encoding PCB1, and related sequences include the nucleic acid accession number NM_006196, SEQ ID NO:32; protein accession number NP_006187, SEQ ID NO:33; and the functional screen hit, SEQ ID NO:5-31. An antisense version of the gene encoding PCB1 was identified as a functional hit in the screen for modulators of angiogenesis.

30 SLC1A5, an amino acid transporter, has ten transmembrane spanning segments. Relevant sequence data for the protein, nucleic acids encoding SLC1A5, and related sequences include the nucleic acid accession number NM_005628, SEQ ID NO:43; protein accession number NP_005619, SEQ ID NO:44; and the functional screen hit, SEQ ID

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NO:34-42. An antisense version of the gene encoding SLC1A5 was identified as a functional hit in the screen for modulators of angiogenesis.

Chromobox homolog 6 is involved in chromatin regulation. Relevant sequence data for the protein, nucleic acids encoding chromobox homolog 6, and related sequences include the nucleic acid accession number NM_014292, SEQ ID NO:57; protein accession number NP_055107, SEQ ID NO:58; and the functional screen hit, SEQ ID NO:45-56. An antisense version of chromobox homolog 6 was identified as a functional hit in the screen for modulators of angiogenesis.

Cytochrome C oxidase subunit 1 is encoded by a mitochondrial gene and transfers electrons from cytochrome C to O₂ (Ingman *et al.*, *Nature* 408:708-713 (2000); (Leninger, *Principles of Biochemistry* (1984); Stryer, *Biochemistry* (1995)) Relevant sequence data for the protein, nucleic acids encoding cytochrome C oxidase, and related sequences include the nucleic acid accession number NC_001807, SEQ ID NO:63; protein accession number NP_536845, SEQ ID NO:64; and the functional screen hit, SEQ ID NO:59-62. A sense version of the gene encoding cytochrome C oxidase, encoding a 21 amino acid peptide, was identified as a functional hit in the screen for modulators of angiogenesis.

Δ -5 fatty acid desaturase (FADSD5 or Δ 5FADS) introduces double bonds into a fatty acyl chain. The protein is involved in arachadonic acid synthesis and has a fatty acid desaturase domain and a heme-binding domain. Relevant sequence data for the protein, nucleic acids encoding Δ -5 fatty acid desaturase, and related sequences include the nucleic acid accession number NM_013402, SEQ ID NO:68; protein accession number NP_037534, SEQ ID NO:69; and the functional screen hit, SEQ ID NO:65-67. An antisense version of Δ -5 fatty acid desaturase gene was identified as a functional hit in the screen for modulators of angiogenesis.

The dynactin p27 subunit protein was shown to be an angiogenesis regulatory protein. The protein has an RGD domain. Relevant sequence data for the protein, and the nucleic acid encoding dynactin p27 subunit protein, include the nucleic acid accession number NC_006571, SEQ ID NO:70; and protein accession number NP_006562.1, SEQ ID NO:71. An antisense version of the gene encoding dynactin p27 subunit protein was identified as a functional hit in the screen for modulators of angiogenesis.

Elongation factor 1 alpha (EF1 α) was shown to be involved in regulation of angiogenesis. Relevant sequence data for the protein, nucleic acids encoding EF1 α , and related sequences include the nucleic acid accession number NC_001402, SEQ ID NO:76;

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functional screen hit. Relevant sequence data for the protein, nucleic acids encoding HSPA5, and related sequences include the nucleic acid accession number NM_005347, SEQ ID NO:128; protein accession number NP_005338, SEQ ID NO:129; a new sequence determination, SEQ ID NO:127; and the functional screen hit, SEQ ID NO:122-126.

5 Interferon gamma receptor 1 (IFN γ R1) is a cytokine receptor that induces antiangiogenic genes. Relevant sequence data for the protein, nucleic acids encoding IFN γ R1, and related sequences include the nucleic acid accession number NM_000416, SEQ ID NO:139; protein accession number NP_000407, SEQ ID NO:140; and the functional screen hit, SEQ ID NO:130-138. An antisense version of the IFN γ R1 gene was identified as
10 a functional hit in the screen for modulators of angiogenesis.

Importin α 4 (karyopherin α 3) is a subunit of the nuclear localization signal receptor. Relevant sequence data for the protein, nucleic acids encoding importin α 4, and related sequences include the nucleic acid accession number NM_002267, SEQ ID NO:153; protein accession number NP_002258.1, SEQ ID NO:154; and the functional screen hit, SEQ
15 ID NO:141-152. An antisense version of the importin α 4 gene was identified as a functional hit in the screen for modulators of angiogenesis.

The lysosomal pepstatin-insensitive protease (CLN2) is encoded by a gene associated with juvenile neuronal ceroid lipofuscinosis disease. Relevant sequence data for the protein, nucleic acids encoding CLN2, and related sequences include the nucleic acid
20 accession number NM_000391, SEQ ID NO:163; protein accession number NP_000382, SEQ ID NO:164; and the functional screen hit, SEQ ID NO:155-162. An antisense version of the CLN2 gene was identified as a functional hit in the screen for modulators of angiogenesis.

A novel protein disulfide isomerase was shown to have a role in angiogenesis.
25 Relevant sequence data for the nucleic acid encoding the novel protein disulfide isomerase, includes SEQ ID NO:165. An antisense version of gene encoding the novel protein disulfide isomerase was identified as a functional hit in the screen for modulators of angiogenesis. The antisense hit encodes a 45 or 32 amino acid peptide that may also be useful as a therapeutic or to modulate angiogenesis.

30 Microtubule-associated protein 4 (MAP4) binds tubulin and may link microtubules to other elements of the cytoskeleton. See *e.g.*, Chapin & Bulinski, *J. Cell. Sci* 98:27-36 (1991); and Chapin *et al.*, *Biochemistry* 34:2289-2301 (1995). Four isoforms of MAP4 are known. Relevant sequence data for the proteins, nucleic acids encoding MAP4 isoforms, and related sequences include the nucleic acid accession numbers NM_002375,

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Plasminogen activator inhibitor 1 (SERPINE1 or PAI-1) was identified as an angiogenesis regulatory protein. PAI-1 is a protease inhibitor. Relevant sequence data for the protein, nucleic acids encoding PAI-1, and related sequences include the nucleic acid accession number NM_000602, SEQ ID NO:419; protein accession number NP_000593, SEQ ID NO:420; and the functional screen hit, SEQ ID NO:410-418. The functional screen hit is in the antisense orientation.

Proteosomal subunit Y, an $\text{INF}\gamma$ regulated proteosomal subunit, was identified as an angiogenesis regulatory protein. Relevant sequence data for proteosomal subunit Y includes the functional screen hit, SEQ ID NO:421. The functional screen hit is in the antisense orientation.

Rap2B was identified as an angiogenesis regulatory protein. Rap2B is a member of the RAS family of GTPases. Relevant sequence data for the protein, nucleic acids encoding Rap2B, and related sequences include the nucleic acid accession number XM_003032, SEQ ID NO:428; protein accession number XP_003032, SEQ ID NO:429; and the functional screen hit, SEQ ID NO:422-427. The functional screen hit is in the antisense orientation.

Semaphorin 3F was identified as an angiogenesis regulatory protein. Semaphorin 3F is a ligand for NP2. Relevant sequence data for the protein, nucleic acids encoding semaphorin 3F, and related sequences include the nucleic acid accession number U38276, SEQ ID NO:437; protein accession number AAB18276, SEQ ID NO:438; and the functional screen hit, SEQ ID NO:430-436. The functional screen hit is in the antisense orientation.

SPARC was identified as an angiogenesis regulatory protein. Relevant sequence data for the protein, nucleic acids encoding SPARC, and related sequences include the nucleic acid accession number NM_003118, SEQ ID NO:439; and protein accession number NP_003109, SEQ ID NO:440.

ssDNA binding protein-3 was identified as an angiogenesis regulatory protein. Relevant sequence data for the protein, nucleic acids encoding ssDNA binding protein-1, and related sequences include the nucleic acid accession number NM_018070, SEQ ID NO:445; protein accession number NP_060540, SEQ ID NO:446; and the functional screen hit, SEQ ID NO:441-444. The functional screen hit is in the sense orientation.

Sumo protease (SUSP-1) was identified as an angiogenesis regulatory protein. Relevant sequence data for the protein, nucleic acids encoding SUSP-1, and related sequences include the nucleic acid accession number NM_015571, SEQ ID NO:456; protein

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The terms “angiogenesis regulatory protein or nucleic acid” or a nucleic acid encoding “angiogenesis regulatory protein” refer to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino acid sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to a polypeptide encoded by a nucleic acid of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, and SEQ ID NO:519, or an amino acid sequence of SEQ ID NO:4, SEQ ID NO:33, SEQ ID NO:44, SEQ ID NO:58, SEQ ID NO:64, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:77, SEQ ID NO:82, SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:121, SEQ ID NO:129, SEQ ID NO:140, SEQ ID NO:154, SEQ ID NO:164, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:203, SEQ ID NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, SEQ ID NO:331, SEQ ID NO:341, SEQ ID NO:352, SEQ ID NO:366, SEQ ID NO:378, SEQ ID NO:385, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:420, SEQ ID NO:429, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:457, SEQ ID NO:463, SEQ ID NO:482, SEQ ID NO:485, SEQ ID NO:494, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:520, SEQ ID NO:522, and SEQ ID NO:524 or other sequences listed herein; (2) specifically bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence of SEQ ID NO:4, SEQ ID NO:33, SEQ ID NO:44, SEQ ID NO:58, SEQ ID NO:64, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:77, SEQ ID NO:82, SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:121, SEQ ID NO:129, SEQ ID NO:140, SEQ ID NO:154, SEQ

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ID NO:164, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:203, SEQ ID NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, SEQ ID NO:331, SEQ ID NO:341, SEQ ID NO:352, SEQ ID NO:366, SEQ ID NO:378, SEQ ID NO:385, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:420, SEQ ID NO:429, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:457, SEQ ID NO:463, SEQ ID NO:482, SEQ ID NO:485, SEQ ID NO:494, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:520, SEQ ID NO:522, and SEQ ID NO:524, immunogenic fragments thereof, and conservatively modified variants thereof; (3)

specifically hybridize under stringent hybridization conditions to a nucleic acid encoding
SEQ ID NO:4, SEQ ID NO:33, SEQ ID NO:44, SEQ ID NO:58, SEQ ID NO:64, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:77, SEQ ID NO:82, SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:121, SEQ ID NO:129, SEQ ID NO:140, SEQ ID NO:154, SEQ ID NO:164, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:203, SEQ ID NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, SEQ ID NO:331, SEQ ID NO:341, SEQ ID NO:352, SEQ ID NO:366, SEQ ID NO:378, SEQ ID NO:385, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:420, SEQ ID NO:429, SEQ ID NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:457, SEQ ID NO:463, SEQ ID NO:482, SEQ ID NO:485, SEQ ID NO:494, SEQ ID NO:497, SEQ ID NO:499, SEQ ID NO:520, SEQ ID NO:522, and SEQ ID NO:524, e.g., a nucleic acid sequence of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ ID NO:523; or its complement, and conservatively modified variants thereof; (4) have a nucleic acid sequence that has greater than about 95%, preferably greater than about 96%, 97%, 98%, 99%, or higher nucleotide

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sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ ID NO:523, or the complement of any of those sequences. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or any mammal. The nucleic acids and proteins of the invention include both naturally occurring or recombinant molecules. When available, accession numbers for the human angiogenesis regulatory proteins and genes are provided.

The phrase “functional effects” in the context of assays for testing compounds that modulate activity of an angiogenesis regulatory proteins includes the determination of a parameter that is indirectly or directly under the influence of an angiogenesis regulatory protein polypeptide, e.g., a chemical or phenotypic effect such as loss-of angiogenesis phenotype represented by a change in expression of a cell surface marker, such as $\alpha v\beta 3$ integrin, or changes in cellular proliferation, especially endothelial cell proliferation; or enzymatic activity, or, e.g., a physical effect such as ligand binding or inhibition of ligand binding. A functional effect therefore includes ligand binding activity, the ability of cells to proliferate, expression in cells undergoing angiogenesis, and other characteristics of angiogenic cells. “Functional effects” include *in vitro*, *in vivo*, and *ex vivo* activities.

Angiogenesis assays are described, e.g., in *Angiogenesis Protocols* (Murray, ed., 2001).

By “determining the functional effect” is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an angiogenesis regulatory proteins, e.g., measuring physical and chemical or phenotypic effects. Such functional effects can be measured by any means known to those skilled in the

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family, the integrin family, the selectin family, and the like; *see, e.g.,* Pigott & Power, *The Adhesion Molecule Facts Book I* (1993). Similarly, toxins and venoms, viral epitopes, hormones (e.g., opiates, steroids, etc.), intracellular receptors (e.g. which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D; peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes, polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly Gly sequences of between about 5 and 200 amino acids (SEQ ID NO:526). Such flexible linkers are known to persons of skill in the art. For example, poly(ethylene glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent which fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups which are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. *See, e.g.,* Merrifield, *J. Am. Chem. Soc.* 85:2149-2154 (1963) (describing solid phase synthesis of, e.g., peptides); Geysen *et al.*, *J. Immun. Meth.* 102:259-274 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron* 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al.*, *Science*, 251:767-777 (1991); Sheldon *et al.*, *Clinical Chemistry* 39(4):718-719 (1993); and Kozal *et al.*, *Nature Medicine* 2(7):753759 (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

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AKIVLRRHLSQDHTVPCFAASELHSRAEHTKENGLPYQSPSPVPGSMKLSPOBPRPLSPGALQLAGEKSS
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 HPLLLAQPRNSLPASPAHQLSSSPRLGGAAQGPLPEASKGDLPSDSGFSDPESEAKRRIVFTITTGAGSA
 5 KQSPSSKHSPLTASARGDCVPSHGDSTRRRGRKRASAGTPSLSAGVSPKRRALPSVAGLFTQPSGSPLN
 LNSMVSININQPLEITAISSPETSLSKSSPVYQDHDQPPVLKKERPLSQTNGAHYSPLTSDEEPGSEDEPS
 SARIERKIATISLESKSPPKTLENGGGLAGRKPAPAGEPVNSSKWKSTFSPISIDIGLAKSADSPLQASSA
 LSQNSLFTFRPALEEPSADAKLAAHPRKGFPGSLSGADGLSPGTNPANGCTFGGGLAADLSLHSFSDGAS
 10 LPHKGPEAAGLSSPLSFPSQRGKEGSDANPFLSKRQLDGLAGLKGEGRGKEAGEGGLPLCGPTDKTPLL
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 GPMSLQANLGSVAGSSVLSLFSVPAAGLVHVSSAATRLTNSHAMGSFSGVAGGTGGVFNHVPSPAS
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 VLHAPPPPNAAALPPPPTLLASNPEPALLQSLASLPPNQAFLPPTSAASLPPANASLSIKLTSPLHKGARP
 15 SFTVHHQPLPRLALAQAAPGIPQASATGPSAVWVSLGMPPPYAAHLSGVKPR

SEQ ID NO:320

Novel (maps to chromosome 4)

Novel (Chromosome 4) >

GGAATAAAAGAGTGGAAATGGGGATTTCCAGGTGCTCCCCTGGTTCATCTAGGCACCAGAGAGCTGCACTAGCAG
 20 GTCTATCATGAATCTCCTTGAATGCTCATTTTATGCTTACTTGATGTGTCTGTTTCTGGAAATGCAGTATTTT
 TAATGTATCTCAACAAAATATTTTATGATTAGTAAGCTTATTCCTATATAAAGGACAATTTTTTCTCTTTTTCAC
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 25 GAAAGATATGAGATCTTGAATTATATCTTACAGACTAGTCCCCAAAAGAATACGTGTTTCTTACCTTTAAT
 TTCTCATGGTAGTTAGTCTGTGAAT

SEQ ID NO:321

Novel peroxidase-like/ melanoma antigen

>GL2-86-4M13F Direction: sense

CGACCTGGCCAGCCACCGCGGCTGCTGCGGCAGGGCATCGTGCAGCGGTCCGGGAAGCCGCTGCTCCCCTTCGC
 30 CACCGGGCCGCCACGGAGTGCATGCGGGACGAGAACGAGAGCCCCATCCCCTGCTTCTGGCCGGGGACCACCG
 CGCCAACGAGCAGCTGGGCCTGACCAGCATGCACACGCTGTGGTTCCGCGAGCACAACCGCATTGCCACGGAGCT
 GCTCAAGCTGAACCCGCACTGGGACGGCGACACCATCTACTATGAGACCAGGAAGATCGTGGGTGCGGAGATCCA
 GCACATCACCTACCAGCACTGGCTCCCGAAGATCCTGGGGGAGGTGGGCATGAGGACGCTGGGAGAGTACCACGG
 35 CTACGACCCCGGCATCAATGCTGGCATCTTCAACGCCTTCGCCACCGCGGCCTTCAGGTTTGGCCACACGCTTGT
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 CTTCTCTCCCTTCCGGATTG

SEQ ID NO:322

>GL2_93_2B08_G3F1 Direction: sense

CGACCTGGCCAGCCACCGCGGCTGCTGCGGCAGGGCATCGTGCAGCGGTCCGGGAAGCCGCTGCTCCCCTTCGC
 40 CACCGGGCCGCCACGGAGTGCATGCGGGACGAGAACGAGAGCCCCATCCCCTGCTTCTGGCCGGGGACCACCG
 CGCCAACGAGCAGCTGGGCCTGACCAGCATGCACACGCTGTGGTTCCGCGAGCACAACCGCATTGCCACGGAGCT
 GCTCAAGCTGAACCCGCACTGGGACGGCGACACCATCTACTATGAGACCAGGAAGATCGTGGGTGCGGAGATCCA
 45 GCACATCACCTACCAGCACTGGCTCCCGAAGATCCTGGGGGAGGTGGGCATGAGGACGCTGGGAGAGTACCACGG
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SEQ ID NO:323

Novel peroxidase-like/ melanoma antigen>

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 GCTCAAGCTGAACCCGCACTGGGACGGCGACACCATCTACTATGAGACCAGGAAGATCGTGGGTGCGGAGATCCA
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 55 CTACGACCCCGGCATCAATGCTGGCATCTTCAACGCCTTCGCCACCGCGGCCTTCAGGTTTGGCCACACGCTTGT
 CAACCCACTGCTTTACCGGCTGGACGAGAACTTCCAGCCCATTGACAAAGATCACCTCCCCCTTCACAAAGCTTT
 CTTCTCTCCCTTCCGGATTGTGAATGAGGGCGGCATCGATCCGCTTCTCAGGGGGCTGTTCCGGGGTGGCGGGGAA
 AATGCGTGTGCTTCGCGAGTGTGAACACGGAGCTCACGGAGCGGCTGTTCTCATGGCACACAGGTGGCTCT
 60 GGACCTGGCGGCCATCAACATCCAGCGGGGCGGGACACGGGATCCACCCCTACCACGACTACAGGGTCTACTG
 CAATCTATCGGCGGCACACAGTTTCGAGGACCTGAAAAATGAGATTAAAAACCCTGAGATCCG

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WHAT IS CLAIMED IS:

1 1. A method for identifying a compound that modulates angiogenesis,
2 the method comprising the steps of:

3 (i) contacting the compound with a nucleic acid, or a polypeptide or a
4 fragment thereof encoded by a nucleic acid, wherein the nucleic acid hybridizes under
5 stringent conditions to a second nucleic acid comprising a nucleotide sequence selected
6 from the group consisting of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID
7 NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID
8 NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID
9 NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID
10 NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID
11 NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID
12 NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID
13 NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID
14 NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID
15 NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID
16 NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID
17 NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID
18 NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ
19 ID NO:523 ; and

20 (ii) determining the functional effect of the compound upon the nucleic
21 acid or polypeptide.

1 2. The method of claim 1, wherein the functional effect is determined
2 *in vitro*.

1 3. The method of claim 2, wherein the functional effect is a physical
2 effect.

1 4. The method of claim 2, wherein the functional effect is determined
2 by measuring ligand or substrate binding to the polypeptide.

1 5. The method of claim 2, wherein the functional effect is a chemical
2 effect.

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1 ID NO:76, SEQ ID NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID
2 NO:128, SEQ ID NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID
3 NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID
4 NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID
5 NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID
6 NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID
7 NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID
8 NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID
9 NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID
10 NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID
11 NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID
12 NO:521, and SEQ ID NO:523.

1 19. The method of claim 1, wherein the polypeptide comprises a
2 sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:33, SEQ ID
3 NO:44, SEQ ID NO:58, SEQ ID NO:64, SEQ ID NO:69, SEQ ID NO:71, SEQ ID
4 NO:77, SEQ ID NO:82, SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:121, SEQ ID
5 NO:129, SEQ ID NO:140, SEQ ID NO:154, SEQ ID NO:164, SEQ ID NO:170, SEQ ID
6 NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:203, SEQ ID
7 NO:287, SEQ ID NO:298, SEQ ID NO:309, SEQ ID NO:319, SEQ ID NO:325, SEQ ID
8 NO:331, SEQ ID NO:341, SEQ ID NO:352, SEQ ID NO:366, SEQ ID NO:378, SEQ ID
9 NO:385, SEQ ID NO:407, SEQ ID NO:409, SEQ ID NO:420, SEQ ID NO:429, SEQ ID
10 NO:438, SEQ ID NO:440, SEQ ID NO:446, SEQ ID NO:457, SEQ ID NO:463, SEQ ID
11 NO:482, SEQ ID NO:485, SEQ ID NO:494, SEQ ID NO:497, SEQ ID NO:499, SEQ ID
12 NO:520, SEQ ID NO:522, and SEQ ID NO:524.

1 20. The method of claim 1, wherein the compound is an antibody.

1 21. The method of claim 1, wherein the compound is an antisense
2 molecule.

1 22. The method of claim 1, wherein the compound is a small organic
2 molecule.

1 23. The method of claim 1, wherein the compound is a peptide.

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1 24. A method for identifying a compound that modulates angiogenesis,
2 the method comprising the steps of:

3 (i) contacting the compound with a nucleic acid, or a polypeptide or a
4 fragment thereof encoded by a nucleic acid, wherein the nucleic acid hybridizes under
5 stringent conditions to a second nucleic acid comprising a nucleotide sequence selected
6 from the group consisting of SEQ ID NO:3, SEQ ID NO:32, SEQ ID NO:43, SEQ ID
7 NO:57, SEQ ID NO:63, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:76, SEQ ID
8 NO:81, SEQ ID NO:86, SEQ ID NO:89, SEQ ID NO:120, SEQ ID NO:128, SEQ ID
9 NO:139, SEQ ID NO:153, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:169, SEQ ID
10 NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:202, SEQ ID
11 NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID
12 NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID
13 NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID
14 NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:340, SEQ ID NO:351, SEQ ID
15 NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID NO:406, SEQ ID NO:408, SEQ ID
16 NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID NO:437, SEQ ID NO:439, SEQ ID
17 NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID NO:481, SEQ ID NO:484, SEQ ID
18 NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID NO:519, SEQ ID NO:521, and SEQ
19 ID NO:523;

20 (ii) determining the functional effect of the compound upon the nucleic
21 acid or polypeptide; and

22 (iii) expressing the nucleic acid or polypeptide in a cell, contacting the
23 nucleic acid or polypeptide with the compound, and determining the phenotypic or
24 chemical effect upon the cell.

1 25. A method of modulating angiogenesis in a subject, the method
2 comprising the step of administering to the subject a therapeutically effective amount of a
3 compound identified using the method of claim 1.

1 26. The method of claim 25, wherein the subject is a human.

1 27. The method of claim 25, wherein the compound is an antibody.

1 28. The method of claim 25, wherein the compound is an antisense
2 molecule.

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12 NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:329, SEQ ID NO:330, SEQ ID
13 NO:340, SEQ ID NO:351, SEQ ID NO:365, SEQ ID NO:377, SEQ ID NO:384, SEQ ID
14 NO:406, SEQ ID NO:408, SEQ ID NO:419, SEQ ID NO:421, SEQ ID NO:428, SEQ ID
15 NO:437, SEQ ID NO:439, SEQ ID NO:445, SEQ ID NO:456, SEQ ID NO:462, SEQ ID
16 NO:481, SEQ ID NO:484, SEQ ID NO:493, SEQ ID NO:496, SEQ ID NO:498, SEQ ID
17 NO:519, SEQ ID NO:521, and SEQ ID NO:523.

1 35. An isolated nucleic acid, wherein the nucleic acid hybridizes
2 under stringent conditions to a polynucleotide comprising a nucleotide sequence selected
3 from the group consisting of SEQ ID NO:165, SEQ ID NO:202, SEQ ID NO:210, SEQ
4 ID NO:218, SEQ ID NO:227, SEQ ID NO:232, SEQ ID NO:248, SEQ ID NO:274, SEQ
5 ID NO:285, SEQ ID NO:286, SEQ ID NO:297, SEQ ID NO:307, SEQ ID NO:308, SEQ
6 ID NO:317, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:323, SEQ ID NO:324, SEQ
7 ID:329, and SEQ ID:330.

1 36. The isolated nucleic acid of claim 35, wherein the nucleic acid
2 comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:165,
3 SEQ ID NO:202, SEQ ID NO:210, SEQ ID NO:218, SEQ ID NO:227, SEQ ID NO:232,
4 SEQ ID NO:248, SEQ ID NO:274, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:297,
5 SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:320,
6 SEQ ID NO:323, SEQ ID NO:324, SEQ ID:329, and SEQ ID:330.

1 37. An isolated polypeptide comprising an amino acid sequence
2 selected from the group consisting of SEQ ID NO:287, SEQ ID NO:298, SEQ ID
3 NO:309, SEQ ID NO:319, SEQ ID NO:325, and SEQ ID NO:331.

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INFORMAL SEQUENCE LISTING

SEQ ID NO:1

5 ABC Transporter
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ATGTAGAACATGCGCTGGGGTGGGGGCTTGTAGAGCACACCACCGTACGTGGGCCAGAGCCCACCCAGGATCCGG
AATAGGGAGCTCTTGCCGAGCCATTGGGGCCTGTGATGAGCAGATGCATGCCTATCCTCCACCTGATGTTGAGG
10 CTGGGGCACCACAACCTCTCCTGANGGCGTGAACGAATCGGGGAATGTTTCCATCCCGTGCGAAGGAAGTCTNNGTG
TCGACGCGCTCTCGNCTCATCACAACACTCCAACAAACACGTGGGCTCGGAATCTTCAAGGGGGGGGGCCATCCAG
AAAACAGCGAACAACCACTGAACCTGGGGCGTAGATGAGGCTCNCACCCAAGATAAAACACCCCGGGGCGCCTT
GGGAAGACCCGGGTCTCCCGTCCCTTAANACGTTCTCCCATGTGGCGGGGCCACTCCCTTCTTGGTNACAACN
GGCTTGGCACCAAGACCAGGCCGCTCGCAACACCGCAGTCCGCGTTTTCTCAGACAGCAAAGTTTANCNCCCT
15 TTGTAGGAAGAAAACCCAAAGAGTTTCCGATTCCACAGGAGTTTGGGCCGCAATGCAACAGNCCCAGGAGCGGGG
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AGNTTACACNCCCGGGGGTATCCGGTCAAAGCAGCCNTTACCCTCCCTTNTTTTGGTGGTTAATACCGGCG
GAAAAAC

SEQ ID NO:2

20 ABC transporter>
GGACGCGCTGGTGCCCCGGGGAGGGGCGCCACCGGGGGAGGAGGAGGAG
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CCTGACCTCAGGGGCCAGGGCACTGACAGGACAGGAGAGCAAGTTCTC
25 CACTTGGGCTGCCCCAAGAGGGCCGCGACCTTGGAGGGCCCTGAGCCACC
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GGCCATCGCAAGGTTTCCAGTTGCCCTAGACAACAGGGCCAGGGTCAGAGC
AACAATCCTTCCAGCCACCTGCCCTCAACTGCTGCCCCAGGCACCAGCCCC
AGTCCCTACGCGGCAGCCAGCCAGGTGACATGCCGGTGCTCTCCAGGCC
CCGGCCCTGGCGGGGGAACACGCTGAAGCGCACGGCCGTGCTCCTGGCCC
30 TCGCGCCCTATGGAGCCCAAGTCTACCCCTTGGTGCGCCAGTGCCTG
GCCCCGGCCAGGGGTCTTCAGGCGCCCGCGGGGAGCCACGCAGGAGGC
CTCCGGGGTTCGCGCGGCCAAAGCTGGCATGAACCGGTATTCTGCAGC
GGCTCCTGTGGCTCCTGCGGCTGCTGTTCCCCCGGGTCTGTGCCGGGAG
ACGGGGCTGCTGGCCCTGCACTCGGCCGCTTGGTGAGCCGCACCTTCCT
35 GTCGGTGTATGTGGCCCGCCTGGACGGAAGGCTGGCCCGCTGCATCGTCC
GCAAGGACCCGCGGGCTTTTGGCTGGCAGCTGCTGCAGTGGCTCCTCATC
GCCCTCCCTGCTACCTTCGTCAACAGTGCCATCCGTTACCTGGAGGGCCA
ACTGGCCCTGTCGTTCCGCAGCCGTCTGGTGGCCACGCCTACCGCCTCT
ACTTCTCCAGCAGACACTACTACCGGGTCAGCAACATGGACGGGCGGCTT
40 CGCAACCCTGACAGTCTCTGACGGAGGACGTGGTGGCCTTTGCGGCCTC
TGTGGCCACCTCTACTCCAACCTGACCAAGCCACTCCTGGACGTGGCTG
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GCCTGGCCCTCGGCCATCGCCGCCCTCGTGGTGTTCCTCACGGCCAACGT
GCTGCGGGCCTTCTCGCCCAAGTTTCGGGGAGCTGGTGGCAGAGGAGCGC
45 GGCGGAAGGGGGAGCTGCGCTACATGCACTCGCGTGTGGTGGCCAACCTCG
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GCGCTCCTACCAGGACCTGGCCTCGCAGATCAACCTCATCTTCTGGAAC
GCCTGTGGTATGTTATGCTGGAGCAGTTCCCTCATGAAGTATGTGTGGAGC
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50 CTCAGAGTCAGATGCAGAGGCGTGAAGAAGGCAGCCTTGGAAGGAAGG
AGGAGGAGCTGGTGAGCGAGCGCACAGAAGCCTTCACTATTGCCCCGAAC
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GGAGGTGACGGAGCTGGCTGGCTACACAGCCCGGGTGCACGAGATGTTCC
AGGTATTTGAAGATGTTTCAGCGCTGTCACTTCAAGAGGCCAGGGAGCTA
55 GAGGACGCTCAGGCGGGTCTGGGACCATAGGCCGGTCTGGTGTCCGTGT
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TCATCTGCGAGAACATCCCCATCGTCACGCCCTCAGGAGAGGTGGTGGT
GCCAGCCTCAACATCAGGGTGGAGGAAGGCATGCATCTGCTCATCACAGG

CCCCAATGGCTGCGGCAAGAGCTCCCTGTTCCGGATCCTGGGTGGGCTCT
GGCCACGTACGGTGGTGTGCTCTACAAGCCCCACCCAGCGCATGTTT
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GATCTACCCGGAAGCTCAGTGGAGGACATGCAAAGGAAGGGCTACTCGGAGC
5 AGGACCTGGAAGCCATCCTGGACGTCGTGCACCTGCACCACATCCTGCAG
CGGGAGGGAGGTTGGGAGGCTATGTGTGACTGGAAGGACGTCCTGTGCGG
TGCGGAGAAGCAGAGAATCGGCATGGCCCGCATGTTCTACCACAGGCCCA
AGTACGCCCTCCTGGATGAATGCACCAGCGCCGTGAGCATCGACGTGGAA
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10 CACCCACCGGCCCTCCCTGTGGAAATACCACACACACTTGCTACAGTTCTG
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15 CAGGGTGCCTCCACCTGACACAACCGTCCCCGGCCCCCTGCCCGCCCCCA
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CACTCCCTGGGGCGCTGTTCCACAGTGACTGGGCCCTGTCCAGGGCAGT
20 GAGTCCCTCTACTTTGCTCCGTGGAGGAAGCTGGGGTACAAGGGGCCAGT
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CCCCTGGCACTGCAGGTGGCCTCCCTCCAGAGACTCGAGTCCCCATGATT
CCCTCCTCGTCAGTCTCTCAAAGACCCCATGGTCCATCCCCTGAGGGTGG
TCAGCCAAGGCTCCCGTTCCGTGGGATGCCATAAAAGCCGCCAGTGGGA
25 CCCACAGTCACACAGAGCGCCTCACCTGCATCCTCTCCCCCACAGAGCC
CCAAAGATCCCACGGGAGAGGGGAGAGGGACGCACAGCACTGCCTGCCAA
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CCTAATTTTATTGGATTCCCTATTCTGTAGCCATCTCCGTGGCCAATGTGAC
TACCGTGCCAGCAGCGGGGGCGGCCAGCCTCTGAGTCCCGTGGGGCCCC
30 GGCTCCACCGGTGCCAAACCCAGCCCCCTGCGGCCGTACCCCGCCAGCC
TACACTGCCAGCCGCCACCGGGGCACACGGGCCTCTGCTTGCCAGCCAGG
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35 CCCCAGTAAAAGCCTCCACTGGCAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO:3

>gi|7262392|ref|NM_000033.2| Homo sapiens ATP-binding cassette, sub-family
D (ALD), member 1 (ABCD1), mRNA

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GAAGAGACGCCCCCTCTGCCCGAGACCTCTCAAGGCCCTGACCTCAGGGGCCAGGGCACTGACAGGACAG
GAGAGCCAAGTTCTTCACTTGGGCTGCCCGAAGAGGCCGCGACCCCTGGAGGGCCCTGAGCCCACCGCAC
CAGGGGCCCCAGCACACCCCGGGGGCCTAAAGCGACAGTCTCAGGGGCCATCGCAAGGTTTCCAGTTGC
CTAGACAACAGGCCCAGGGTCAGAGCAACAATCCTTCCAGCCACCTGCCTCAACTGCTGCCCCAGGCACC
45 AGCCCCAGTCCCTACGCGGACAGCCAGCCAGGTGACATGCCGGTGTCTCCAGGCCCGGCCCTGGCGGG
GGAACACGCTGAAGCGCACGGCCGTGCTCCTGGCCCTCGCGGCTATGGAGCCACAAAGTCTACCCCTT
GGTGCGCCAGTGCCTGGCCCCCGGCCAGGGGTCTTCAGGCGCCCGCGGGGAGCCACGCAGGAGGCCTCC
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TGTTCCCCCGGGTCTGTGCGGGGAGACGGGGCTGCTGGCCCTGCACTCGGCCGCCTTGGTGAGCCGCAC
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5 CACTATTGCCCGCAACCTCCTGACAGCGGCTGCAGATGCCATTGAGCGGATCATGTCGTCGTACAAGGAG
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SEQ ID NO:4

>gi|7262393|ref|NP_000024.2| ATP-binding cassette, sub-family D (ALD),
member 1; adrenoleukodystrophy protein [Homo sapiens]
35 MPVLSRPRPWRGNTLKR TAVLLALAA YGAHKVYPLVRQCLAPARGLQAPAGEPTQEASGVAAAKAGMNRV
FLQRLWLLRLLFPRVLCRETGLLALHSAALVSRTFLSVYVARLDGRLARCIVRKDPRAFGWQLLQWLLI
ALPATFVNSAIRYLEGQLALSFRSRLVAHAYRLYFSQQTYYRVSNM DGLRLNPDQSLTEDVVAFAASVAH
LYSNLT KPLLDVAVTSYTL LRAARSRGAGTAWPSA IAGLVVFLTANVLRAFSPKFGELVAEEARRKGELR
40 YMHSRVVANSEEIAFYGGHEVELALLQRSYQDLASQINLILLERLWYVMLEQFLMKYVWSASGLLMVAVP
IITATGYSESDAEAVKKALEKKEEELVSERTEAFTIARNLLTAAADAIERIMSSYKEVTELAGYTARVH
EMFQVFEDVQRCHFKRPRELEDAQAGSGTIGRSGVRVEGPLKIRGQVVDVEQGIICENIPIVTPSGEVVV
ASLNIRVEEGMHLLITGPNCGKSSLFRILGGLWPTYGGVLYKPPPQRMFYIPQRPYMSVGLSLRDQVIYP
DSVEDMQRKGYSEQDLEAILDVVHLHHILQREGWEAMCDWKDVLSGGEKQIRIGMARMFYHRPKYALLDE
45 CTSAVSIDVEGKIFQAAKDAGIALLSITHRPSLWKYHTLLQFDGEGGWKFEKLDSAARLSLTBEKQRL
QQLAGIPKMQRRLQELCQILGEAVAPAHVPAPSPQGPGLQAST

SEQ ID NO:5

PCBP1
GL2_131_2_M13F
50 GCTGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACATCATGACCGGCCCAACATGCCATC
TTTAAGAGCTTTTCGTATGATCATCGACAAGACTGGAGGAAGATATCAACAGCTCCATGACCAACAGTACCGCGG
CACAGCAGGCCCCACGGGTACCCTGAGGCTGGATGGTGCCGGCCACCCAGATGCGGCTCCCTGATANGGGAAG
GCGGGTGTAAAGATCAAAGAGATCANNAGAGAGTACGGGGNGCGCAGGTCCAAGGAATGGCAGGAGGGATATGCAT
55 GCCCAAAAACAACCGAGACGGGCCAAANACCATAGCTGGACAGTGCCGAAGGACTGTCACCNAAAGAT

SEQ ID NO:6

GL2-77-2M13R
60 CGCTGCGGCCTCCCGCCCGCTCCCGCTCGCTCCCGCGGCCTCGCTCGCCTCGCGCCGGCAGTTTTGGGCCTACAC
CTCCCCCTCCCCCGCCAGCCGCCAAAGACTTGACCACGTAACGAGCCCAACTCCCCCGAACGCCGCCCGCGCTCG
CCATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCATTCCGGCTTCTTATGCACGGAAAGGAAG

TAGGAAGCATCATTTGGGAAGAAAGGGGAGTCGGTATAAGAGGATCCGCGAGGAGAGTGGNGCGCGGATCAACATC
TCGGAGGGGAATTTGTACCGGAGAGAATCATCACTCTGACCGGCNCCCAACAAATGCACAANCNTAAAGGACNTA
AACGACAAATAGAAATCATACGACAAANCTAGAGAGAAGATATCAACAGACTCCAATGAACAAAANAAACCGCAGA
GACAGACAGGAACCCCNNGGAAC

SEQ ID NO:7

GL2_209_3_M13R

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
ACCGATCTTGCCCGCCCGCGCAGATGACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCC
ACTTGGCGGAGACCTGGGCAGAGGCCGGTTCTCCAGGGCAATGACCCAGGCAAATCTGCTTGAGACACACCTA
CGGTGCACAGACTGGCGGGGCAACGGCACAGAGCAGAAGTTGCGGTGAACAGCTGGGCACACAAGGACGA

SEQ ID NO:8

GL2_131_3_M13F

CATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCATTTCGGCTTCTTATGCACGGAAGGAAGT
AGGAAGCATCATTTGGGAAGAAAGGGGAGTCGGTTAAGAGGATCCGCGAGGAGAGTGGCGCGCGGATCAACATCTC
GGAGGGGAATTTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAATGCCATCTTTAAGACTTTTCGCTATGAT
CATCGACAAGCTGGAGGAAGATATCAACAGCTCCATGACCAACAGTACCGCGGCCAGCAGGCCCCCGGTACCCCT
GAGGCTGGTGGTGCCGGCCACCCAGTGCGGCTCCCTGATTGGGAAAGGCGGGTGTAAAGATCAAAGAGATCCGCG

SEQ ID NO:9

GL2_205_C05_G3F1

AGAGGCGCAGCGGTTCGCGAGCGNTGGCTCAGTGTGCTGGGTTCTTGCGGCTTGAATCGAGTAGGCATCCAGAGGTG
GTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGCACCGATCTTGGCGCCCGCGCAGATGAC
TGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCCCTTGCGGAGACTGGGAGAGCGTCTCCAG
CATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCACGCCAGCGATGGTGTATGGCCCGCTCGGT
GGAGTTTGGGCAGCATATCCCCGCAACTGGACCTGCGCCCCCGTACTCTCGCGGATCTCTTTGATCTTACACCC
GCCTTTCCCAATCAGTGGAGCCGCACTGGGTGGGCGGCAACAACAGCTCAGGGTGACCGGGGGCCTGCTGGCCGC
GGTACTGTTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGATGATCATAGCGAAAGCCTTAAAGATGG
CATTGGTGGGGCCGGTCAGAGTGATGATTCTCTCCGACAATTCCTCCGAGATGTTTGATCCGGGCGCCACTC
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AATGGTGAGAGTCACATTTTAGTCCACTTTTCAGTCACACCGGGGATCCATGGNCGANCGGGCGGGGACGGGCGT
ACGGGGGAATTGGGCTCGTAACAGTTGGNCCAGNTCNTTAGGCGGTGAGAGGGAGGGAAGGGGAGGCCAACAAATGG
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SEQ ID NO:10

GL2_131_3_M13R

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CCTTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGC
ACGCCAGCGATGGTGTATGGCCCGCTCGGNGAGAGTTAGGGCAGCAATATCCCCACGAACAACTGGAATGACG
GCCCCGAAACTCTACGCNAGATACTCNTTAAGAACTTNACACCCGACTTATACCCAAATCAGAGAAGCCGCA
ACATGGGTGGCACCGAAAAACAACAGAACTCCAGGGGATGAACCGGAGGGGACATAGAAAGGGAACAGACGGGGA
TACCATAGGTCTGGCGGTCCCAATGGGGAGGCTGCNTATGAATAAATCCTTACCCTTCCCAANCACATAGGNA
TCCGGAATGGAAATCAAATAGGCGGAAAAANGTCCCTTTAAACAGAAAAATNGGGCAACTTNGNAAGGGGGGAC
CACGAGACANAACAAACCGAAGACATACGCAACCAGGGAACAAAANTTACCCGACACGCAGAGAAGGNTGGACA
NCACGGCACAGACCACAGTACCCATCNNAGACGGACCCG

SEQ ID NO:11

GL2_209_1_M13R

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
ACCGATCTTGCCCGCCCGCGCAGATGACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCC
CTTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCA
CGCCAGCGATGGTGTATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCACACCTGGACCTGCGCCCCGTA
CTCTCGCGGATCTCTTATGATCTTAACAACACACGACACNTTTTTNCANCAAAATCCAGGGAGCCGACAACATG
GAGTGAGCCCGACACCACACAGACCTCAGGGTGACCGGGGCTGCATGGCCGACGGATACNGAANGGTATGG
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AGATNGGGGCGGCCCGGGATCCAGGAAGGTTGCGACTAGGAACCTNACGTACCATTATCCCCAGGGAGAAAACNCC
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SEQ ID NO:12

GL2_131_2_M13R

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
GCCGATCTTGCCCGCCCGCGCAGATGACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCC
5 CTTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCA
CGCCAGCGATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCACGAGCANCTGGACCTGCGCCCCCGA
TACTCTCGACGGATCTCTTTGATCTTACACCCGACCTTTCCCAATCAGGGAAGCCGCACATGGGATGGCAGGCA
CCACCAGACCTCAGGGATGACCAGGGAGGCCTGCATGGACCGCAGGATACTGATAGGATCATGGAGNCTGATAGA
10 TATCTTCCCTCCAGACTATGNTCGATGATCAATAAGGCGGAAAAGGCCATAAANAGNAATGGGCAATTAGGGATC
GGGAGGACCAGGATCAAGA

SEQ ID NO:13

GL2_81_1_M13F

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCAGTAATGGCCGGGTTTTTTTGGGTNNGGGGCCAAAT
15 TTTCCGGGGGAAGGAGTAAAGGCCCCACCGGGACCAATTGGCAGGGTCCGCTGCNACCGATACTTGGCCTGCCGC
GCAGATGACTGGGGAGCTGGTCCGCATGGGCTGGTACGGAATGGTCATGACTCTCCCTTGCGGAGACTGGGAGAG
CGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCACGCCAGCGATGGTGATGGC
CCGCTCGGTGGAGTTGGGCAGCATATCCCCGCCACCTGGACCTGCGCCCCCGTACTCTCGCGGATCTCTTTGAT
20 CTTACACCCGCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCTCAGGGTGACCGGGGGCCT
GCTGGCCGCGGTACTGTTGGTTCATGGGGCTGTTGATATCTTCCTCCAGCTTGTCTG

SEQ ID NO:14

GL2_77_1_M13F

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
25 ACCGATCTTGCCCGCCCGCGCAGATACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCCC
TTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACCCCTCGGTGACAGACTGCGGCAC
GCCAGCGATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCGCCACCTGGACCTGCGCCCCCGTACT
CTCGCGGATCTCTTTGATCTTACACCCGCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCT
30 CAGGGTGACCGGGGGCCTGCTGGCCGCGGTACTGTTGGTTCATGGAGCTGTTGATAT

SEQ ID NO:15

GL2_77_1_M13R

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GGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGCCCCACCAATGCCATCTTTAAGG
35 CTTTCGCTATGATCATCGACAAGCTGGAGGAAGATATCAACAGCTCCATGACCAACAGTACCGCGGCCAGCAGGC
CCCCGGTCAACCTGAGGCTGGTGGTGCCGGCCACCCAGTGC GGCTCCCTGATTGGGAAAAGGCGGGTGTAAAGATCA
AAGAGATCCGCGAGAGTACGGGGGCGCAGGTCCAGGTGGCGGGGGATATGCTGCCCAACTCCACCGAGCGGGCCA
TCACCATCGCTGGCGTGCCGCAGTCTGTACCGAGGGTGTCAAGCAGATTTGCTTGGTTCATGCTGGAGACGCTCT
40 CCCAGTCTCCGCAAGGGAGAGTCATGACCATTCCTGACCAGCCATGCCGGCCAGCTCCCCAGTATCTGCGCGGG
CGGCCAAGATCGGTGCAGCGACGCTGCGGGCTACCCCATGCCACCCATGACCTGGAGGGACCACCTCTGGATGC
CTACTCGATTCAAG

SEQ ID NO:16

GL2_77_2_M13F

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
45 ACCGATCTTGCCCGCCCGCGCAGATACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCCC
TTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCAC
GCCAGCGATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCGCCACCTGGACCTGCGCCCCCGTACT
CTCGCGGATCTCTTTGATCTTACACCCGCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCT
50 CAGGGTGACCGGGGGCCTGCTGGCCGCGTACTGTTGGTTCATGGAGCTGTTGATATCTTCCTCCAGCTTGTCTGAT
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CGAGATGTTGATCCGCGCGCCATCTCTCGCGGATCTCTTAAACCGATCCCCTTTCTTCCCAATGATGCTTCTA
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SEQ ID NO:17

GL2_77_3_M13F

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
55 ACCGATCTTGCCCGCCCGCGCAGATACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCCC
TTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCAC
GCCAGCGATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCGCCACCTGGACCTGCGCCCCCGTACT

CTCGCGGATCTCTTTGATCTTACACCCGCCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCT
CAGGGTG

SEQ ID NO:18

GL2_77_4_M13F

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
ACCGATCTTGGCCGCCCCGCGCAGATACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCCC
TTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCAC
GCCAGCGATGGTGATGGCCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCCACCTGGACCTGCGCCCCCGTACT
CTCGCGGATCTCTTTGATCTTACACCCGCCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCT
CAGGGTGACCGGGGGCCTGCTGGCCGCGGTACTGTTGGTCATGGAGCTGTTGATATCTTCTCCAGCTTGTTCGAT
GATCATAGCGAAAGCCTTAAAGATGGCATTTGGTGGGGCCGGTCAGAGTGATGATTCTCTCCGACAATTTCCCTC
CGAGATGTTGATCCGCGCGCCACTCTCTCGCGGATCTCT

SEQ ID NO:19

GL2_77_5_M13F

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
ACCGATCTTGGCCGCCCCGCGCAGATACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCCC
TTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCAC
GCCAGCGATGGTGATGGCCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCCACCTGGACCTGCGCCCCCGTACT
CTCGCGGATCTCTTTGATCTTACACCCGCCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCCT
CAGGGTGACCGGGGGCCTGCTGGCCGCGGTACTGTTGGTCATGGAGCTGTTGATATCTTCTCCAGCTTGTTCGAT
GATCATAGCGAAAGCCTTAAAGATGGCATTTGGTGGGGCCGGTCAGAGTGATGATTCTCTCCGACAATTTCCCTC
CGAGATGTTGATCCGCGCGCCACTCTCTCGCGGATCTCTTAAACCGACTCCCCTTTCTTCCCAATGATGCTTC
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SEQ ID NO:20

GL2_131_1_M13F

NGCTGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACATCATGACCGGCCCCACCAATGCCA
TCTTTAAGAGCTTTCGCTATGATCATCGACAAGACTGGAGGAAGATATCAACAGCTCCATGACCAACAGTACCGC
GGCACAGCAGGCCCCACGGGTACCCCTGAGGCTGGATGGTGGCCGCCACCCAGATGCGGCTCCCTGATANGGGAA
AGGCGGGTGTAAGATCAAAGAGATCANNAGAGAGTACGGGGNGCGCAGGTCCAAGGAATGGCAGGAGGGATATGC
ATGCCCCAAAACAACCGAGACGGGCCAAANACCATAGCTGGACAGTGCCGAAGGACTGTCCACNGAAGAT

SEQ ID NO:21

GL2_131_1_M13R

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
ACCGATCTTGGCCGCCCCGCGCAGATGACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCC
CTTGCGGGGAGAACTGGGGAAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGC
GGCACGCCAGCAATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCCACCTGGACCTGCGCCCCC
GTACTCTCGCGGATCTCTT

SEQ ID NO:22

GL2_209_2_M13R

GGCGCCAGTGCTGCNATTCGNTATCTCTCGGCATGGACGAGCTGGTACAAAAAGGAGGAGGGCCCGCAAGTC
GGTGGCAGCGGTGGCTCCAGTGTTGGCTGGGGGGTTCTGCGGCTTGAATCGGAAGGTTTAAGGGGGCATCCAGA
GGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGCACCGATCTTGGCGCCGCGCCAGA
TGACTGGGGGAAGCTGGCCGGCATGGGCTTGGTACGGAA

SEQ ID NO:23

GL2_209_3_M13F

CGCTGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAATGCCATCT
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GCAGGCCCCCGGTACCCCTGAGGCTGGTGGTGCCGGCCACCCAGTGCGGCTCCCTGATTGGGAAAGGCGGGTGTA
AGATCAAAGAGATCCGCGAGAGTACGGGGGCGCAGGTCCAGGTGGCGGGGGATATGCTGCCCCAACTCCACCGAGC
GGCCATCACCATCGCTGGCGTCCGCGAGTCTGTCCAGGAGTGTGTCAAGCAGATTTGCCTGGTCATGCTGGAGA
CGCTCTCCAGTCTCCGCAAGGGAGAGTCATGACCATTCCGTACCCAGCCCCATGCCGGCCAGCTCCCCAGTCATCT
GCGCGGGCGGCCAAAGATCGGNGCAGCGACGCTGCGGGCTACCCACAATAGACACACCATGACCTGGAGGGAAC
AACTACTGGATGCTACATCCGANNTCAAGCCGGAAAAANCCAACAACTGGGAACCACACGATAGACACACGTCG
CCTTGGCAGGCATCACACCTATGAA

SEQ ID NO:24

GL2_209_4_M13R

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5 ACCGATCTTGGCCGCCCCGCGCAGATGACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCC
CTTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCA
CGCCAGCGATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCCACCTGGACCTGCGCCCCCGTAC
TCTCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGGCCGGCACCACCAGCC
10 TCAGGGTGACCGGGGGCCTGCTGGCCGCGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGACTTGTGCG
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CCTTCGAAGATGTGATCCGCGCGCACATCTCCTCGCGGATCTCTTAAACCGAGTCCCNTTTCATCCAAGAATGNA
CTCCTACTCCCTATACCGGCCATAANAANGCCGAAATGGGTGAAGAANGTCACACTTTAAGGTCCACACTTATCA
GCACANCCCGGGATCCACAGGGGCAAACGGCCGGGAGCAGGAAGGCCCGAGAGGCCCGGAAAAACCCANACAACA
GGGTTAAATAAAAATAAAGGGCCGCAAAAAAATCGAAGGAATCGAGAAAAACANGCCGCCAATCGGCACACTAA
15 TGAACGATAACAACATAAGACAGA

SEQ ID NO:25

GL2_131_4_M13F

CGCTGCGGGCTCCCGGCCCCGGCTCGCCATGGATGGCCGGTGTGACTGAAAGTGGACTAAATGTGANTCTCACCAT
20 TCGGCTTCTTATGCACGGAAAGGAAGTAGGAAGCATCATTGGGAAGAAAGGGGAGTCNGT'TAAGANGATCCGTGA
GGAGAGTGGCGCGCGGATCAACTATCTCGTGAGGGAATTGTCNCGGAGAGAANCATCACTCTGACCGGCCCCACC
AATGANCANCTTTAAGGCTTGCGCATATGATCATCGACAAGCNGGAGGAAGATATCAACAGANTACCATGACC
CAGTACCGCGGGACAGACANGCCCCCGGNCAGACANGAGGCTGGAGGNAGCCCGACCAGC

25 SEQ ID NO:26

GL2_205_C04_G3F1

CTTGAATCGAGTAGGCATCCAGAGGTGGTCCCTCCAGGTCATGGGTGGCATGGGGGTAGCCCGCAGCGTCGCTGC
ACCGATCTTGGCCGCCCCGCGCAGATGACTGGGGAGCTGGCCGGCATGGGCTGGTACGGAATGGTCATGACTCTCC
30 CTTGCGGAGACTGGGAGAGCGTCTCCAGCATGACCAGGCAAATCTGCTTGACACACTCGGTGACAGACTGCGGCA
CGCCAGCGATGGTGATGGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGCACTGGACCTGCGCCCCCGTACTC
TCGCGGATCTCTTTGATCTTACACCCGCCTTTCCCAATCAGGGAGCCGCACTGGGTGTGCCGGCACCACCAGCCT
CAGGGTGACCGGGGGCCTGCTGGCCGCGGTACTGTTGGTCATGGAGCTGTTGATATCTTCCCTCCAGCTTGTGAT
GATCATAGCGAAAGCCTTAAAGATGGCATTGGTGGGGCCGGTCAGAGTGATGATTCTCTCCGGACAATTCCTC
CGAGATGTTGATCCGCGCGCCACTCTCCTCGCGGATCTCTTAAACGATCCCCCTTCTTCCCAATGATGCTTCCA
35 TACTTCTTTCCGTGCATAAGAAGCCGAAATGGTGAGAGTCACCATTTAGGTCCACTTTTCAGTCAACACCGGATC
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SEQ ID NO:27

GL2_77_4_M13R

CGCTGCGGCTCCCGCCCCGCTCCCGCTCGCTCCCGCGGCCCTCGCTCGCCTCGCGCCGGCAGTTTTGGGCCTACA
40 CCTCCCCCTCCCCCGCCAGCCGCCAAAGACTTGACCACGTAACGAGCCCAACTCCCCCGAACGCCGCCCGCGCT
CGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCATTGGCTTCTTATGCACGGAAAGGA
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45 TGATCATCGACAAGCTGGAGGAAGATATCAACAGTCCATGACCAACAGTACCGCGGCCAGCAGGCCCCCGGTCA
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SEQ ID NO:28

GL2_77_5_M13R

CGCTGCGGCTCCCGCCCCGCTCCCGCTCGCTCCCGCGGCCCTCGCTCGCCTCGCGCCGGCAGTTTTGGGCCTACA
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CGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCATTGGCTTCTTATGCACGGAAAGGA
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50 CTCGGAGGGGAATTTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAATGCCATCTTTAAGGCTTTCGCTA
GATCATCGACAAGCTGGAGGAAGATATCAACAGTCCATGACCAACAGTACCGCGGCCAGCAGGCCCCCGGTCA
CCTGAGGCTGGTGGTNGCCGGCCACCCAGTGCGGCTCCCTGATTGGGAAAGGCGGGTGTAAAGATCAAAGAGATCCG
55 CGAGAGTACGGGGGCGCAGGTCCAGGT

SEQ ID NO:29

GL2_209_4_M13F

CGCTGCGGCTCCCGCCCGCGCTCGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCAT
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 5 GGAGAGTGGCGCGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAA
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 CGCGGCCAGCAGGCCCCCGGTCACCTGAGGCTGGTGGTGCCGGCCACCCAGTGGGCTCCCTGATTGGGAAAGG
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 10 ACCGAGCGGGCCATCACCATCGCTGGCGTGCCGAGTCTGTTACCCGAAGTGTGTACAGCNAGATTTGCCTGGT
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 AACCAACAGCCCCCAAATGGGCCCCGGGGCCACAGGCTCCCCCAAGGACANATCNGGAGGCCGGGGGGACGGGGCC
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SEQ ID NO:30

GL2_205_C06_G3F1

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 20 CCAGCGATGGTGTATGNGCCCGCTCGGTGGAGTTGGGCAGCATATCCCCCGGCACCTGGANCTGCGCCCCCGTACT
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 CCTCAGGGTGACCGGGGTGCTGCTGGCCGCGGTACTGTTGGTCATGGAGCTGTTGATATCTTCTCCAGCTTG
 TCGATGATCATAGCGAAAGCCTTAAAGATGGCATTTGGTGGGGCCGGTCAGAGTGATGATTCTCTCCGACAATTC
 CCTCCGAGATGTTGATCCGCGCGCAATCTCCTCGCGGATCCTCTTAACGAATCCCCTTTCTTCCAAANGATGAT
 25 TCCTANTTCTTTACCGTGCATATAGAAAGCCCGAAATGGTTGACGAGTCCACATTTAGTCCACACTTTTCAGTCA
 CACCCGGAATCCAATGGGCGAGCGGAGGGACGGAGACGGGGGAAGATGGGCGCCGAACGTTGGGCCAAGAATA
 GAGCAAGAGAGNAGAAGGAAAAANGACAAAGAGCACAAACAGAAAAAAGACAAAAAGGNAGCAAGCACACNAAAA
 AA

SEQ ID NO:31

GL2_209_2_M13F

CGCTGCGGCTCCCGCCCGCGCTCGCCATGGATGCCGGTGTGACTGAAAGTGGACTAAATGTGACTCTCACCAT
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 GGAGAGTGGCGCGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAATCATCACTCTGACCGGCCCCACCAA
 35 TGCCATCTTTAAGGCTTTTCGCTATGATCATCGACAAGCTGGAGGAAGATATCAACAGCTCCATGACCAACAGTAC
 CGCGGCCAGCAGGCCCCCGGTCACCTGAGGCTGGTGGTGCCGGACACCCAGTGGGCTCCCTGATTGGGAAAGG
 CGGGATGTAAGATCAAAG

SEQ ID NO:32

>gi|14141164|ref|NM_006196.2| Homo sapiens poly(rC) binding protein 1
 (PCBP1), mRNA

GACGCCGCCCGACCTGCGACTACGCTGCGGACTCCCGCCCGCTCCCGCTCGCTCCCGCGGTCTCTCGCTC
 GCCTCGCCCGGTAGTTTTGGGCCTACACCTCCCCCTCCCCCGCCAGCCGCAAAGACTTGACCACGTAA
 CGAGCCCCAACTCCCCGAACGCCGCCCGCGCTCGCCATGGATGCGGGTGTGACTGAAAGTGGACTAAAT
 45 GTGACTCTCACCATTTCGCTTCTTATGCACGGAAGGAAGTAGGAAGCATCATTTGGGAAGAAAGGGGAGT
 CGGTAAAGAGGATCCGCGAGGAGAGTGGCGCGCGGATCAACATCTCGGAGGGGAATTGTCCGGAGAGAAT
 CATCACTCTGACCGGCCCCACCAATGCCATCTTTAAGGCTTTTCGCTATGATCATCGACAAGCTGGAGGAA
 GATATCAACAGCTCCATGACCAACAGTACCGCGGCCAGCAGGCCCCCGGTCACCTGAGGCTGGTGGTGC
 CGGCCACCCAGTGCGGCTCCCTGATTGGGAAAGGCGGGTGTAAAGATCAAAGAGATCCGCGAGAGTACGGG
 50 GGCGCAGGTCCAGGTGGCGGGGGATATGCTGCCCAACTCCACCGAGCGGGCCATCACCATCGCTGGCGTG
 CCGCAGTCTGTACCGAGTGTGTCAAGCAGATTTGCTGGTTCATGCTGGAGACGCTCTCCAGTCTCCGC
 AAGGAGAGTCATGACCATTCCTGACAGCCATGCGCGGCGAGCTCCCGAGTCATCTGCGCGGGCGGCCA
 AGATCGGTGCAGCGACGCTGTGGGCTACCCCCATGCCACCCATGACCTGGAGGGACCACCTCTAGATGCC
 TACTCGATTCAAGGACAACACACCATTTCTCGCTCGATCTGGCCAAGCTGAACCAGGTGGCAAGACAAC
 55 AGTCTCACTTTGCCATGATGCACGGCGGGACCGGATTGCGCGGAATTGACTCCAGCTCTCCAGAGGTGAA
 AGGCTATTGGGCAAGTTTGGATGCATCTACTCAAACCCCATGAACTCACCATTCCAAATAACTTAATT
 GGCTGCATAATCGGGCGCCAAGGCGCCAACATTAATGAGATCCGCCAGATGTCCGGGGCCAGATCAAAA
 TTGCCAACCCAGTGAAGGCTCCTCTGGTAGGCAGGTTACTATCACTGGCTCTGCTGCCAGTATTAGTCT
 GGCCCAGTATCTAATCAATGCCAGGCTTTCTCTGAGAAGGGCATGGGGTGCAGCTAGAACAGTGTAGGT
 60 TCCCTCAATAACCCCTTTCTGCTGTTCTCCCATGATCCAATGTGTAATTTCTGGTCAGTGATTCCAGGT

TTTAAATAATTTGTAAGTGTTCAGTTTCTACACAACCTTTATCATCCGCTAAGAATTTAAAAATCACATTC
TCTGTTTCAGCTGTTAATGCTGGGATCCATATTTAGTTTTATAAGCTTTTCCCTGTTTTTAGTTTTGTTTT
GGGTTTTTTGGCTCATGAATTTTATTTCTGTTTGTGCGATAAGAAATGTAAGAGTGGAATGTTAATAAATT
TCAGTTTAGTTCTGTAATGTCAAGAATTTAAGAATTAACAAACGGATTGGTTAAAAAATGCTTCATATTT
5 GAAAAAGCTGGGAATTGCTGTCTT

SEQ ID NO:33

>gi|5453854|ref|NP_006187.1| poly(rC)-binding protein 1; heterogenous
nuclear ribonucleoprotein X; alpha-CP1; nucleic acid binding protein sub
10 2.3; heterogenous nuclear ribonucleoprotein E1 [Homo sapiens]
MDAGVTESGLNVTLTIRLLMHGKEVGSIIIGKKGESVKRIRESGARINISEGNCPERIITLTGPTNAIFK
AFAMIIDKLEEDINSSMTNSTAASRPPVTLRLVVPATQCSLIGKGGCKIKEIRESTGAQVQVAGDMLPN
STERAITIAGVPQSVTECVKQICLVMLETLQSPOQGRVMTIPYQMPASSPVICAGGQDRCSDAVGYPHA
THDLEGPPLDAYSIQGQHTISPLDLAKLNQVARQQSHFAMMHGGTGFAGIDSSPEVKGYWASLDASTQT
15 THELTIPNNLIGCIIGROGANINEIRQMSGAQIKIANPVEGSSGRQVTITGSAASISLAQYLINARLSSE
KGMGCS

SEQ ID NO:34

Amino acid transporter (SLC1A5)

>G3_8_66_PCR_G3F1

CTCGCCCGGTGAAGACGAAGTGCCTCAAGCGCTCCAGTGCCCAACGCCAGCGCACCCCCGGCCCCCGACACCCC
CAGTCCCACGCCACGCCCGCCACCACGGCACCACCTTACAACAACGGTTGCTCAAGCAGCGGCACCTTGTCCTGGGA
ACCGCAGTAGCCGCTGCTCCCGCCTTGCTCGATGGAGGCCAGCGCCAGGCCCCGTTGGCGGTGGCTCC
25 GCCGCTCGAGCCCCCTTGAGTCTCGAGGAGGATCGGCCACCATGATGGAAGCACCGGGGTTTCTTAGCGCCTGGA
AGCTGGCTGGGAGCGCTTGGGCTCCTTCCCAGGACCCGACGTTCTTAGGACTGAGTTGAGTAACAGCACCTGGAG
ACTGGAACCTTGGAGGGCTCCTTAGAGTTGTGAGTTCACAGCACTAAGTTCCTTGGCTCTTGAAGCTGGAGTGT
TTAAATCCCCAGGCTGGGCGCTAGGCTTCTC

SEQ ID NO:35

>GL3_8.66_A_M13F

CTCGCCCGGGAAGACGAAGGCGCTCAAGCGCTCCAGGCCCAACGCCAGCGCACCCCCGGCCCCCGACACCCCCAG
TCCAGCGCCACGCCCGCCACCACGGCCACCACTGTGAGCAGCACAAGCAGGTTGGCTCGAAGGCAGCGGCGCAC
CTGGTCCCGGGAACCGCAGTACCGCGCTGCTGCCGCGCTTGGTCTCGATGGAGGCCAGCGCCAGGCCCCCGTT
35 GGCGGTGGGCTCCGCCGCTGCGAGCCCCCTTGGAGTCTCGAGGAGGATCGGCCACCATGATGGGAAGCACCGGGGT
TTCTTAGCGCCTGGAAGCTGGCTGGGAGCGCTTGGGCTCCTTCCCAGGACCCGACGTTCTTAGGACTGAGTTGAG
TAACAGCACCTGGAGACTGGAACCTTGGAGGGCTCCTTAGAGTTGTGAGTTCACAGCACTGAAGTTCCTTGGCTC
TTGGAAGCTGGAGTGTTTAAATCCCCAGGCTGGGCGCTGAGGCTTCTCTGCTCTGCCCCGTGTGCCAGATGTCC
GAAAGCTGGGAGTTCGGAGCGCCCCGGGTTCCT

SEQ ID NO:36

>GL3_8.66_A_M13R Direction: anti-sense

CTCCTAGGGCCAAGGAACCCGGGCGCTCCGAACTCCAGCTTTCGGACATCTGGCACACGGGGCAGAGCAGAGAA
GCCTCAGCGCCAGCCTGGGGAATTTAAACACTCCAGCTTCCAAGAGCCAAGGAACCTCAGTGCTGTGAATCAC
45 AACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGTGCTGTTACTCAACTCAGTCTTAGGAACGTCGGGTCCTG
GGAAGGAGCCCAAGCGCTCCAGCCAGCTTCCAGGCGCTAAGAAAACCCCGGTGCTTCCCATCATGGTGGCCGATC
CTCCTCGAGACTCCAAGGGGCTCGCAGCGGCGGAGCCACCGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGG
ACCAAGGCGCGGCAGCAGGCGGCTACTGCGGTTCCTGGGACCAGGTGCGCCGCTGCCTTCGAGCCAACCTGCTTG
TGCTGCTGACAGTGGTGGCCGTGGTGGCCGGCGTGGCGCTGGGACTGGGGGTGTCGGGGGCGGGGGTGGCGCTGG
50 CGTTGGGCTGGAGCGCTTGAGCGCTTCGTCTTCCCGGGCAGCCGGAACCCAGCACACTGGAGCCACC

SEQ ID NO:37

>GL3_8.66_B_M13F Direction: sense

CTATAGGGCGAATGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATTCGCCCT
TCTCTCGGCATGGACGAGCTGTACAAGGAGGAGGCCGCCAAGGCCGGTGGCAGCGGTGGCTCCAGTGTGCTGGGT
55 TCCGCTCGCCCGGAAGACGAAGGCGCTCAAGCGCTCCAGGCCCAACGCCAGCGCACCCCCGGTCCCCGACACC
CCCAGTCCCAGCGCCACGCCGGCCACCACGGCCACCACCTGTGTCAGCAGCACAAGCAGGTTGGCTCGAAGGCAGCGG
CGCACCTGGTCCCGGGAACCGCAGTAGCCGCTGCTGCCGCGCTTGGTCTCGATGGAGGCCAGCGCCAGGCCC
CCGTTGGCGGTGGGCTCCGCCGCTGCGAGCCCCCTTGGAGTCTCGAGGAGGATCGGTACCATGATGGGAAGCACC
GGGGTTTCTTAGCGCCTGGAAGCTGGCTGGGAGCGCTTGGGCTCCTTCCCAGGACCCGACGTTCTTAGGACTGAG
60 TTGAGTAACAGCACCTGGAGACTGGAACCTTGGAGGGCTCCTTAGAGTTGCGAGTTCACAGCACTGAAGTTCCTT

GGCTCTTGGAAGCTGGAGTGTAAATTTCCCAAGGCTGGGCGCTGAGGCTTCTCTGCTCTGCCCCGTGTGCCAGA
TGTCCGAAAGCTGGGAGTTCGGAGCGCCCGGGTTCCTTGGCCCTAGGAG

SEQ ID NO:38

5 >GL3_8.66_B_M13R Direction: anti-sense
CTCCTAGGGCCAAGGAACCCGGGCGCTCCGAAGTCCAGCTTTCGGACATCTGGCACACGGGGCAGAGCAGAGAA
GCCTCAGCGCCCAGCCTGGGGAATTTAAACACTCCAGCTTCCAAGAGCCAAGGAACCTTCAGTGCTGTGAACTCGC
AACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGTGCTGTTACTCAACTCAGTCCTAGGAACGTCGGGTCTTG
10 GGAAGGAGCCCAAGCGTCCCAGCCAGCTTCCAGGCGCTAAGAAACCCCGGTGCTTCCCATCATGGTGACCGATC
CTCCTCGAGACTCCAAGGGGCTCGCAGCGGCGGAGCCACCGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGG
ACCAAGGCGCGCAGCAGGCGGCTACTGCGGTTCCCGGGACCAGGTGCGCCGCTGCCTTCGAGCCAACCTGCTTG
TGCTGCTGACAGTGGTGGCCGTGGTGGCCGGCGTGGCGCTGGGACTGGGGGTGTGCGGGACCGGGGTGCGCTGG
CGTTGGGCTTGAGCGCTTGAGCGCCTTCGTCTTCCCGGGCGAGCCGGAACCCAGCACACTGGAGCCACCGCTGC
15 CACCGGCTTGGCGGCTCCTCCTTGACAGCTCGTCCATGCCGAGAGAAGGGCGAATTCTGCAGATATCCATCA
CACTGG

SEQ ID NO:39

>GL3_8.66_C_M13F Direction: anti-sense
CTCCTAGGGCCAAGGAACCCGGGCGCTCCGAAGTCCAGCTTTCGGACATCTGGCACACGGGGCAGAGCAGAGAA
20 GCCTCAGCGCCCAGCCTGGGGAATTTAAACACTCCAGCTTCCAAGAGCCAAGGAACCTTCAGTGCTGTGAACTCAC
AACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGTGCTGTTACTCAACTCAGTCCTAGGAACGTCGGGTCTTG
GGAAGGAGCCCAAGCGTCCCAGCCAGCTTCCAGGCGCTAAGAAACCCCGGTGCTTCCCATCATGGTGGCCGATC
CTCCTCGAGACTCCAAGGGGCTCGCAGCGGCGGAGCCACCGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGG
ACCAAGGCGCGCAGCAGGCGGCTACTGCGGTTCCCGGGACCAGGTGCGCCGCTGCCTTCGAGCCAACCTGCTTG
25 TGCTGCTGACAGTGGTGGCCGTGGTGGCCGGCGTGGCGCTGGGACTGGGGGTGTGCGGGGCGCGGGGTGCGCTGG
CGTTGGGCTTGAGCGCTTGAGCGCCTTCGTCTTCCCGGGCGAGCCGGAACCCAGCACACTGGAGCCACCGCTGC
CACCGGCTTGGCG

SEQ ID NO:40

30 >GL3_8.66_C_M13R Direction: sense
GATCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTCTCTCGGCATGGACGAGCTGTACAAGGAGGAGGC
CGCCAAGGCCGGTGGCAGCGGTGGCTCCAGTGTGCTGGGTTCCGGCTCGCCCCGGGAAGACGAAGGCGCTCAAGCG
CTCCAGGCCCAACGCCAGCGCACCCCCGGCCCCCGACACCCCCAGTCCAGCGCCACGCCGGCCACCACGGCCAC
CACTGTTCAGCAGCACAAAGCAGGTTGGCTCGAAGGCAGCGCGCACCTGGTCCCGGGAACCGCAGTAGCCGCTGC
35 TGCCGCGCTCTGGTCTCGATGGAGGCCAGCGCAGGCCCCCGTTGGCGGTGGGCTCCGCGCTGCGAGCCCCCTT
GGAGTCTCGAGGAGGATCGGCCACCATGATGGGAAGCACCGGGGTTTCTTAGCGCTGGAAGCTGGCTGGGAGCG
CTTGGGCTCCTTCCAGGACCCGACGTTCTTAGGACTGAGTTGAGTAACAGCACCTGGAGACTGGAACCTTTGGAG
GGCTCCTTAGAGTTGTGAGTTCACAGCACTGAAGTTCTTGGCTCTTGGAAGCTGGAGTGTAAATTTCCCAAGG
40 CTGGGCGCTGAGGCTTCTCTGCTCTGCCCCGTGTGCCAGATGTCCGAAAGCTGGGAGTTCGGAGCGCCCGGGTTC
CTTGGCCCTAGGAG

SEQ ID NO:41

>GL3_8.66_D_M13F Direction: N/A
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45 CTTCTCTCGGCATGGACGAGCTGTACAAGGAGGAGGCCCGCAAGGCCGGTGGCAGCGGTGGCTCCAGTGTGCTGG
GTTCCGGCTCGCCGGAAGACGAAGGCGCTCAAGCGCTCCAGGCCCAACGCCAGCGCACCCCCGGCCCCCGACA
CCCCAGTCCAGCGCCACGCCGGCCACCACGGCCACCACTGTTCAGCAGCACAAAGCAGGTTGGCTCGAAGGCAGC
GGCGCACCTGGTCCCGGGAACCGCAGTAGCCGCTGCTGCCGCGCTTGGTCTCGATGGAGGCCAGCGCCAGGC
CCCCGTTGGCGGTGGGCTCCGCGCTGCGAGCCCCCTTGAGTCTCGAGGAGGATCGGCCACCATGATGGGAAGCA
50 CCGGGGTTTCTTAGCGCTGGAAGCTGGCTGGGAGCGCTTGGGCTCCTTCCAGGACCCGACGTTCTTAGGACTG
AGTTGAGTAACAGCACCTGGAGACTGGAACCTTTGGAGGGCTCCTTAGAGTTGTGAGTTCACAGCACTGAAGTTC
TTGGCTCTTGGAAGCTGGAGTGTAAATTTCCCAAGGCTGGGCGCTGAGGCTTCTCTGCTCTGCCCCGTGTGCCA
GATGTCCGAAAGCTGGGAGTTCGGAGCGCCCGGGTTCCTTGGCCCTAGGAGCCGC

55 SEQ ID NO:42

>GL3_8.66_D_M13R Direction: anti-sense
CTCCTAGGGCCAAGGAACCCGGGCGCTCCGAAGTCCAGCTTTCGGACATCTGGCACACGGGGCAGAGCAGAGAA
GCCTCAGCGCCCAGCCTGGGGAATTTAAACACTCCAGCTTCCAAGAGCCAAGGAACCTTCAGTGCTGTGAACTCAC
AACTCTAAGGAGCCCTCCAAAGTTCCAGTCTCCAGGTGCTGTTACTCAACTCAGTCCTAGGAACGTCGGGTCTTG
60 GGAAGGAGCCCAAGCGTCCCAGCCAGCTTCCAGGCGCTAAGAAACCCCGGTGCTTCCCATCATGGTGGCCGATC

CTCCTCGAGACTCCAAGGGGCTCGCAGCGGCGGAGCCCCACCGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGG
ACCAAGGCGCGGCAGCAGGCGGCTACTGCGGTTCCCCGGGACCAGGTGCGCCGCTGCCCTTCGAGCCAACCTGCTTG
TGCTGCTGACAGTGGTGGCCGTGGTGGCCGGCGTGGCGCTGGGACTGGGGGTGTCGGGGGCGGGGGTGCCTGG
CGTTGGGCTTGGAGCGCTTGGAGCGCTTCGTCTTCCGGGCGAGCCGGAACCCAGCACACTGGAGCCACCGCTGC
5 CACCGGCCTTGGCGGCCTCCTCCTTGTACAGCTCGTCCATGCCGAGAGAAGGGCGAATTCTGCAGATATNCATCA
CACTGGCGG

SEQ ID NO:43

>gi|5032092|ref|NM_005628.1| Homo sapiens solute carrier family 1 (neutral
10 amino acid transporter), member 5 (SLC1A5), mRNA
GTAACCGCTACTCCCGGACACCAGACCACCGCCTTCCGTACACAGGGGCCCCGCATCCCACCCTCCCGGAC
CTAAGAGCCTGGGTCCCCCTGTTTCCGGAGGTCCGCTTCCCGGCCCCAGATTCTGGCATCCCAGCCCTCA
GTGTCCAAAGACCCAGGCAGCCCGGGTCCCCGCTCCCGGATCCAGGCGTCCGGGATCTGCGCCACCAGAA
15 CCTAGCCTCCTGCAGACCTCCGCCATCTGGGGGCACTCAACCTCCTGGAGCCAAGGGGCCCCACGTCCAC
CCAGAGAAACTCTCGTATTCCCAGCTCCTAGGGCCAAGGAACCCGGGCGCTCCGAACCTCCCAGCTTTCGG
ACATCTGGCACACGGGGCAGAGCAGAGAAGCTCAGCGCCAGCCTGGGGAATTTAAACACTCCAGCTTCC
AAGAGCCAAGGAACCTTCAGTGCCTGTGAACCTCAAACTCTAAGGAGCCCTCCAAAGTTCAGTCTCCAGGT
GCTGTTACTCAACTCAGTCTTAGGAACGTGGGTCTGGGAAGGAGCCCAAGCGCTCCAGCCAGCTTCC
AGGCGCTAAGAAACCCCGTGCTTCCCATCATGGTGGCCGATCCTCCTCGAGACTCCAAGGGGCTCGCAG
20 CGGCGGAGCCACCGCCAACGGGGGCTGGCGCTGGCCTCCATCGAGGACCAAGGCGCGGCAGCAGGCGG
CCTATGCGGTTCCCGGGACAGGTGCGCGCTGCTTCCGAGCCAACTGCTTGTGCTGCTGACAGTGTG
GCGTGGTGGCCGGCTGGCGCTGGGACTGGGGGTGTCGGGGGCGGGGGTGCCTGGCGTGGCGTGGGCCCCG
AGCGCTTGAGCGCTTCTGCTTCCCGGCGAGCTGCTGCTGCGTCTGCTGCGGATGATCATCTTGCCGCT
GGTGGTGTGACGCTTGATCGGCGGCGCCGACGCTGGACCCGGCGCGCTCGGCCGCTTGGGCGCCTGG
25 GCGCTGCTCTTTTCTGCTCACCACGCTGCTGGCGTGGCGCTCGGAGTGGGCTTGGCGCTGGCTCTGC
AGCCGGGCGCCGCTCCGCCGCCATCAACGCTCCGTGGGAGCCGCGGCGAGTGGCGAAATGCCCCAG
CAAGGAGGTGCTCGATTCTTCTTGGATCTTGGCGAGAAATATCTTCCCTTCCAACCTGGTGTGACAGCC
TTTCGCTCATACTCTACCACCTATGAAGAGAGGAATATCACCGGAACAGGGTGAAGGTGCCCGTGGGGC
AGGAGGTGGAGGGGATGAACATCCTGGGCTTGGTAGTGTGTTGCCATCGTCTTTGGTGTGGCGCTGCGGAA
30 CTGGGGCTGAAGGGGAGCTGCTTATCCGCTTCTTCACTCCTTCAATGAGGCCACCATGGTCTCTGGTC
TCCTGGATCATGTGTTACGCCCTGTGGGATCATGTTCTCTGGTGGCTGGCAAGATCGTGAGATGGAGG
ATGTGGGTCTTACTCTTTGCCCGCTTGGCAAGTACATTCTGTGCTGCTGCTGGGTACGCCATCCATGG
GCTCCTGGTACTGCCCCCTCATCTACTTCTTCAACCGCAAAAACCCCTACCGCTTCTGTGGGGCATC
GTGACGCGCTGGCCACTGCTTTGGGACCTCTTCCAGTTCGCCACGCTGCCGCTGATGATGAAGTGGC
35 TGGAGGAGAATAATGGCGTGGCCAAGCACATCAGCCGTTTCATCCTGCCCATCGGCGCCACCGTCAACAT
GGACGGTGCCGCGCTCTTCCAGTGGCGTGGCCGAGTGTTTATTGCACAGCTCAGCCAGCAGTCTTGGAC
TTCGTAAAGATCATCACCATCCTGGTCACGGCCACAGCGTCCAGCGTGGGGGCGAGCGGGCATCCCTGCTG
GAGGTGCTCTCACTCTGGCCATCATCCTCGAAGCAGTCAACCTCCCGGTGCGACCATATCTCCTTGATCCT
GGCTGTGACTGGCTAGTTCGACCGGCTGTACCGTCTCAATGTAGTAGGCTGACGCTCTGGGGGCGAGGA
40 CTCCTCCAAAATTATGTGGACCGTACGGAGTTCGAGAAGCACAGAGCCTGAGTTGATACAAAGTGAAGAGTG
AGCTGCCCCCTGGATCCGCTGCCAGTCCCCACTGAGGAAGGAACCCCTCCTCAAACACTATCGGGGGCC
CGCAGGGGATGCCACGGTCGCTCTGAGAAGGAATCAGTCATGTAAACCCCGGGAGGGACCTTCCCTGCC
CTGCTGGGGGTGCTCTTTGGACACTGGATTATGAGGAATGGATAAATGGATGAGCTAGGGCTCTGGGGGT
CTGCCTGCACACTCTGGGGAGCCAGGGGCCCCAGCACCTCCAGGACAGGAGATCTGGGATGCCTGGCTG
45 CTGGAGTACATGTGTTTCAAGGGTTACTCCTCAAACCCCCAGTCTCTCACTCATGTCCCCAACCTCAAGG
CTAGAAAACAGCAAGATGGAGAAATAATGTTCTGCTGCGTCCCCACCGTGACCTGCCTGGCCTCCCCCTGT
CTCAGGGAGCAGGTACAGGTACCATGGGGAATTCTAGCCCCACTGGGGGGATGTTACAACACCATGC
TGGTTATTTTGGCGGCTGTAGTTGTGGGGGGATGTGTGTGTGTCACGTTGTGTGTGTGTGTGTGTGTGTGT
TGTGTGTGTGTCTGTGACCTCCTGTCCCCATGGTACGTCCCACCTGTCCCCAGATCCCCCTATTCCCTC
50 CACAATAACAGAAACACTCCCAGGGACTCTGGGGAGAGGCTGAGGACAAATACCTGCTGTCACTCCAGAG
GACATTTTTTTAGCAATAAAATTGAGTGTCAACTATTTAAAAA

SEQ ID NO:44

>gi|5032093|ref|NP_005619.1| solute carrier family 1 (neutral amino acid
55 transporter), member 5; baboon M7 virus receptor; RD114 virus receptor;
neutral amino acid transporter B [Homo sapiens]
MVADPPRDSKGLAAAEPTANGGLALASIEDQAAAGGYCGSRDQVRRCLRLANLLVLLTVVAVVAGVALGL
GVSGAGGALALGPERLSAFVFPGEILLRLRMIIPLVVCSLIGGAASLDPGALGRLGAWALLFLVTTL
LASALGVGLALALGPAGASAINASVGAAGSAENAPSKEVLDSFLDLARNIFPSNLVSAAFRSYSTTYEE
60 RNITGTRVKVPVQGVEGMNIGLVVFAIVFGVALRKLGPGEILLIRFFNSFNEATMVLVSWIMWYAPVG
IMFLVAGKIVEMEDVGLLFARLGKYLCLLGHAIHGLLVLP LIYFLFTRKNPYRFLWGIIVTPLATAFGT

SSSSATLPLMMKCVEENNGVAKHISRFLPIGATVNMDGAALFQCVAAVFIAQLSQSLDFVKIITILVT
ATASSVGAAGIPAGGVLTLAILLEAVNLPVDHISLILAVDWLVDRSCTVLNVEGDALGAGLLQNYVDRTE
SRSTEPELIQVKSELPLDPLVPTEEGNPLLKHRYRGPAGDATVASEKESVM

5 SEQ ID NO:45

Chromobox homologue 6

>GL3_37C_2_M13F

ACGCAGGACGCTCTCGCTGAACCTTCTTGCTCTTGCCCTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCAG
CGCCCCGGCCCCCTGCCCCGGGCCCCCGCCGAGCGCCCTTTGTGCGATCACCTTCAGGTCAGGATGATGCGGTCCG
10 CTTGGGCATCCCGCNCCTTACACCTTGCGGTTGATGATGCGCACCGTCTCCGAGAAGGGCGAAATGAGGCGGGCA
GCAGTCCGGGGCTGCCCCCTGCAGGTTCCGGGCGGGGGCAGGGGACGGCGGGACATACGGTTGGGCAAGNCGGG
CCGGCGAATGTTCTTATACCTTGAAGCCCGGTTGCCACGGGATTAGACGCCTTTGGGAGATTGCACGCATATGG
GGCAAAGGAAGGCNACCTTGCGCCCTCGGGCNTTTNGACACGGAAGGNAATTTGCCACATTCCACTTGAATT
15 TGCGCCAGAATANGGCGNCCACTTNCGTGAGCGACCACTTTGGGCCCCCAGGGGANGGNACGCCGTTTATCA
TCAAAGAGGGGAAAAGGCNGAAAAAAGCGTTNTATCAGTAGAGGGGACAGGGGAATTATTAGGGGGGATTAC
CCCCCCCAGTTACAATTTTACCATATTGAGGAGGAGNCCGCCCANAGTATTAAACATAGGACGTGTTNCAAACG
GGGACNTTACACCAGCATTANCAATTTCCGCAATTTATTATAGTATGGGGATTTCNAGAACAAANGTGGGCGCTTT
TGTCGAAAAATTTAGGAATAGGTCCCCACGG

20 SEQ ID NO:46

>GL3_35L_1_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCGAGGAGAACATCCTGGACTCGCGGCTCATTGCAGCCTTCGAACAAAAGGAGAGGGAGC
GTGAGCTGTATGGGCCCAAGAAGAGGGGACCCAAACCCAAACTTTCTCCTGAAGGCGCGGGCCAGGCCGAGG
CCCTNTCCGCATCAGTGTATGTGCAATTTCTCTGTCAAGCCGAGCGCCAGTGCCTCCTCGCCCAAGCTGCACTCCAG
25 CGCAGCCGTGCACCGGCTCAAGAAGGACATCCGCCGCTGCCACCGTATGTCCCGCGTCCCTGCCCCGCCCCGA
CCCGCAGGGGGGCGAGCCCGGACTGCGCCCGCCCATTTGCGCCTTCTCGGAGACGGTGCGCATCATCAACCGCCA
AGGTGAAGCCGCGGGAGCCCAAGGCGGAACCGCATCATCCTGAACCTGAAGGTGATCGGAACAAGGGCGCTGGCA
CGGCAGGGGGCGCCGGGCAAGGGGGCGGGGACGCTGGCCCGCCAAAAAAGGNTCNCCTATCNGCGGGGAAAC
CCGGCGGTGTAATAGGGGGCAAGAGGCAAGAACAGGTACCAGGCAAAGGAAGCCGGGTACATGGCAGGTNCGCG
30 GNCANAGAAACCCAGCAACACTTGGGAGGCCACACCGGTNGCNCAACCGGACCTTTNGGGGGGGCCTCACATC
ACCNATGGTACCAAGGGTCTGTCACCAATCGAGCACGGACAAGAAAGGGGGCGAAATTC

SEQ ID NO:47

>GL3_35L_3_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCGAGGAGAACATCCTGGACTCGCGGCTCATTGCAGCCTTCGAACAAAAGGAGAGGGAGC
GTGAGCTGTATGGGCCCAAGAAGAGGGGACCCAAACCCAAACTTTCTCCTGAAGGCGTGGGCCAGGCCGAGG
CCCTCCGCATCAGTGTATGTGCAATTTCTCTGTCAAGCCGAGCGCCAGTGCCTCCTCGCCCAAGCTGCACTCCAGCG
CAGCCGTGCACCGGCTCAAGAAGGACATCCGCCGCTGCCACCGTATGTCCCGCGTCCCTGCCCCGCCCCGACC
40 CGCAGGGGGGCAAGCCCCGGAACCTGNGCCCGCCCAATTTGCGCCTTCTCGGAGACCGGTGCGCATCATCAACCGC
AAGTGAAGCCGCGGGAGCCAAGCGGAACCGATCATCCTGAAACCTGAAGGTGATCGGACAAGGGCGCTGGCGGAC
GGGGGCGCCGGGCGAGGGGGGCGGGGGCGCCTGGGCCCCGGCCCCCAAAANAGTCCCCCACCATCAGGGCGAGG
GAAAACCCCGGAGGANAAGTAGCGGGCAAANGAAGCCAANAGGAAANGTTCAACAAGGAGAGAAGAACGNGA
CGACCANGCGAGATCCCGGGGAAGAGAAACGCNNAAGGCAAAACAAGATTGGGAGAAGCNACAACNGGTGAGC
ACAACAGCCGGGGCACTAGGCGGGCGGNACCTACCCTCCCCCTATTGGAACGCAGCNCNCGGGCANCAATTGCCGA
45 GAAAGAAAGGGGGGCGAATCTNCGA

SEQ ID NO:48

>GL3_35L_4_M13F Direction: N/A

ACGCAGGACGCTCTCGCTGAACCTTCTTGCTCTTGCCCTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCAG
50 CGCCCCGGCCCCCTTGCCCGGCGCCCCCGCCGCGCCAGCGCCCTTTGTGCGATCACCGTTTCAGGTTTCAGGATGATGCG
GTTCCGGCTTTGGGCATCCCGGGGGGCTTACCTTTGCNNGGTTGACTGATGCGCACCGGACATCTGAGAAAGGG
CGAAATGGGACGGGACGCAGATCCGGGGCNTGCCCCCCTTGCCGGGGGGACTTCCAGGGGCACGGGGGANGA
CAAGGGGGGAACGGGGACGGGTGAACCAATTACCGGNGGTGGGCCAGCCGGGCGGGGAATGGGTCCCTTCTTGGA
AGACCGGGTGCCAA

55

SEQ ID NO:49

>GL3_37C_1_M13F Direction: sense

ACGCAGGACGCTCTCGCTGAACCTTCTTGCTCTTGCTTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCAG
60 CGCCCCGGCCCCCTTGCCCTGGAGCCCCCGCCGCGCCAGCAGGCCCATTTGTGAGAATTCAACCTTTCAAGGNTNCAAG
GGATGAATTGCGNGGTCCCGCTNTATGGGGATTCCNCAAGAGGGACTTTTCAACCTTTTGCCAGGGATATGGAA

CGTGGNATTTGCCGGCCAAACCCGGGGTNACTCCCCAGAAAGGAAAAAGGGGGGCGGGAAAAAATTTGGGCGCT
GGGGGCCGACGGC

SEQ ID NO:50

>GL3_35L_1_M13F Direction: N/A

ACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCCCTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCA
GCGCCCGGGCCCCCTTGCCCCGGGGCCCCCGCCCGCCNAGCGGCCCTTTGTTCGGATCAACCTTCAGGTCAGGATGA
TGCGGTTCCGCTTTGGGCTTCCCGCGGGTTTACCTTGCGGGTTGATGATGCGGCAACCCGGGTCTTCCCAGA
AGAACAGGGGGCGGACAATTGGNGCGCAGGGGC

SEQ ID NO:51

>GL3_35L_3_M13F Direction: N/A

ACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCCCTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCCAG
CGCCCCGGCCCCCTTGCCCCGGGGCCCCCGCCCGCCAGCGCCCTTGTCGATCACCTTCAGGTNCAGGATGATGCGGTT
CCGCTTGGGCTCCCGCGGCTTACCTTGCGGTTGATGATGCGCACCGTCTCCGAGAAGGGCGAAATGGGCGGGCG
CAGTCCGGGGCTGCCCCCTTGCGGGATCCGGGCGGGGCGAGGGACCGGCGGGCACCATACGGTGGCAGCGGGC
GGAATGTCTTCTGAAGCCGGTGACGGCTTGCGCTTGAAGTTGCAGCTTGGGCCAAGG

SEQ ID NO:52

>GL3_35L_4_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCCGAGGAGAACATCCTGGACTCGCGGCTCATTGCAGCCTTCGAACAAAAGGAGAGGGAGC
GTGAGCTGTATGGGCCCAAGAAGAGGGGACCCAAACCCAAAACCTTCTCTCTGAAGGCGCGGGGCCAGGCCGAGG
CCCTCCGCATCAGTGATGTGCATTTCTCTGTCAAGCCGAGCGCCAGTGCCCTCCTCGCCCAAGCTGCACTCCAGCG
CAGCCGTGCACCGGCTCAAGAAGGACATCCGCCGCTGCCACCGTATGTCCCGCCGTCCCCTGCCCGCCCCGGACC
CGCAGGGGGGCGAGCCCCGACTGCGCCCGCCATTTCGCCCTTCTCAGAGACGGTGCGCATCATC

SEQ ID NO:53

>GL3_35L_PCR_G3F1 Direction: N/A

GACGCAGGACGCTCTCGCTGAACTTCTTGCTCTTGCCCTATAACGCGGTTCCGCGAGGGGACTTTGGGGCGGGCC
AGCGCCCCGGCCCCCTGCCCGGGCCCCCGCGCGGCCCTTTATACCTTCAGTTCAGATGATGCGGTTCCGCTTGGG
CTCCCGCGGCTTACCTTGCGGTTGATGATGCGCACCGTCTCCGAGAAGGGCGAAATGGGCGGGCGCAGTCCGGG
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CCGGTGACGGCTGCGCTGGAGTGACGCTTGGGCGAGGAGGCACTGGCGCTCGGCTTGACAGAGAAATGCACATC
ACTGATGCGGAGGGCCTCGGCCTGGGCCCCGCGCCTTCAGGAGGAAAGTTTGGGTTTGGGTCCCCTCTTCTTGGG
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SEQ ID NO:54

>GL3_37C_1_M13R Direction: anti-sense

ACAGCACTTGGGAGCCCCGAGGAGAACATCCTGGACTCGCGGCTCATTGCAGCCTTCGAACAAAAGGAGAGGGAGC
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CCCTCCGCATCAGTGATGTGCATTTCTCTGTCAAGCCGAGCGCCAGTGCCCTCCTCGCCCAAGCTGCACTCCAGCG
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CGCAGGGGGGCGAGCCCCGACTGCGCCCGCCATTTCGCCCTTCTCGGAGACGGTGCGCATCATCAACCGCAAGG
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AAGCAAGGAAGGTCAGGCGAGAGGCGGTCCCTGCGTCCGNAGAAACCCAGCACACCTGGACGGCCACCGATGCCA
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SEQ ID NO:55

>GL3_37C_2_M13R Direction: anti-sense

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GGTGAAGCCGCGGGAGCCCAAGCGGAANCGCATCATCCATGAACCTGAA

>GL3_37C_PCR_G3F1 Direction: N/A

[illegible]

SEQ ID NO:37
 >gi|10140848|ref|NM_014292.1| Homo sapiens chromobox homolog 6 (CBX6), mRNA

15 AAGTACAGCACTTTGGGAGCCCCGAGGAGAACATCTGGACTCGCGGGCTCATTTGACAGCTTCGAAACAAAGGAGAGGGGAGCGTGAGCTGTATGGGGCCCAAGAAGAGGGGACCCAAACCCAAAACCTTTCCTCCTGAAGCCGCGGGCCCAGGCCGAGGCCCTCCGATCAGTGTATGTGCATTTCTCTGTCAAGCCGAGCGCCAGTGCCTCCTCGCCCAAGCTGCACTCCAGCGCAGCCGTGCACCGGCTCAAGAAGGACATCCGCGCTGCCACCGTATGTCCCGCGTCCCCCTGCCCGCCCCGAGGCCGAGGCCGAGGCCGAGCCCGGACTGCGCCCGCCCATTTGCGCCCTTCTCGAGACGGTGCGCATCATCAACCGCAAGGTGAAGCCGCGGGAGCCCAAGCGGAACCGCATCATCCTGAACCTGAAGGTGATCGACAAGGGCGCTGGCGGCGGGGCGCCGGGCAGGGGGCGGGGGCGCTGGCCCCGCCCCAAGTCCCCCTCGCGGAACCGCGTTATAGGCAAGAGCAAGAAGTTCAGCGAGAGCGTCTCTGCGTACACAGATCCGCCACATGAAGTTCGGCGCCTTTGCGCTGTACAAGCCTCCGCCCCGCCCCCTGGTAGCCCCGTCCCCGGCAAGGCTGAGGCCTCAGCCCCGGGCCCTGGGCTACTTCTGGCCGCCCGCCCGCCCCCTACGACGCCGCAGCTCTGGCTCCTCCGGCTGCCCCCTCGCTACACCACAGTCTCTGACCCCCGACGACGCCCCCAA

20 GCTCCTCCCCGAGACCGTGAGCCCATCCGCCCCAGCTGGCGCGAGCCGGAGGTGCTCGACCTGTCCCTCCTCCCGAGTCGGCAGCCACGAGCGGCGACGCGCTGAGGTACAGCTGCTGCCGGCCCGGCACCTCCACGGCCCCCTGAGCCCCGCGGTGCTCCTCCGAGCCCGAGGCTGGGGACTGGCGCCCCGAGATGTCACCCTGCTCCAATGTGGTTCGTCACCGATGTCACCAGCAACCTCCTGACGGTCACAATCAAGGAATTCTGCAACCTTGAGGATTTGAGAAGGTGGTCTGCTGGGGTAGCAGGCGCCGCTGGGGGCGGTGGCAGCATTGGGGCGA

25 GCAAGTGGAGGGGCTCCACCAAGGAGGGGGGCTTGGGGGGGCCCCCTCTGCCCCGAGTCACTCTTGCTCCACCCACCCCTTGCCCCAGCCCTCTCTCCCTGTGCTTTGCTTGTCTCAAATGCTCGGTGTTTGACCCAGGGATGGGGCTGGGTAGTTGGGGTCCCAGAAAGCCGGGGTAGGGGCCACCTTGAATGGGGCAGGGGAA

30 GGGCACACCCCCCTGCCATGTCATGTGTAGCCACTGGGTGGTGGTGGAAAGCCCTAGAAACTAGGGTTCCCTGCTCCCTTCCACATCCCACTGTCTCTCTAGCTTGCTTCTGCTCTCCTGTGCGGCGTCTGATTCTCTGCTGCTAACCTGGCAGCTGTGGGGCCCTTAGGAGCCCCCACCAGGGTGGACACAGTCCCTTTCCTTCC

35 TGCAGATGCCTAGGCAGGAGGAGGGCTTCCCTGCCTGTTTGGCAAAGTCCCAGGCAGAGGCCAAGGATGAGGCCTGACTCGGCTCCTCCCTCCACATCAGCCAGGGCATCAGAAGTTGGGCCAGGGCGGGGTCTTCCCTGCTCGATTTTGGACGAGGCCTAAGTAGACCCCCATAGCCCTGCCCCAGCCCTGGCTCTTTCCCTAACCCCTCAACGGTGGGAGGAAC

40 TGGCAGAGGGTGC

45 GCGCTGCCCCGACGCTTGTCCCAGCCCCCTCTTTTGCTTCTGACCACGGAGGCTTTCTCACAGCCACGCTGCCTGAAGCAAAGGAGGCTCCCGTGTCTGGGACGCTTCTGTTTCCCTCTGCTGCTGGGAGCTGAGGCA

50 CCGTGCCAGTGCGAGAGCCACAGCCCCAGCCTTAGGCCAGGCCCTGGGAGGGCAGGCAGGCAAGGGGAGACCAAGGGTCTGTCTCCAGGAGAATGAGGGTGTGGTCCAGAAATTGGACCGGGGCCCCGCTG

55 GCCAGCCCTGGGCACTTCCCGGGTCTCCATTGTGCGTGGGTGGCGTGTTCAGGCGTGGCTGGAGCTGGCTTCCCTGGCTGTGCTGCCATGGGCCCCCTCCCTCAGAAGCACGTTGGCAGGAGGCCGATCAGAACCCTAGCGCCTTTGGTCCCTAAGAATGGGAGGCTGCCTTCCCTTCCCAATCTCCCTGCCAGGGCCCCACAGCGTGGCCCTAGCCCTCCCCCTCCCGGGATGTAGAACGGGGACCCCTCGCAGGGTTGGGGCGGGGGCTGATACTCTCGGC

60 CCTTCCCTACCTTGCCCTGTGTGTTGGCTTTGTGGCCGTC

5

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40

>gi|10140849|ref|NP_055107.1| chromobox homolog 6 [Homo sapiens]
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KRGPKPKTFLLKARAQAEALRISDVHFSVKPSASASSPKLHSSAAVHRLKKDIRRCHMSRRPLPRDPQ
GGSPGLRPPISPFSETVRIINRKVKPREPKRNRIILNLKVIDKGAGGGGAGQGAGALARPVKVPSRNRVIG
KSKKFSESVLRTQIRHMKFGAFALYKPPPAPLVPASPGEAEASAPGPGLLLAAPAYDARRSSGSSGCPS
PTPQSSDDPTPKLLPETVSPSPASWREPEVLDSLFLNPESAATSKRAPPEVTAAGAPAPPTAPEPAGAS
SEPEAGDWRPEMSPCSNVVVDVTSNLLVTIKEFLSCNPEDFEKVAAGVAGAAGGGGIGASK

50

ACTTTTCTCGGCCATATCCGGAATGCCCGACGTTACTCGGACTACCCCGATGCATACACCACATGAAACATCCTAT
CATCTGTAGGCTCATTCATTTCTCTAACAGCAG

55

CTGCTGTTAGAGAAATGAATGAGCCTACAGATGATAGGATGTTTCATGTGGTGATGCATCGGGGTAGTCCGAGT
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SEQ ID NO:61

>GL2_226_2_2_M13R Direction: sense

ACTTTCTCGGCTATCCGGAATGCCCCGACGTTACTCGGACTAACCCGATGCATACACCACATGAAACATCCTATN
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SEQ ID NO:62

>GL2_226_2_4_M13F Direction: anti-sense

CTGCTGTTAGAAGAAATGAATGAGCCTTACAGATGATAGGATGTTTCATGTGGTGTATGCATCGGGGTAGTCCGA
GTAACGTCGGGGCATTCGGGATAGGCCGAGAAAGT

SEQ ID NO:63

5905-7446

/gene="COX1"

/codon_start=1

/transl_table=2

/product="cytochrome c oxidase subunit I"

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5941 aaagacattg gaacactata cctattattc ggcgcagtga ctggagtcct aggcacagct
6001 ctaagcctcc ttattcgagc cgagctgggc cagccaggca accttctagg taacgaccac
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6181 gcgtttcccc gcataaacia cataagcttc tgactcttac ctccctctct cctactcctg
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6301 gcagggaact actcccaccc tggagcctcc gtagacctaa ccatcttctc cttacaccta
6361 gcagggtgtc cctctatctt agggggccatc aatttcatca caacaattat caatataaaa
6421 cccctgcca taaccaata ccaaacgccc ctcttcgtct gatccgtcct aatcacagca
6481 gtctactctc tcctatctct cccagtccta gctgctggca tcaactact actaacagac
6541 cgcaacctca acaccacctt ctctgacccc gccggaggag gagaccccat tctataccaa
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6661 ataattctcc atattgtaac ttactactcc ggaaaaaaag aaccatttgg atacataggt
6721 atgggtctgag ctatgatatc aattggcttc ctagggttta tcgtgtgagc acaccatata
6781 tttacagtag gaatagacgt agacacacga gcatatttca cctccgctac cataatcatc
6841 tctatcccca ccggcgtcaa agtatttagc tgactcgcca cactccacgg aagcaatatg
6901 aatgatctg ctgcagtgct ctgagcccta ggattcatct ttcttttcac cgtaggtggc
6961 ctgactggca ttgtatttag aaactcatca ctagacatcg tactacacga cagtactac
7021 gttgtagctc acttccacta tgtcctatca ataggagctg tatttgccat cataggaggc
7081 ttcattcaact gatttcccct attctcaggc tacaccctag accaaacctc cgccaaaatc
7141 catttccacta tcatattcat cggcgtaa atctaacttct tcccacaaca ctttctcggc
7201 ctatccggaa tgccccgacg ttactcggac taccctgatg catacaccac atgaacatc
7261 ctatcatctg taggctcatt catttctcta acagcagtaa tattaataat tttcatgatt
7321 tgagaagcct tcgcttcgaa gcgaaaagtc ctaatagtag aagaacctc cataaacctg
7381 gagtgactat atggatgccc ccaccctac cacacattcg aagaacctg atacataaaa
7441 tctagacaaa
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SEQ ID NO:64

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>gi|17981855|ref|NP_536845.1| cytochrome c oxidase subunit I [Homo sapiens]
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GGLTGIVLANSSLDIVLHDITYYVVAHFHYVLSMGAVFAIMGGFIHWFP LFSGYTLDQTYAKIHFTIMFIG
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SEQ ID NO:65

Delta-5 Fatty Acid Desaturase (FADS1; FADS5)

>GL1_10_3_G3F1 Direction: sense

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CCATCCGCTCCACTGTGGNCCGCANACTCCCGAACTCATCTGTCAGCTCTTTATTCTTGGTGGGNTCAAAGCTG
GGCTGNTCTGGAGACAGTTCTCCAATCAGGAGAGAGTTTCATATACTTCTTCACAAGGCCCTTGTGGATGTGGAAG
GCCACAAAGGGATCCGTGGNATCCTGNCCGGNGTAGTGGCTGATGANCCGGGAGCCCCCTGNATGCCGGCGGAGT
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SEQ ID NO:66

>GL1_10_3_G3R1 Direction: anti-sense

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TGAGCCACCAAGAATAAAGAGCTGACAGATGAGTTCCGGGAGCTGCGGGCCACAGTGGAGCGGATGGGGCTCAT
GAAGGCCAACCATGTCTTCTTCTGCTGTACCTGCTGCACATCTTGCTGCTGGATGGTGCAGCCTGGCTCACCTT
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SEQ ID NO:67

delta5-Fatty acid desaturase>

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CGGCATCCAGGGGGCTCCCGGGTTCATCAGCCACTACGCCGGGAGGATGC
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CAAGTCTGCCTTCAATGACTGGTTTCAAGTGGACACCTCAACTTCCAGATTG
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CCCCTGGTGCAGTCCTTGTGTGCCAAGCATGGCATAGAGTACCAGTCCAA
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SEQ ID NO:68

>gi|14141179|ref|NM_013402.3| Homo sapiens fatty acid desaturase 1 (FADS1), mRNA

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50 SEQ ID NO:69
>gi|11181775|ref|NP_037534.2| fatty acid desaturase 1; delta-5 fatty acid
desaturase; linoleoyl-CoA desaturase (delta-6-desaturase)-like 1; delta-5
desaturase [Homo sapiens]
MAPDPVAAETAAGQPTPRYFTWDEVAQRSGCEERWLVIDRKVYNISEFTRRHPPGGSRVISHYAGQDATDP
55 FVAFHINKGLVKKYMNSLLIGELSPEQPSFEPTKNKELTDEFRELRAFTERMGLMKANHVFFLLYLLHIL
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60 SAFADIHSLKESQGLWLDAYLHQ

SEQ ID NO:70

Dynactin 6, p27 subunit

>gi|18426895|ref|NM_006571.2| Homo sapiens novel RGD-containing protein (WS-3), mRNA

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10 CTTACCCAGATAATATCACTCCTGACACTGAAGATCCAGAACCAAAACCTATGATCATTGGCACCATAA
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SEQ ID NO:71

>gi|5730116|ref|NP_006562.1| novel RGD-containing protein [Homo sapiens]

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25 TPDTEDEPEPKPMIIGTNNVFEVGCYSQAMKMGDNNVIESKAYVGRNVILTSGCIIGACCNLNTFEVIPEN
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SEQ ID NO:72

Elongation factor 1 alpha (EF1 α)

>GL1_34_LOW_3_G3F1 Direction: sense

30 ACTGTNCTTGCTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGATATGGTGGTGCACCTTTGCTCCAGCTCAAC
GTTACAACGGAAGTAAATCTGTGCAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATGTGGGC
TTCAATGTCAAGAATGTGTCTGTCAAGGATGTTCTGTCGTGGCAACGTNGCTGGTGACAGCAAAATGACCCACCA
ATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCC

SEQ ID NO:73

>GL1_34_LOW_3_G3R1 Direction: anti-sense

35 GGCCTTTATTTGGCCTGGATGGTTCAGGATAATCACCTGAGCAGTGAAGCCAGCTGCTTCCATTGGTGGGTGCTATT
TTTGCTGTCCAGCAACGTTGCCACGACGAACATCCTTGACAGACACATTCTTGACATTGAAGCCACATTGTC
CCCAGGAAGAGCTTCACTCAAAGCTTCATGGTGCATTTGACAGATTTTACTTCCGTTGTAACGTTGACTGGAGC
40 AAAGGTGACCACCATAACCGGTTTGAGAACACCAGTCTCCACTCGGCCAACAGGAACAGT

SEQ ID NO:74

>GL1_34_LOW_4_G3F1 Direction: sense

45 ACTGTTCTTGTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTGCACCTTTGCTCCAGTCAACGTT
ACAACGGAAGTAAATCTGTGCAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATGTGGGCTTC
AATGTCAAGAATGTGTCTGTCAAGGATGTTCTGTCGTGGCAACGTTGCTGGTGACAGCAAAATGACCCACCAATG
GAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGCGCC

SEQ ID NO:75

>GL1_34_LOW_4_G3R1 Direction: anti-sense

50 GGCCTTTATTTGGNCTGGATGGTTCAGGATAATCACCTGAGCAGTGAAGCCAGCTGCTTCCATTGGTGGGTGCTATT
TNTGNTGTCACCAGCAACGTTGCCACGACGAACATCCTTGACAGACACATTCTTGACATTGAAGCCACATTGTC
CCCAGGAAGAGCTTCACTCAAAGCTTCATGGTGCATTTGACAGATTTTACTTCCGTTGTAACGTTGACTGGAGC
55 AAAGGTGACCACCATAACCGGTTTGAGAACACCAGTCTCCACTCGGCCAACAGGAACAGT

SEQ ID NO:76

>gi|20127674|ref|NM_001402.3| Homo sapiens eukaryotic translation

elongation factor 1 alpha 1 (EEF1A1), mRNA

GGCACGAGGGTTTGGCCGAGAACACAGGTGTCGTGAAAACCTACCCCTAAAGCCAAAATGGGAAAGGAA
60 AAGACTCATATCAACATTGTCGTCAATTGGACACGTAGATTCCGGGCAAGTCCACCCTACTGGCCATCTGA

TCTATAAATGCGGTGGCAATGACAAAAGAACCATTGAAAAATTTGAGAAGGAGGCTGCTGAGATGGGAAA
GGGCTCCTTCAAGTATGCCTGGGTCTTGGATAAACTGAAAGCTGAGCGTGAACGTGGTATCACCATTGAT
ATCTCCTTGTGGAAATTTGAGACCAGCAAGTACTATGTGACTATCATTGATGCCCCAGGACACAGAGACT
5 TTATCAAAAACATGATTACAGGGACATCTCAGGCTGACTGTGCTGTCTGATTGTTGCTGCTGGTGTGG
TGAATTTGAAGCTGGTATCTCCAAGAATGGGCAGACCCGAGAGCATGCCCTTCTGGCTTACACACTGGGT
GTGAAACAACATAATTGTCGGTGTAAACAAAATGGATTCCACTGAGCCACCCTACAGCCAGAAGAGATATG
AGGAAATTGTTAAGGAAGTCAGCACTTACATTAAGAAAATTGGCTACAACCCCGACACAGTAGCATTGT
GCCAATTTCTGGTTGGAATGGTGACAACATGCTGGAGCCAAGTGCTAACATGCCTTGGTTCAAGGGATGG
10 AAAGTCACCCGTAAGGATGGCAATGCCAGTGGAAACCACGCTGCTTGAGGCTCTGGACTGCATCCTACCAC
CAACTCGTCCAAGTACAAGCCCTTGGCGCTGCCTCTCCAGGATGTCTACAAAATTGGTGGTATTGGTAC
TGTTCTCTGTTGGCCGAGTGGAGACTGGTGTCTCAAACCCGGTATGGTGGTCACCTTTGCTCCAGTCAAC
GTTACAACGGAAGTAAAATCTGTGCAAAATGCACCATGAAGCTTTGAGTGAAGCTCTTCTGGGGACAATG
TGGGCTTCAATGTCAAGAATGTGTCTGTCAAGGATGTTCTGCTGGCAACGTTGCTGGTGACAGCAAAAA
15 TGACCCACCAATGGAAGCAGCTGGCTTCACTGCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGC
GCCGGCTATGCCCCCTGTATTGGATTGCCACACGGCTCACATTGCATGCAAGTTTGCTGAGCTGAAGGAAA
AGATTGATCGCCGTTCTGGTAAAAAGCTGGAAGATGGCCCTAAATCTTGAAGTCTGGTGTATGCTGCCAT
TGTTGATATGGTTCTTGGCAAGCCCATGTGTGTTGAGAGCTTCTCAGACTATCCACCTTTGGGTCGCTTT
GCTGTTCTGTATATGAGACAGACAGTTGCGGTGGGTGTCTCAAAGCAGTGGACAAGAAGGCTGCTGGAG
20 CTGGCAAGGTACCAAGTCTGCCAGAAAGCTCAGAAGGCTAAATGAATATTATCCCTAATACCTGCCAC
CCCCTCTTAATCAGTGGTGAAGAACGGTCTCAGAACTGTTTGTTCATTGGCCATTTAAGTTTAGTA
GTAAAAGACTGGTTAATGATAACAATGCATCGTAAACCTTCAGAAGGAAAGGAGAATGTTTTGTGGACC
ACTTTGGTTTTCTTTTTTTCGCTGTGGCAGTTTTTAAGTTATTAGTTTTTTAAATCAGTACTTTTTTAATGGA
AACAACTTGACCAAAAATTTGTACAGAATTTTGAGACCCATTAAAAAAGTTAAATGAGAAAAA
25 AA
AAAAAAAAAAAAA

SEQ ID NO:77

>gi|4503471|ref|NP_001393.1| eukaryotic translation elongation factor 1
alpha 1 [Homo sapiens]
30 MGKEKTHINIVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAEMGKGSFKYAWVLDKLKAERERG
ITIDISLWKFETSKYYVTIIDAPGHRDFIKNMITGTSQADCAVLIVAAGVGEFEAGISKNGQTREHALLA
YTLGVKQLIVGVNKM DST EPPYSQKRYEEIVKEVSTYIKKIGYNPDVAFVPISGWNGDNMLEPSANMPW
FKGWKVRTRKDGNASGTTLLLEALDCILPPTRPDKPLRLPLQDVYKIGGIGTVVPVGRVETGVLKPGMVVTF
35 APVNVTTTEVKSVMHHEALSEALPGDNVGFNVKNVSKDVRRGNVAGDSKNDPPMEAAGFTAQVIILNHP
QGISAGYAPVLDCHTAHIACKFAELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVPKPKMCVESFSDYPP
LGRFAVRDMRQTVAVGVKAVDKKAAGAGKVTKSAQKAQKAK

SEQ ID NO:78

Elongation factor 4 gamma (Elf4 γ)
40 >GL1_3_1_G3F1 Direction: sense
GTCCAACCTCAAAGATATGGGAGAGGATTTGGAGTGCCTCTGTCTAGATAATGAGGACAGTGGGACCTAGATTAGAC
CATGAACGAGCCAAGTCCTTAATGGATCAGT

SEQ ID NO:79

>GL1_3_1_G3R1 Direction: anti-sense
45 ACTGATCCATTAAGGACTTGGCTCGTTCATGGTCTAATCTAGGTCCCACTGGTCCTCATTATCTGACAGAGGCAC
TCCAAATCCTCTCCCATATCTTTGAGTTGGAC

SEQ ID NO:80

>GL1_3_2_G3R1 Direction: anti-sense
50 ACTGATCCATTAAGGACTTGGNTCGTTCATGGTCTAATCTANAGTCCCACTGGTCCTCATTATCTGACAGGAGAG
CACTCCAAATCCTCTCCCATATCTTTGAGTTGGAC

SEQ ID NO:81

>gi|4503538|ref|NM_001418.1| Homo sapiens eukaryotic translation initiation
factor 4 gamma, 2 (EIF4G2), mRNA
55 CAGCAGTGAGTCGGAGCTCTATGGAGGTGGCAGCGGGTACCGAGTGGCGGCTGCAGCAGCGACTCCTCTG
AGCTGAGTTTGAAGCCGTCCCCGACTCCTTCCTCCCCCTTCCCTCCCCCTTTTTTTTGTTCCTGTTCCGTTCC
CTTCCCCCTCCTTCCCTATCCCCGACGACCGGATCCTGAGGAGGCAGCTGCGGTGGCAGCTGCTGAGTT
60 CTCGGTGAAGGTATTTCAATTTCTCTGTCCCCCTCCCCCTCCCCACCCATCTATTAATATTATCTTTTGA

[illegible]

SEO ID NO:82

55 >gi|4503539|ref|NP_001409.1| eukaryotic translation initiation factor 4
gamma, 2; Eukaryotic translation initiation factor 4G-like 1; p97 [Homo
sapiens]
MESAIAEGGASRFSASSGGGSGRGAPQHYPKTAGNSEFLGKTPGONAQKWIPARSTRRDDNSAANNSSANE
KERHDAIFRKVRGILNKLTPKFKDLKLELLNVGVESKLILKGVILLIVDKALEEPKYSSSLYAQLCLRLA
EDAPNEDGPAEGQPGQKQSTTFRLLLSKLQDEFENRTRNVDDVDKRENPLPEEEEEQRAIAKIMKMLGN
60 IKFIGELGKLDLHESILHKCIKLTLEKKRVQLKMGDELECLCQIMRTVGPRLDHERAKSLMDQYFAR
MCSLMLSKELPARIRFLQDQTVELREHHWVPRKAFLDNGPKPTINQIRODAVKDLGVFIAPAPAOGRMSDF

FLEGPFMPPRMKMDRDPGLCLADMFGQMPGSGIGTGPGVIQDRFSPTMGRHRSNQLFNHGGHIMPPTQS
QFGEMGGKFMKSQGLSOLYHNQSQGLLSQLQGQSKDMPPRFSSKKGQLNADEISLRPAQSFLMNKNQVPKL
QPQITMIPPSAQPPRTQTPPLGQTPQLGLKTNPLIQEKPAKTSKKPPPSKEELLKLTETVVTEYLNSGN
5 ANEAVNGVREMRAPKHFLPEMLSKVIIISLDRSDEDKEKASSLISLLKQEGIIATSDNFMQAFNLVLDQCP
KLEVDIPLVKSYLEAQAARAIISELVSISELAQPLESGTHFPLFLLCLQQLAKLQDREWLTELFOQSKVN
MQKMLPEIDQNKDRMLEILEGKGLSFLFPLLKLEKELLKQIKLDPSPQTIYKWKDNISPKLHVDKGFVN
ILMTSFLQYISSEVNPPSDETDSSSAPSKEQLEQEKQLLSFKPVMQKFLHDHVDLQVSALYALQVHCYN
SNFPKGMLLRFFVHFYDMEIIIEEEAFLAWKEDITQEFPGKGKALFQVNQWLWLETAEEEESEEEAD

10 SEQ ID NO:83

Filamin A

>GL3_11C_PCR_G3F1 Direction: sense

ACATCCAGGACACGGTGATGGCACGCACACCATTACCTACATTCCCCTCTGCCCCGGGGCCTACACCGTCACCAT
CAAGTACGGCA

15 SEQ ID NO:84

>GL3_15A_2_M13R Direction: anti-sense

TGCCGTACTTGATGGTGACGGTGATAGGCCCGGGGAGAGGGGAATGTAGGTAATGGTGTGCGTGCCATCACCGT
GGTCCCTGGATGTTTCGCAGAAACCAGCACACTGGAGCCACCGCTGCACCGGGCTTGGGGGCTCCTCCTTGACAGC
20 TCGTCCATGCCGAGAGAAGGGCGAATTCTTGACAGATATNCATCACACTGGCGGGCGCTCGAGC

SEQ ID NO:85

>GL3_32C_PCR_G3F1 Direction: sense

ACATCAGGACCACGGATGATGGCACGCACACCATACTACATCCCCTCTGCCCCGGGGCCTACACCGTCACCATC
25 AAGTACGGCACCGNAGAACCAGCACAGTGGTNAGATAGATAAAGCGGCCGCTCGACTAGTCTGAGGTCTGAATA
CTCAACTGAACTGTACGTAAAAACAA
AA
AAAAA

30 SEQ ID NO:86

>gi|4503744|ref|NM_001456.1| Homo sapiens filamin A, alpha (actin binding
protein 280) (FLNA), mRNA

GCGATCCGGGCGCCACCCCGCGGTCATCGGTACCGGTGCTCTCAGGAACAGCAGCGCAACCTCTGCTC
CCTGCCTCGCCTCCCGCGCGCTAGGTGCTGCGACTTTAATTAAAGGGCCGTCCTCGCCGAGGCTGC
35 AGCACCGCCCCCGGCTTCTCGCGCCTCAAATGAGTAGCTCCCACTCTCGGGCGGGCCAGAGCGCAGC
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GAGGACGCGCCGTGGAAGAAGATCCAGCAGAACACTTTTCACGCGCTGGTGCAACGAGCACCTGAAGTGG
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40 GCTCAGCCAGAAGAAGATGCACCGCAAGCACAACCAGCGGCCCACTTTCCGCCAATGCAGCTTGAGAAC
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CATGTGGGACGAGGAGGAGGATGAGGAGGCCAAGAAGCAGACCCCCAAGCAGAGGCTCCTGGGCTGGATC
CAGAACAAGCTGCCGCGAGCTGCCCATCACCAACTTCAGCCGGGACTGGCAGAGCGGGCCGGGCCCTGGGCG
45 CCCTGGTGGACAGCTGTGCCCCGGGCTGTGTCTGACTGGGACTCTTGGGACGCCAGCAAGCCCGTTAC
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50 GCACCTTCTCCGTCTGCTACGTCCCGAGGTGACGGGGACTCATAAGGTTACTGTGCTCTTTGCTGGCCA
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55 CACGTACGTTTGCCGGCGGTGCCCATCCCTCGCAGCCCTACACTGTCACTGTTGGCCAAGCCTGTAACC
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5 CCCCAGGACTTCCACCCAGACAGGGTGAAGGCACGTGGGCCTGGATTGGAGAAGACAGGTGTGGCCGTCA
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10 GCTCAAGGCCCCACGAGCCACCTACTTCACTGTGGACTGCGCCGAGGCTGGCCAGGGGACGTCAGCATC
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15 AAGCTGCTGGCAAAGGCAAGCTGGACGTCCAGTTCTCAGGACTCACCAAGGGGGATGCAGTGCGAGATGT
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CAAATCAAAGGGTGTCTGGTGTCAAGGCAAAGTGGCATCCAAGATTGTGGGCCCCCTCGGGTGCAGCGGTG
20 CCCTGCAAGGTGGAGCCAGGCCCTGGGGGCTGACAACAGTGTGGTGGCTTCTGCCCCGTGAGGAAGGGC
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25 GTACAACATCAACATCCTCTTCGCTGACACCCACATCCCTGGCTCCCCATTCAAGGCCCCAGTGGTTCCC
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30 AACCTGCGGTGGACACTTCCGGTGTCCAGTGCTATGGGCCTGGTATTGAGGGCCAGGGTGTCTTCCGTGA
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35 AGTGGCACCACCAACAAGCCCCAAGTTCACTGTGGAGACCAGGGGAGCTGGCACGGGCGGCCTGGGCC
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50 CCGGGCAAATACGTCACTGTGTGCGCTTTGGTGGCGAGCAGTGCCCAACAGCCCCCTTCCAAGTGACGG
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55 ACCCAGCGAGGCTGGCCTGCACGAGATGGACATCCGCTATGACAACATGCACATCCCAGGAAGCCCCCTTG
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5 CTACATCATCAACATCAAGTTTGGCCAGCAGCTGCAGCCCTTCTCTGTGAAGGTGACAGGC
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10 ATGGGCACACACACAGTCAGCGTCAAGTACAAGGGCCAGCAGTGCCTGGGAGCCCCCTCCAGTTCACCG
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15 GTCAACCAGCCAGCCTCTTTTGCAGTCAGCCTGAACGGGGCCAAGGGGGCGATCGATGCCAAGGTGACACA
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25 TAGACTGCAGCAAAGCAGGCAACAACATGCTGTGGTGGGGGTTTCATGGCCCCAAGGACCCCTGCGAGGA
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30 ACCTGCCTCCCCAGCCAGCCGCTGACCTCTCGGCTTTCACTTGGGCAGAGGGAGCCATTTGGTGGCGCTG
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SEQ ID NO:87

>gi|4503745|ref|NP_001447.1| filamin 1 (actin-binding protein-280); filamin
35 A, alpha (actin-binding protein-280); filamin 1; actin-binding protein-280
[Homo sapiens]
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LSDGLRLIALLEVLSQLKMRKHNRPTFRQMQLENVSVALEFLDRESIKLVSIDSKAIVDGNLKLILGL
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40 PDWDSWDASKPVTNAREAMQQADDWLGIPOVITPEEIVDPNVDEHSMVTYLSQFPKAKLKPGAPLRPKLN
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45 IGRSPFEVKGTECGNQKVRWGPGLGGVVGKSADFVVEAIGDDVGTGLGFSVEGPSQAKIECDDKGDGS
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50 FSGLTKGDAVRDVIDIDHHDNTYTVKYTPVQQGPVGVNVTYGGDPIPKSPFSVAVSPSLDLSKIKVSGLG
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PVPGPSFPLEAVAPTTPSKVKAFGPGLQGGGAGSPARFTIDTKGAGTGGGLGLTVEGPCEAQLECLDNGDG
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AELTIEICSEAGLPAEVYIQDHGDGTHITITYIPLCPGAYTVTIKYGGQPVPNFPKSLQVEPAVDTSGVQC
55 YGPGIEGQGVFREATTETFSVDARALTQTGGPHVKARVANPSGNLTETYVQDRGDMYKVEYTPYEGLHS
VDVTYDGSPPVSSPFPVPTGCDPSRVVHGPQIGSGTTNKPKNFTVETRGAGTGGLGLAVEGPSEAKM
SCMDNKDGSCSVEYIPYEAGTYSLVNTYGGHQVPGSPFKVPVHDVTDASKVKCSGPGLSPGMVRANLPQS
FQVDTSKAGVAPLQVKVQGPGLVEPVDVVDNADGTQTVNYVPSREGPYSISVLYGDEEVPRSPFKVKVL
PTHDAKVKASGPGLNTTGVPASLPVEFTIDAKDAGEGLLAVQITDPEGKPKKTHIQDNHDGTYTVAYVP
60 DVTGRYTILIKYGGDEIPFSPYRVRAVPTGDASKCTVTVSIGGHGLGAGIGPTIQIGEETVITVDTKAAG
KGKVTCTVCTPDGSEVDVDVVENEDGTFDIFYTAPQPGKYVICVRFGGEHVPNSPFPQVTALAGDQPSVQP

PLRSQQLAPQYTYAQQGQQTWAPERPLVGVNGLDVTSLRPFDLVIPFTIKKGEITGEVRMPSGKVAQPTI
 TDNKDGTVTTRYAPSEAGLHEMDIRYDNMHIPGSPLQFYVDYVNCGHVTAYGGLTHGVVNKPATFTVNT
 KDAGEGGLSLAIEGPSKAEISCTDNQDGTCSVSYLPVLPDYSILVKYNEQHPGSPFTARVTGDDSMRM
 SHLKVGSAADIPINISSETDLSSLTATVVPSPGREEPCLLKRLRNHVGISFVVPKETGEHLVHVKNKGQHV
 5 ASSPIPVVISQSEIGDASRVRVSGQLHEGHTFEPAEFIIDTRDAGYGGLSLSIEGPSKVDINTEDLEDG
 TCRVTYCTPEPGNYIINIKFADQHVPGSPFSVKVTGEGRVKESITRRRRAPS VANVGSHCDLSLKIP EIS
 IQDMTAQVTSPSGKTHEAEIVEGENHTYCIRFVPAEMGTHTVSVKYKGQHVPGSPFQFTVGPLGEGGAHK
 VRAGGPGLERAEGVPAEFSIWTR EAGAGGLAIAVEGPSKAEISFEDRKDGSCGVAYVVEPGDYEVSVK
 FNEEHIPDSPFVVPVSPSGDARRLTVSSLOESGLKVNQPASFAVSLNGAKGAIDAKVHSPSGALEECYV
 10 TEIDQDKYAVRFIPRENGVYLIDVKFNGTHIPGSPFKIRVGEPGHGGDPGLVSA YGAGLEGGVTGNPAEF
 VVNTSNAGAGALSVTIDGPSKVKMDCQECPEGYRVTYTPMAPGSYLSISIKYGGPYHIGGSPFKAKVTGPR
 LVSNHSLHETSSVFVDSLTKATCAPQHGAPGPGPADASKVVAKGLGLSKAYVGQKSSFTVDCSKAGNNML
 LVGVHGPRTPCEEILVKHVGSR LYSVSYLLKDKGEYTLVVKWGHEHIPGSPYRVVVP

15 SEQ ID NO:88

Gα13 protein

>GL2_46_3_M13R Direction: sense

CCGCGAGGGCAGCGGCGGCGCAAGATGGCGGACTTCCTGCCGTGCGGGTCCGTGCTGTCCGTGTGCTTCCCCGG
 GNCTGCCTGCTGACGAGTGCGGAGG

20

SEQ ID NO:89

>gi|5729847|ref|NM_006572.1| Homo sapiens guanine nucleotide binding
 protein (G protein), alpha 13 (GNA13), mRNA

25 TGGGGCCGGAGAGGCGGCGAGGCGGCGGCGGCGGCGCAAGATGGCGGACTTCCTGCCGTGCGGGTCCGT
 GCTGTCCGTGTGCTTCCCCGGCTGCTGCTGACGAGTGCGGAGGCCGAGCAGCAACGCAAGTCCAAGGAG
 ATCGACAAAATGCCTGTCTCGGGAAAAGACCTATGTGAAGCGGCTGGTGAAGATCCTGCTGCTGGGCGCGG
 GCGAGAGCGGCAAGTCCACCTTCCTGAAGCAGATGCGGATCATCCACGGGCAGGACTTCGACCAGCGCGC
 GCGCGAGGAGTTCCGCCCCACCATCTACAGCAACGTGATCAAAGGTATGAGGGTGCTGGTTGATGCTCGA
 30 GAGAAGCTTCATATTCCCTGGGGAGACAACCTCAAACCAACAACATGGAGATAAGATGATGTGCTTTGATA
 CCCGGGCCCCCATGGCAGCCCAAGGAATGGTGGAACAAGGGTTTTCTTACAATATCTTCCTGCTATAAG
 AGCATTATGGGCAGACAGCGGCATACAGAATGCCTATGACCGGCGTCGAGAATTTCAACTGGGTGAATCT
 GTAAAATATTTCTGGATAAATTTGGATAAATTTGGAGAACCAGATTATATTCATCACAACAAGATATTC
 TGCTTGCCAGAAGACCCACCAAAGGCATCCATGAATACGACTTTGAAATAAAAAATGTTCTTTTCAAAT
 35 GCTTGATGTAGGTGGTCAGAGATCAGAAAGGAAACGTTGGTTTGAATGTTTCGACAGTGTGACATCAATA
 CTTTTCTTGTTCCTCAAGTGAATTTGACCAGGTGCTTATGGAAGATCGACTGACCAATCGCCTTACAG
 AGTCTCTGAACATTTTGAACAATCGTCAATAACCGGGTTTTTCAGCAATGTCTCCATAATTCTGTTCTT
 AAACAAGACAGACTTGCTTGAGGAGAAGGTGCAAAATGTGAGCATCAAAGACTATTTCTAGAAATTTGAA
 GGGGATCCCCACTGCTTAAGAGACGTCCAAAAATTCCTGGTGGAATGTTTCCGGAACAAACGCCGGGACC
 40 AGCAACAGAAGCCCTTATACCACCCTTCACCACTGCTATCAACACGGAGAACATCCGCCTTGTTTTCCG
 CGACGTGAAGGATACTATTCTGCATGACAACCTCAAGCAGCTTATGCTACAGTGATGTACAAAAGACTTG
 CTGTTTTAATATCTTTTTGTGTTTTTGATGTTTTCTGTTTTGTTTTTAAATAGCAGTTTACAAC
 CAGAATTAGAACAATCTTAATCTACGTTTAACTTCTTGAAAATCTTAGTACTTTTTCTGCGGCCTTTGG
 TTTGTGGCTGAAAGCTGTTGAGTGACTCATCGCAAGATTGCTGTAATGCAGGCTTTGATCTGTTTCAC
 45 CC

SEQ ID NO:90

>gi|5729848|ref|NP_006563.1| guanine nucleotide binding protein (G
 protein), alpha 13; guanine nucleotide binding protein, alpha-13 [Homo
 sapiens]

50 MADFLPSRSVLSVCFPGCLLTSGEAEQQRKSKEIDKCLSREKTYVKRLVKILLGAGESGKSTFLKQMRI
 IHGQDFDQRRAREEFRPTIYSNVIKMRVLVDAREKLHIPWGDNSNQHGDKMMSFDTRAPMAAQGMVETR
 VFLQYLPALRALWADSGIQNAYDRRREFQLGESVKYFLDNLDKLGEPDYIPSQQDILLARRPTKGIHEYD
 FEIKNVFPKMLDVGQRSEKRWFECDVSTILFLVSSSEFDQVLMEDRLTNRLTESLNIFETIVNNRV
 FSNVSIILFLNKTDLLEEKVQIVSIKDYFLEFEGDPHCLRDVQKFLVECFRNKRDRDQQQKPLYHHFTTAI
 55 NTENIRLVFRDVKDTILHDNLKQLMLQ

SEQ ID NO:91

HOXB2

>GL3_11D_1_M13R Direction: sense

5 TTTGCCCTGACCCGGGCCATTGCCAGAAGACGTCTTCTCGGGGCGCCAGGATTCACCTTTCCTTCCCGACCTCAA
CTTCTTCGCGGCCGACTCCTGTCTCCAGCTATCCGGAGGCCTCTCCCCTAGCCTACAGGGTTCTCTCGACAGCCC
TGGTCCCTTTTCCGATGGACAAAGAGCTTGGATTTTTTCACCAAGTACCGCTCTGTGCCCAATTCTGGAGCCTGC
NAGGTTTTACCCCCCCTTTAAAAAGCCCCCTTTGGTTATATACCCCTTACCCTTACCCCCCGTGGGTTACCCC
TTNTATACGGAACCCCCCTGGTCGGCCTTCCCCTTTATGGGGCCCCGGTCTTAAACCTGGGGAAACACAAN
10 AACTTCCGGAAGGGACCCCCATTTCGATTTACCCCGCAAAAGCCCCCNCTTTCCCAAANGGATACCGGCCA
AGTTNTAAAGGAAACCTTTTAAANATTTGGATTGAGGATTATTTATTATAGGGGCCCTATTAAAAACAAACAACAA
CACTTCTTTTTATCCACAAAGTGGNGGGATNTAAATGATTTATCAAANCCCGTTTGTGGTAACAAAACAATTTT
TTTACAAAACGNCCCGGAGTATATTAGTTATAAAAAAATATTCCTCCCGAAAAACATTATTTCTCCCCCCCCC
CTTATATATTTTAAACCCCCATATATTCAACNGCTATTTATTATTGCCACCATATTTTACCCCATAAATA

15 SEQ ID NO:92

>GL3_21C_1_M13F Direction: N/A

TTTGCCCTGACCCGGGCCATTGCCAGAAGACGTCTTCTCGGGGCGCCAGGATTCACCTTTCCTTCCCGACCTCAA
CTTCTTCGCGGCCGACTCCTGTCTCCAGCTATCCGGAGGCCTCTCCCCCTTAGCCTACAGGGTTCTCTCGACAGC
20 CCGTCCCGGTTTTTTATTTCCCGGAAGGGGGAAGGGAAGGCTGGGGATTGTGTTTCGACGCAGTACGCTCTGT
GCCATCGACCTGCAGTTTCCCTAACCTGTTTCTCTCCCGTCTTTTCGACCCCCGCGCTCCTTGGCCGTCTAC
TGGA

SEQ ID NO:93

>GL3_11D_1_M13F Direction: anti-sense

25 AAAANGTATAGACTCACTATAGTGGCGAATTGGGNCCATCTAGATGCATGCTCGAGCGGCCGCCAGGTGTGATGG
ATATCTGCAGAATTGCTGCCGCTTACGACAGTCAGTGAGTATCAGACCTCAGAGCTAGATCGAGCGGCCGCTTTA
TCTATCTAACCAC'TGTGCTGGGTTTCGTGCGNCCCCGCTAGAGTTTAAATGTATTCTGAGATTTCACTGGACAGG
AGTCTACCAAACGGAATTTTTCTGTGTGAATTTTAAAGATAACCGAGTGCCCAATATTTTAGAACGAAGAAGAA
30 AGGGAGTGGATTAAACGCTAAGTTTCAGTAATACCNCTGAAGTTTTTAGCAAAAGCGACATAAGTTCTATGGCGACT
GAGGGGTGGGAGAGGCTCGACGNNTTNAACCAAGTAGACGGGCCAAGGAAGGCGCGNNGGGGTCCGGAAACANGG
GACCCGGGGCAGGGGGAGGGGAAAAAACCGGGTTACAGCGNGAAAAACCTGGCCAAGGGACTACCCGGAACGTAT
GAGGGCCAAACAAAAGAAAGGCCGATTAAACCTATGGGGGATTGGAAAAAAAATCCCAAAGGGCTTCCTAT
ATCCCCCTCCGGGGGAAAAAACACAGGGGGGAAACCCCCGGGAGGCCCTATGGATCCAGGACACGAAAGCGAA
35 AACCCCCCTGGGTAAGAGAGCCCTAAGGGGGGA

SEQ ID NO:94

>GL3_27D_2_M13R Direction: anti-sense

CCCCCTAGAGTTTAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTTCTGTGTGAATTTT
AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG
40 AATTTTAGCAAAACACATAAGTCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTTCCAGTAGACGGCCAAGGAG
CGCGGGGTGCGAAAGGACCGGAGGAGGAACAGGTTAGGGAAACTGCAGGTCGATGGCACAGAGCGTACTGGTG
AAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGGCTGTGCGAGAGAACCCTGTAGGCTAGGAGGAGCCTCCG
GATAGCTGGAGACAGGAGTGGCCGCGAAGAAGTTGAGGTGCGGAAGGAAAGGTGAATCCTGGCGCCCCGAGAAG
45 ACGTCTTCTGGCAATGGCCCGGGCTCCAGCCCCACGGCCCCGCGCAGCGCGCAAGCCGGGACTTCGAACGCACNC
NTGCAGCCCTCATAAGCGAACGGCATAAAAGGCCCGGGGGTCCAGCGCATTAAAGGGCCCCCGGACCATCCTCC
GGGCGAGGTGAACAAGCGGGTTACCCAAGGCCGGCGAGAGGTCCCGAGGCCATTNGACTAGGGNT

SEQ ID NO:95

>GL3_45B_3_M13F Direction: N/A

50 TTTGCCCTGACCCGGGCCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGCGGGGCGCGCAGGCTGCGCACGGGTTTACACCAACACGCAGCTGCTGGAACCTGGGAAG
GAATTCACCTTTAATAAGTACCTGTGCGGCCACGCCGCTCGAGATCGCGGCCCTTGTGGACCTCACCAGAAAGG
CAGGTCAAAGTCTGGTTTTCAGAACCGGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCGGATGGG
55 GAGCCTGCCTGCCCGGAGCCCTGGAGGACATCTGCGACCCTGCCGAGGAACCTGCGGCCAGCCCGGGCGGCC
CTCCGCTCGCGGGCGCGTGGGAAGCCTGCTGTACCCGCCGAGGTGGTTGCCGGGGGCC

SEQ ID NO:96

>GL3_27D_1_M13R Direction: anti-sense

60 CCCCCCTAGAGTTTAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAAACGGAATTTTTCTGTGTGAATTTT
AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG

AATTTTAGCAAAACACATAAGTCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTTCCAGTAGACGGCCAAGGAG
CGTGGGGGTGCAAAAGGACCGGGAGGAGGAAACAGGTTAGGGAAACTGCAGGTCGATGGCACAGAGCGTACTGGTG
AAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGGCTGTCGAGAGAACCCTGTAGGCTAGGGGAGAGGCCTCCG
GATAGCTGGAGACAGGAGTCGGCCGCGAAGAAGTTGAGGTCGGGAAGGAAAGGTAATTCCTTCTCCAGTTCCAGC
AGCTGCGTGTGGTGTAAAGCCGTG

SEQ ID NO:97

>GL3_45B_1_M13R Direction: sense

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGCGGGGCGCGCAGGCTGCGCAGGTTACACCAACACGCAGCTGCTGGAACCTGGAGAAGGA
ATTCCACTTTAATAAGTACCTGTGCGGCCACGCCGCTCGAGATCGCGGCTTGCTGGACCTACCGAAAGGCA
GGTCAAAGTCTGGTTTCAGAACCGGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCGGATGGGGA
GCCTTGCCCTTGCCCGGGAGCCCTTGAGGACATCTGCGACCCTGCCGAGGAACCCGCGGGCCAGCCCGGGCGGCC
CCTTCCGCCTCGCGGGCGGGCG

SEQ ID NO:98

>GL3_11D_3_M13R Direction: anti-sense

CCCCCTAGAGATTCTAATGTACTTCTGAGATTATCACTGGAAGGAGATCTACCAAACGGAATTTCTTCCGTGT
GAATTTTAACAGAGATAACCGAGTGCCCATATTTTAGAAGAAGAAGAAAGGAGTGGATTAAACGCTAATTCAGT
AATACCTGAATTTTAGCAAAGACACATAAGTCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTTCCAGTAGACG
GCCAAGGAGCGCGGGGTCGAAAGGACCGGGAGGAGGAAACAGGTTAGGGAAACTGCAGGTCGACTGGCACAGAG
CGTACTGGTGAAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGGCTGTCGAGAGAACCCTGGTAGGCTAGGGG
AGAGGCCTCCGATAGCTGGAGACAGGAGTCGGCCGCGAANGAAGTTGAGGTCGGGAAGGAAAGGTGAATCC

SEQ ID NO:99

>GL3_11D_4_M13F Direction: sense

AAATTGGAAATAGACTCACTATAGGGCGAATTGGGCCCTCTAGAATGACATGCTCGAGCGGCCAGNCCAAGGTGT
GATGGATATCTGCAGAAATCTGCCCTTACGACAGTCAGTGAGTATCAGACCTCAGAGCTAGATCGTAGCGGCCGC
TTTATCTATCTAACCCTGTGCTGGGTNTCTGCGGCCCCCGCTAGAGTTTAATTATTCCTGAGATTTCACTGGCC
AGGGAGTCTACCAACAGGGAATTTTCTGTGTGAATTTTAAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGA
AGAAAGGAGTGGATTAAACGCTAATTCAGTAATACCTGAATTTTAGCAAAACACATAAGTCTATGCGACTGAGG
GTGGGAGAGGCTCGATTTTCCAGTAGACGGCCAAGGAGCGCGGGGNCGAAAGGACCGGGAGGAGGAAACAGGT
TAGGGAAACTGCAAGTTCGATGGCACAGAGCGTACTGGTGAAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGG
GTGTAAGAGAGAACCCTGGNAAGGCCAGCGGGA

SEQ ID NO:100

>GL3_41D_1_M13R Direction: anti-sense

CCCCCTAGAGTTTAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAACGGAATTTTTCTGTGTGAATTTT
AAGAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCT
GAATTTTAGCAAAACACATAACGTCTATGCGACTGAGGGTGGGAGAGGCTCGATTTTGTCCAGTACGACGGCCAA
GGAGCGCGCGGGGTCGAAAGGACCGGGAGGAGGAAACAGGTTAGGGAAACTGCAGGTCGATGGCACAGAGCGTAC
TGGTGAAAAATCCAGCTCTACCTCGGAAAAAGGGACCGGGACCNATCGAGAGAACCCTGTAGGCTAGGGGAGA
GGCATCCGGATAGACTGGAGACAGGAGTCGGAACGCGAAGAAGTACGAGGTCGNGGAAGG

SEQ ID NO:101

>GL3_41D_3_M13R Direction: anti-sense

CCCCCTAGAGTTTAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAACGGAATTTTTCTGTGTGAATTTT
AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG
AATTTTAGCAAAACACATAAGTCTATGCGACTGAGGGTGGGAGGGGCTCGATTTTCCAGTAGACGGCCAAGGAG
CGCGGGGTGCAAAAGGACCGGGAGGAGGAAACAGGTNAGGGAAACTGCAGGTCGATGGCACAGAGCGTACTGGTG
AAAAAATCCAGCTCTTCTCGGAAAAAGGGACCGGGCTGTCGAGAGAACCCTGTAGGCTAGGGGAGAGGCCTCCG
GATAGCTGGAGACAGGAGTCGGCCGCGAAGAAGTNGAGGTGCGGAAGGAAAGCGTGAAAGTCCCTGGCACAGCCA
CCGAAGGCAAGAAGACGGATCNTTTTCATNGGACAAAAATGGGACCCAGGAGCATCCCAAGCACCCGGANCGGGCG
CCCCGGACGCAGNAGCGCAAGACAGGGNGAATCAGGAAAGGCAGNACNTGACGACCCCATTCAAAAAG
GAGAGAACAANGGNATAAAAAGGGACCAGGAGAAGANCAAG

SEQ ID NO:102

>GL3_41D_4_M13R Direction: anti-sense

CCCCCTAGAGTTTAATTATTCCTGAGATTTCACTGGAAGGAGTCTACCAACGGAATTTTTCTGTGTGAATTTT
AAAAGATAACCGAGTGCCCAATATTTTAGAAGAAGAAGAAAGGGAGTGGATTAAACGCTAATTCAGTAATACCTG

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>GL3_45B_1_M13F Direction: anti-sense

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>GL3_45B_3_M13R Direction: anti-sense

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>GL3_45B_4_M13R Direction: anti-sense

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>GL3 27D 3 M13F Direction: N/A

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>GL3_27D_3 M13R Direction: anti-sense

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>GL3 27D 4 M13F Direction: N/A

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>GL3 27D 4 M13R Direction: anti-sense

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>GL3 21C 1 M13R Direction: anti-sense

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>GL3_41D_3_M13F Direction: N/A

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>GL3 41D 4 M13F Direction: N/A

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>GL3 41D PCR G3F1 Direction: N/A

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SEQ ID NO:114

>GL3_41E_PCR_G3F1 Direction: sense

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGGCGCGCAGGCTGCGCACGGCTTACACCAACACGCAGCTCTGGAAGTGGAGAAGGA
ATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCTCGAGATCGCGGCCTTGCTGGACCTCACCGAAAGGCA
GGTCAAAGTCTGGTTTCAGAACCGGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGGATGGGGA
GCCTGCCTGCCCGGGAGCCCTGGAGGACATCTGCGACCCCTGCCGAGGAACCCGCGGCCAGCCCGGGCGGGCCCTC
CGCCTTCGCGGGCGGCGTGGGAAGCCTGCTGTACCCGCCGAGGTGGTGGCGGGGGCCTTAAGCGCGGACCCCCG
GCCTTTAGCCGTTTCGCTTAGAGGGCGCAGGCGCGTTCAGTCCCAGGTGCGCGCTGCGCGGGGCGCGGGGCTGGA
GCCCGGGCCATTGCCAGAAGACGTCTT

SEQ ID NO:115

>GL3_45B_4_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGGCGCGCAGGCTGCGCACGGCTTACACCAACACGCAGCTGCTGGAAGTGGAGAAGG
AATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCTCGAGATCGCGGCCTTGCTGGACCTCACCGAAAGGC
AGGTCAAAGTCTGGTTTCAGAACCGGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGGATGGGG
AGCCTGCCTGCCCGGGAGCCCTGGAGGACATCTGCGACCCCTTGCCGAGGAACCCGCGGCCAGCCCGGGCGGGCC

SEQ ID NO:116

>GL3_45B_PCR_G3F1 Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGGCGCGCAGGCTGCGCACGGCTTACACCAACACGCAGCTGCTGGAAGTGGAGAAGG
AATTCCACTTTAATAAGTACCTGTGCCGGCCACGCCGCTCGAGATCGCGGCCTTGCTGGACCTCACCGAAAGGC
AGGTCAAAGTCTGGTTTCAGAACCGGCGCATGAAGCACAAGCGGCAGACGCAGCACCGAGAGCCGCCGGATGGGG
AGCCTGCCTGCCCGGGAGCCCTGGAGGACATCTGCGACCCCTGCCGAGGAACCCGCGGCCAGCCCGGGCGGGCCCT
CCGCCTCGCGGGCGGCGTGGGAAGCCTGCTGTACCCGCCGAGGTGGTGGCGGGGGCCTTAAGCGCGGACCCCC
GGCCTTTAGCCGTTTCGCTTAGAGGGCGCAGGCGCGTTCAGTCCCAGGTGCGCGCTGCGCGGGGCGCGGGGCTGG
AGCCCCGGGCCATTGCCAGAAGACGTCTTCTCGGGGCG

SEQ ID NO:117

>GL3_27D_1_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAGAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGGCGCGCAGGCTTGCGGCCAACGGTTTTACACCAAAACACGCAGCTGCTTGGAA
CTGGAGAAAGGAAATTAACCTTTTTCTTTCCCGAACCTTCAAACCTTTCTTTTCGGCGGGCCGGACTTCTTTGTC
TCCAGCTTATCCGGAGAGCGCTTCTCCCCATTAGCCCTAACAAAGGGGTTCTCTCNGGACAGGCCCGCGGGGTCC
CCTTTTTTCCGGAGAAAGAGCTTGAATTTTCCAACCAAGGTACGGCCATTCTGTTGGTTGCCCCCAATTTTCGT
AGAACCCTTTGCACAAGGTTTTTTCCCCCTATAAAAACCTGTGGTTTTTTCCCTTCCACCTTTCCCCGCGGGGG
TATCCCTTTTTTTCAGGAAGCCGCGCCNACAAAAGGGCCTTCTATTTTGGGCCCCGTGTAATCTTTAGCGTGTGG
GAAAACAGAATTTCGTCGGGAAGGCCCTTCTTCCACAAACCCCCATTCTNAGAGGTCCGGGGCAAGATTTAGAAA
CTTTATTGGACTATGATTTGTGTTGAGGGCCCTTAAACACAAAATTTTCAAGGGGATTATTTTTTA

SEQ ID NO:118

>GL3_27D_2_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGCACTG
CCTGGCGCTTTGGGAAGCGTGCTGTACCCGTCGGAGGGTGGATGCCGTGGGGTCTATGAAGCTGCGGACCCCC
CGGTCTTTAGACCGTACGCTTAGAGCGGCGGACAGGCNCGTCGAGGTCCCGGCTGCGAACAGCGCGGAGCCCGGG
CNGCATGAAGCCTCGTGTNCNAATTTNCCAAGAATGGAAGGGTTCTTACCCTTCNGAGGCGCGGCCAAGNGTA
CTTCTTACCCCTGTGTTTCCCTTTTCCCCGAAACCTCTCGAAGTCTTTCTTTACGGGCGNGGCCAGANACTC
CGTTGTTCTTACCCTANGGATTACANCTGAGAAGACCTTTTNCNACGCCTCNTTGAGGCCTCACTGTAAACNGG
TGGGAGGGTTNGTCTCCGTTCTTNCGGGGACCTAAGCGGGCCGCTGGGCGAACCGGGTTTTTTTTAAACCTCA
CCGGGAGAAAGNAGACAAAANGACAAAGGGTCTTTTGAGGAAGATTCCATCTTTNCACNACCCGTATAGATTAGT
TAACGGGTCTCCCTTGTGCTTCGCCCACATATTTAAGTACCGGCTGTGGGCGAAGCGTTCTTGGCCCNCCAAATTA
CACAGTCCNCTTTGTGATATAACCCNCTTCCACTCTTACCCGNGCGGGGACTCCCACTTTTTTTTTC

SEQ ID NO:119

>GL3_41D_1_M13F Direction: N/A

TTTGCCCTGACCCGGGCGGGGCTGTAGACTAGAGAGGGAGAGAAGAAAACCCAAAAGCAATGGCCTGGGACTGC
CGGAGGCTGGTGGCGGGCGGGGCGCGCAGGCTGCGCNACGGTTACACTCAACTACGCAGCTGCTGGAAGTGGAGA
AGGAATTTCCACTTTAATAAGTACCTTGTGTCCGGGCCACAGCCGGCGGTTCAGAGATCNGCGGGCCTTTGCCTGG

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SEQ ID NO:125

>GL2_1_A03_G3F1 Direction: sense

GTTCTAGATCGCGAGCGGCCGCGTGGAGATCATCGCCAACGATCAGTGGCAACCGCATCACGCCGTCCTATGTCTG
CCTTCACTCCTGAAGGGGAACGTCTGATTGGCGATGCCGCCAAGAACCAGCTCACCTCCAAACCCGAGAACACGG
TCTTTGACGCCAAGCGGCTCATCTGG

SEQ ID NO:126

>GL2_1_A05_G3F1 Direction: sense

GTTCTAGATCGCGAGCGGCCGCGTGGAGATCATCGCCAACGATCAGGGGCAACCGCATCACGCCGTCCTATGTCTG
CCTTCACTCCTGAAGGGGAACGTCTGATTGGCGATGCCGCCAAGAACCAGCTCACCTCCAACCCCGAGAACACGG
TCTTTGACGCCAAGCGGCTCATCTGG

SEQ ID NO:127

HSP5>

ATGGAGGAGGACAAGAAGGAGGACGTGGGCACGGTGGTTCGGCATCGACCT
GGGGACCACCTACTCCTGCGTGGCGTGTTCAGAAGCGGCCGCGTGGAGA
TCATCGCCAACGATCAGGGCAACCGCATCACGCCGTCCTATGTCTGCCTTC
ACTCCTGAAGGGGAACGTCTGATTGGCGATGCCGCCAAGAACCAGCTCAC
CTCCAACCCCGAGAACACGGTCTTTGACGCCAAGCGGCTCATCGGCCGCA
CGTGGAATGACCCGCTCTGTGCAGCAGGACATCAAGTTCTTGCCGTTCAAG
GTGGTTGAAAAGAAAACTAAACCATAATTCAAGTTGATATTGGAGGTGG
GCAAACAAAGACATTTGCTCCTGAAGAAATTTCTGCCATGGTTCTCTACTA
AAATGAAAGAAACCGCTGAGGCTTATTTGGGAAAGAAGGTTACCCATGCA
GTTGTTACTGTACAGCCTATTTTAATGATGCCCAACGCCAAGCAACCAA
AGACGCTGGAACCTATTGCTGGCCTAAATGTTATGAGGATCATCAACGAGC
CTACGGCAGCTGCTATTGCTTATGGCCTGGATAAGAGGGAGGGGGAGAAG
AACATCCTGGTGTGTTGACCTGGGTGGCGGAACCTTCGATGTGTCTCTTCT
CACCATTGACAATGGTGTCTTTCGAAGTTGTGGCCACTAATGGAGATACTC
ATCTGGGTGGAGAAGACTTTGACCAGCGTGTCTATGGAACACTTCATCAAA
CTGTACAAAAAGAACGCGGCAAGATGTCAGGAAAGACAATAGAGCTGT
GCAGAACTCCGGCGCGAGGTAGAAAAGGCCAAACGGGCCCTGTCTTCTC
AGCATCAAGCAAGAAATTGAAATTGAGTCTTCTATGAAGGAGAAGACTTT
TCTGAGACCCCTGACTCGGGCCAAATTTGAAGAGCTCAACATGGATCTGTT
CCGGTCTACTATGAAGCCCGTCCAGAAAGTGTGGAAGATTCTGATTTGA
AGAAGTCTGATATTGATGAAATTGTTCTTGTGTTGGTGGCTCGACTCGAATT
CCAAAGATTTCAGCAACTGGTTAAAGAGTTCTTCAATGGCAAGGAACCATC
CCGTGGCATAAAACCCAGATGAAGCTGTAGCGTATGGTGTCTGTGTCAGG
CTGGTGTGCTCTCTGGTGTATCAAGATACAGGTGACCTGGTACTGCTTGAT
GTATGTCCCCCTTACACTTGGTATTGAAACTGTGGGAGGTGTCTGACCAA
ACTGATTCCAAGGAACACAGTGGTGCCTACCAAGAAGTCTCAGATCTTTT
CTACAGCTTCTGATAATCAACCAACTGTTACAATCAAGGTCTATGAAGGT
GAAAGACCCCTGACAAAAGACAATCATCTTCTGGGTACATTTGATCTGAC
TGGAATTCTCTCTGCTCCTCGTGGGGTCCACAGATTGAAGTCACCTTTG
AGATAGATGTGAATGGTATTCTTCGAGTGACAGCTGAAGACAAGGGTACA
GGGAACAAAAATAAGATCACAATCACCATGACCAGAATCGCCTGACACC
TGAAGAAATCGAAAGGATGGTTAATGATGCTGAGAAGTTTGCTGAGGAAG
ACAAAAAGCTCAAGGAGCGCATTGATACTAGAAATGAGTTGGAAAGCTAT
GCCTATTCTCTAAAGAATCAGATTGGAGATAAAGAAAAGCTGGGAGGTAA
ACTTTCCTCTGAAGATAAGGAGACCATGGAAAAAGCTGTAGAAGAAAAGA
TTGAATGGCTGGAAAGCCACCAAGATGCTGACATTGAAGACTTCAAAGCT
AAGAAGAAGGAACCTGGAAGAAATTGTTCAACCAATTATCAGCAAACTCTA
TGGAAGTGCAGGCCCTCCCCCAACTGGTGAAGAGGATACAGCAGAACTCC
ACCACCACCACCACCAC

SEQ ID NO:128

>gi|21361242|ref|NM_005347.2| Homo sapiens heat shock 70kD protein 5
(glucose-regulated protein, 78kD) (HSPA5), mRNA

ACAGCACAGACAGATTGACCTATTGGGGTGTTCGCGAGTGTGAGAGGGGAAGCGCCGCGGCCTGTATTTC
TAGACCTGCCCTTCGCCTGGTTTCGTGGCGCCTTGTGACCCCGGGCCCTGCCGCTGCAAGTCGGAAATT
GCGCTGTGCTCCTGTGCTACGGCCTGTGGCTGGACTGCCTGCTGCTGCCCAACTGGCTGGCAAGATGAAG

CTCTCCCTGGTGGCCGCGATGCTGCTGCTGCTCAGCGCGGCGCGGGCCGAGGAGGAGGACAAGAAGGAGG
ACGTGGGCACGGTGGTGGCATCGACCTGGGGACCACCTACTCTGCGTGGCGGTTC AAGAACGGCCG
CGTGGAGATCATCGCCAACGATCAGGGCAACCGCATCACGCCGTCTATGTGCGCTTCACTCCTGAAGGG
5 GAACGTCTGATTGGCGATGCCGCCAAGAACCAGCTCACCTCCAACCCCGAGAACACGGTCTTTGACGCCA
AGCGGCTCATCGGCCGACGTGGAATGACCCGTCTGTGCAGCAGGACATCAAGTTCTTGCCGTTCAAGGT
GGTTGAAAAGAAAATAAAACCATACATTCAAGTTGATATTGGAGGTGGGCAAAACAAAGACATTTGCTCCT
GAAGAAATTTCTGCCATGGTTCTCACTAAAATGAAAGAAACCGCTGAGGCTTATTTGGGAAAAGAGTTA
CCCATGCAGTTGTTACTGTACCAGCCTATTTTAATGATGCCCAACGCCAAGCAACCAAAGACGCTGGAAC
10 TATTGCTGGCCTAAATGTTATGAGGATCATCAACGAGCCTACGGCAGCTGCTATTGCTTATGGCTGGAT
AAGAGGGAGGGGAGAAGAACAATCCTGGTGTGTTGACCTGGGTGGCGGAACCTTCGATGTGTCTCTTCTCA
CCATTGACAATGGTGTCTTCGAAGTTGTGGCCACTAATGGAGATACTCATCTGGGTGGAGAAGACTTTGA
CCAGCGTGTCTGGAACACTTCATCAAACGTGACAAAAGAAGACGGGCAAAGATGTCAGGAAAGACAAT
AGAGCTGTGCAGAACTCCGGCGCGAGGTAGAAAAGGCCAAACGGGCCCTGTCTTCTCAGCATCAAGCAA
15 GAATTGAAATTGAGTCTTCTATGAAGGAGAAGACTTTTCTGAGACCCTGACTCGGGCCAAATTTGAAGA
GCTCAACATGGATCTGTTCCGGTCTACTATGAAGCCCGTCCAGAAAGTGTGGAAAGATTCTGATTTGAAG
AAGTCTGATATTGATGAAAATGTTCTTGTGTTGGTGGCTCGACTCGAATTCCAAAGATTCAAGCACTGGTTA
AAGAGTTCTTCAATGGCAAGGAACCATCCCGTGGCATAAACCCAGATGAAGCTGTAGCGTATGGTGCTGC
TGTCAGGCTGGTGGTCTCTGTTGATCAAGATACAGGTGACCTGGTACTGCTTGATGTATGCCCTT
20 ACACCTGGTATTGAAACTGTGGGAGGTGTCTATGACCAAACCTGATTCCAAGGAACACAGTGGTGCCTACCA
AGAAGTCTCAGATCTTTTCTACAGCTTCTGATAATCAACCAACTGTTACAATCAAGGTCTATGAAGGTGA
AAGACCCCTGACAAAAGACAATCATCTTCTGGGTACATTTGATCTGACTGGAATTCCTCCTGCTCCTCGT
GGGGTCCACAGATTGAAGTCACCTTTGAGATAGATGTGAATGGTATTCTTCGAGTGACAGCTGAAGACA
AGGGTACAGGGAACAAAAATAAGATCACAATCACCATGACCAGAATCGCCTGACACCTGAAGAAATCGA
25 AAGGATGGTTAATGATGCTGAGAAGTTTGTGAGGAAGACAAAAGCTCAAGGAGCGCATTGATACTAGA
AATGAGTTGGAAAGCTATGCCATTTCTCTAAAGAATCAGATTGGAGATAAAAGAAAAGCTGGGAGGTAAAC
TTTCTCTGAAGATAAGGAGACCATGGAAAAGCTGTAGAAGAAAAGATTGAATGGCTGGAAAGCCACCA
AGATCTGCATGATGAAGACTTCAAAGCTAAGAAGGAAGTGAAGAAAATGTTCAACCAATTATCAGC
AAACTCTATGGAAGTGCAGGCCCTCCCCCAACTGGTGAAGAGGATACAGCAGAAAAAGATGAGTTGTAGA
30 CACTGATCTGCTAGTGCTGTAATATTGTAAATACTGGACTCAGGAACTTTTGTAGGAAAAAATTGAAAG
AACTTAAGTCTCGAATGTAATTGGAATCTTACCTCAGAGTGGAGTTGAACTGCTATAGCCTAAGCGGC
TGTTTACTGCTTTTCATTAGCAGTTGCTCACATGTCTTTGGGTGGGGGGGAGAAGAAGAAATTGGCCATCT
TAAAAGCAGGTAAAAAACCTGGGTAGGGTGTGTGTTACCTTCAAATGTTCTATTTAACTAAGTGGGT
CATGTGCATCTGGTGTAGGAAGTTTTTCTACCATAAGTGACACCAATAAATGTTTGTATTATTAAGTGG
35 TCTAATGTTTGTGAGAAGCTTCTAATTAGATCAATTACTTATTTTAGGAAATTTAAGACTAGATACTCGT
GTGTGGGGTGAGGGGAGGGAGTATTTGGTATGTTGGGATAAGGAAACACTTCTATTTAATGCTTCCAGGG
ATTTTCTTTTCTTTTAAACCTCCTGGGCCCAAGTGATCCTTCCACCTCAGTCTCCAGCTAATTGA
GACCAAGGCTTGTACCAACCATGCTCGGCTTTTGCAATTAATCTAAGAAAAGGGAGAGAAGTTAATCCA
CATCTTTACTCAGGCAAGGGGCATTTACAGTGCCCAAGAGTGGGGTTTTCTTGAACATACTTGGTTTCC
TATTTCCCTTATCTTTCTAAACTGCCTTTCTGGTGGCTTTTTTTTAAATTAATTAATGATGCTTTT
40 ATAGCTGCTTGGATTCTCTGAGAAATGATGGGGAGTGAGTGATCACTGGTATTAATTTATACACTTGG
TTTCATTTGTAACCTTAGGATGTAAAGGTATATTGTGAACCTAGCTGTGTGAGAAATCTCCATCCCTGAA
ATTTCTCATTAGTGCTACTGGGGTGGGATCTTGGATGGTGACATTGAAACTACACTAAATCCCTCAC'TA
TGAATGGGTTGTTAAAGGCAATGGTTTGTGTCAAACCTGGTTTAGGATTACTTAGATTGTGTTCTGAA
AAAAGAGTCCAGGTAAATGGTATGATCAATAAAGGACAGGCTGGTGCTAACATAAAATCCAATATTGTAA
45 TCCTAGCACTTTGGGAGGCCAAGGCGGGTGGATCACAAGGTCAAGAGATAGAGACCATCTTTGCCAACAT
GGTGAAACTCCATCTCTACTGAAAATACAAAATTAGCTGGGCGTGGTAGTGCAAGCTGAAGGTGAGGC
AGGAGAATCACTCGAACC CGGGAGGAGGTTGAGTGAGCCGAGATCACACCACTGTACTCCAGCCCCG
GCACTCCAGCCTGGCGACAAGAGTGAGACTCCACCTCAAAAAAAAAAAAAAGAAATCCAATACTGCCCAAG
GATAGGTATTTTATAGATGGGCAACTGGCTGAAAGGTTAATTCTCTAGGGCTAGTAGAACTGGATCCCAA
50 CACCAACTCTTAATTAGACCTAGGCCTCAGCTGCACTGCCCCGAAAAGCATTGGGGCAGACCCTGAGCAG
AATACTGGTCTCAGGCCAAGCCCAATACAGCCATTAAAGATGACCTACAGTGCTGTGTACCTGGGGCAA
TAGGGTTAAATGGTAGTTAGCAACTAGGGCTAGTCTTCCCTTACCTCAAAGGCTCTCACTACCGTGGACC
ACCTAGTCTGTAACCTCTTCTGAGGAGCTGTTACTGAATATTAAAAAGATAGACTTCAAAAAAAAAAAAA
55 AAAAA

SEQ ID NO:129

>gi|16507237|ref|NP_005338.1| heat shock 70kD protein 5 (glucose-regulated protein, 78kD); BiP; Heat-shock 70kD protein-5 (glucose-regulated protein, 78kD) [Homo sapiens]

60 MKLSLVAAMLLLLSAARAEEDKKEDVGTGVGIDLGTTYSVGVFKNRVEIANDQGNRITPSYVAFTP
EGERLIGDAKNQLTSNPENTVFDKRLIGRTWNDSVQDQIKFLPFKVVEKTKPYIQVDIGGGQTKTF

APPEISAMVLTKMKETAETGKKVTHAVVTVPAYFNDAQRQATKIDAGTIAGLNVMRIINEPTAAAIAYG
 LDKREGEKNILVFDLGGGTFDVSLLTIDNGVFEVVATNGDTHLGGEDFDQRVMEHFIKLYKKKTGKDVRK
 DNRAVQKLRRVEKAKRALSSQHQAIEIESFYEGEDFSETLTRAKEELNMDLFRSTMKPVQKVLEDS
 LKKSIDEIVLVGGSTRIPKIQQLVKEFFNGKEPSRGINPDEAVAYGAAGVQAGVLSGDQDTGDLVLLDVC
 5 PLTLGIETVGGVMTKLIPRNTVVPTKKSQIFSTASDNQPTVTIKVYEGERPLTKDNHLLGTFDLTGIPPA
 PRGVPQIEVTFEIDVNGILRVTAEDKGTGNKNKITITNDQNRLTPEEIERMVNDAEKFAEEDKKLKERID
 TRNELESYAYSILKNQIGDKKELGGKLSSSEDKETMEKAVEEKIEWLESHQDADIEDFKAKKKELEEIVQPI
 ISKLYGSAGPPPTGEEDTAEKDEL

10 SEQ ID NO:130

IFNgR1

>G3_2_37_PCR_G3F1 Direction: sense

CTGGCTTTAACTCTGACCCAAAGTAGTATTTGATGGATCACCAACATGTATCAGTAAATATTACAATAATGNATG
 TAGTAATATTGATGCAGGCATCAATCCATTCTGAATTCCTAACACCATAGTTCTTTACCTCTACGGTAAAAACAG
 15 GGACCTGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTG
 GTGTAGGCACTGAGGACGGCCCCAGATCCGCGGTGCCATCTCAGCCCTGCTCACACCCTGCATGACAAGGGGTA
 GGAGAAAGAGGAGGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCCGAGCGCCTGCGGGACCAGCCAGCG
 CTGCCC

20 SEQ ID NO:131

>GL3_2.37_A_M13F Direction: sense

CTGGCTTTAACTCTGACCCAAAGAGAATTTGATGGATCACCAACATGTATCAGAAATATTACAATAATGATGAGAA
 ATATTGATGCAGGCATCAATCCATTCTGAATTCCTAACACCATAGTTCTTTACCTCTACGGTAAAAACAGGGACC
 TGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTGGTGTA
 25 GGCATGAGGACGGCCCCAGATCCGCGGTGCCATCTCAGCCCTGCTCACACCCTGCATGACAAGGGGTAGGAGA
 AAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCCGAGCGCCTGCGGGACCAGCCAGCGCTGCC
 C

SEQ ID NO:132

>GL3_2.37_A_M13R Direction: anti-sense

GGGCAGCGCTGGGCTGGTCCCGCAGGCGCTCGGGGTTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCT
 TTCTCCTACCCCTTGTTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGCTCCTCAGTGC
 CTACACCAACTAATGTTACAATTGAATCCTATAACATGAACCCCTATCGTATATTGGGAGTACCAGATCATGCCAC
 AGGTCCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTTAAGAATTCAGAATGGATTGATGCCTGCATCAATA
 35 TTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCTCTTTGGGTCAGAGTTAAAGCCA
 G

SEQ ID NO:133

>GL3_2.37_B_M13F Direction: anti-sense

GGGCAGCGCTGGGCTGGTCCCGCAGGCGCTCGGGGTTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCT
 TTCTCCTACCCCTTGTTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGCTCCTCAGTGC
 CTACACCAACTAATGTTACAATTGAATCCTATAACATGAACCCCTATCGTATATTGGGAGTACCAGATCATGCCAC
 AGGTCCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTTAAGAATTCAGAATGGATTGATGCCTGCATCAATA
 45 TTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCTCTTTGGGTCAGAGTTAAAGCCA
 G

SEQ ID NO:134

>GL3_2.37_B_M13R Direction: sense

CTGGCTTTAACTCTGACCCAAAGAGAATTTGATGGATCACCAACATGTATCAGAAATATTACAATAATGATGAGAA
 ATATTGATGCAGGCATCAATCCATTCTGAATTCCTAACACCATAGTTCTTTACCTCTACGGTAAAAACAGGGACC
 TGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTGGTGTA
 GGCATGAGGACGGCCCCAGATCCGCGGTGCCATCTCAGCCCTGCTCACACCCTGCATGACAAGGGGTAGGAGA
 AAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCCGAGCGCCTGCGGGACCAGCCAGCGCTGCC
 55 C

SEQ ID NO:135

>GL3_2.37_C_M13F Direction: anti-sense

GGGCAGCGCTGGGCTGGTCCCGCAGGCGCTCGGGGTTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCT
 TTCTCCTACCCCTTGTTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGCTCCTCAGTGC
 CTACACCAACTAATGTTACAATTGAATCCTATAACATGAACCCCTATCGTATATTGGGAGTACCAGATCATGCCAC
 60

AGGTCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTTAAGAATTCAGAATGGATTGATGCCTGCATCAATA
TTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCCTTTGGGTCAGAGTTAAAGCCA
G

5 SEQ ID NO:136

>GL3_2.37_C_M13R Direction: sense

CTGGCTTTAACTCTGACCCAAAGAGAATTTGATGGATCACCAACATGATCAGAAATATTACAATAATGATGAGAA
ATATTGATGCAGGCATCAATCCATTCTGAATTCCTTAACACCATAGTTCCTTTACCTCTACGGTAAAAACAGGGACC
TGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTGGTGTA
10 GGCACTGAGGACGGCCCCAGATCCGCGGTGCCCATCTCAGCCCTGCTCACACCTGTCATGACAAGGGGTAGGAGA
AAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCGAGCGCCTGCGGGACCAGCCCAGCGCTGCC
C

15 SEQ ID NO:137

>GL3_2.37_D_M13F Direction: sense

CTGGCTTTAACTCTGACCCAAAGAGAATTTGATGGATCACCAACATGATCAGAAATATTACAATAATGATGAGAA
ATATTGATGCAGGCATCAATCCATTCTGAATTCCTTAACACCATAGTTCCTTTACCTCTACGGTAAAAACAGGGACC
TGTGGCATGATCTGGTACTCCCAATATACGATAGGGTTCATGTTATAGGATTCAATTGTAACATTAGTTGGTGTA
20 GGCACTGAGGACGGCCCCAGATCCGCGGTGCCCATCTCAGCCCTGCTCACACCTGTCATGACAAGGGGTAGGAGA
AAGAGGAGAGCCATGCTGCTACCGACGGTCGCTGGCTCCAACCCGAGCGCCTGCGGGACCAGCCCAGCGCTGCC
C

25 SEQ ID NO:138

>GL3_2.37_D_M13R Direction: anti-sense

GGGCAGCGCTGGGCTGGTCCCGCAGGCGCTCGGGGTTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCT
TTCTCCTACCCCTTGTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGTCCTCAGTGC
CTACACCAACTAATGTTACAATTGAATCCTATAACATGAACCTATCGTATATTGGGAGTACCAGATCATGCCAC
AGGTCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTTAAGAATTCAGAATGGATTGATGCCTGCATCAATA
30 TTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCCTTTGGGTCAGAGTTAAAGCCA
G

30 SEQ ID NO:139

>gi|4557879|ref|NM_000416.1| Homo sapiens interferon gamma receptor 1
(IFNGR1), mRNA

35 CCGCAGGCGCTCGGGGTTGGAGCCAGCGACCGTCGGTAGCAGCATGGCTCTCCTCTTTCTCCTACCCCTT
GTCATGCAGGGTGTGAGCAGGGCTGAGATGGGCACCGCGGATCTGGGGCCGTCCTCAGTGCCTACACCAA
CTAATGTTACAATTGAATCCTATAACATGAACCTATCGTATATTGGGAGTACCAGATCATGCCACAGGT
CCCTGTTTTTACCGTAGAGGTAAAGAACTATGGTGTTAAGAATTCAGAATGGATTGATGCCTGCATCAAT
40 ATTTCTCATCATTATTGTAATATTTCTGATCATGTTGGTGATCCATCAAATTCCTTTGGGTCAGAGTTA
AAGCCAGGGTTGGACAAAAAGAATCTGCCTATGCAAAGTCAGAAGAATTTGCTGTATGCCGAGATGGAAA
AATTGGACCACCTAAACTGGATATCAGAAAGGAGGAGAAGCAAAATCATGATTGACATATTTACCCCTTCA
GTTTTTGTAAATGGAGACGAGCAGGAAGTCGATTATGATCCCCGAAACTACCTGTTACATTAGGGTGTA
ATGTTGATGTGAGAATGAACGGAAGTGAGATCCAGTATAAAATACTCACGCAGAAGGAAGATGATTGTGA
CGAGATTCACTGCCAGTTAGCGATTCCAGTATCCTCACTGAATTCTCAGTACTGTGTTTCAGCAGAAGGA
45 GTCTTACATGTGTGGGTGTTACAACCTGAAAAGTCAAAAGAAGTTTGTATTACCATTTTCAATAGCAGTA
TAAAAGGTTCTCTTTGGATTCCAGTTGTTGCTGCTTTACTACTCTTTCTAGTGCTTAGCCTGGTATTCAT
CTGTTTTTATATTAAGAAAATTAATCCATTGAAGGAAAAAAGCATAATATTACCCAAGTCCTTGATCTCT
GTGGTAAGAAGTGCTACTTTAGAGACAAAACCTGAATCAAAATATGTATCACTCATCACGTCATACCAGC
CATTTTCCTTAGAAAAGGAGGTGGTCTGTGAAGAGCCGTTGTCTCCAGCAACAGTTCCAGGCATGCATAC
50 CGAAGACAATCCAGGAAAAGTGGAACATACAGAGAAGCTTTCTAGTATAACAGAAAGTGGTGACTACTGAA
GAAAATATTCCTGACGTGGTCCCGGGCAGCCATCTGACTCCAATAGAGAGAGAGAGTTCTTCACCTTTAA
GTAGTAACCACTCTGAACCTGGCAGCATCGCTTTAACTCGTATCACTCCAGAAATTGTTCTGAGAGTGA
TCACTCCAGAAATGGTTTTGATACTGATTCCAGCTGTCTGGAATCACATAGCTCCTTATCTGACTCAGAA
TTTCCCCCAAATAATAAAGGTGAAATAAAAAACAGAAGGACAAGAGCTCATAACCGTAATAAAAGCCCCCA
55 CCTCCTTTGGTTATGATAAACCACATGTGCTAGTGGATCTACTTGTGGATGATAGCGGTAAAGAGTCCTT
GATTGGTTATAGACCAACAGAAGATTCCAAAGAATTTTCATGAGATCAGCTAAGTTGCACCAACTTTGAA
GTCTGATTTTCTGGACAGTTTTCTGCTTTAATTTTCATGAAAAGATTATGATCTCAGAAATTGTATCTTA
GTTGGTATCAACCAATGGAGTGACTTAGTGTACATGAAAGCGTAAAGAGGATGTGTGGCATTTTCACTT
TTGGCTTGTAAGTACAGACTTTTTTTTTTTTTTAAACAAAAAAGCATTGTAACCTTATGAACCTTTACA
60 TCCAGATAGGTTACCAGTAACGGAACATATCCAGTACTCCTGGTTCCTAGGTGAGCAGGTGATGCCCCAG

GGACCTTTGTAGCCACTTCACTTTTCTCTCTGCCTTGGTATAGCATATGTTTGTAAAGTTTA
TGCATACAGTAATTTTAAGTAATTTTCAAGAAATTCGAAGCTTTTCAAATTTGGACTTAAAATCTAA
TTCAAATAATAGAATTAATGGAATATGTAAATAGAAACGTGTATATTTTTTATGAAACATTACAGTTAG
AGATTTTAAATAAAGAATTTTAAAACTC

SEQ ID NO:140

>gi|4557880|ref|NP_000407.1| interferon gamma receptor 1; Immune
interferon, receptor for [Homo sapiens]

MALLFLLPLVMQGVSRAMGTADLGPSSVPTPTNVTIESYNMNPVIVWEYQIMPQVPVFTVEVKNYGVKN
SEWIDACINISHYCNISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFVAVCRDGKIGPPKLDIRKEEKQ
IMIDIFHPSVFNVDQEVDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEIQQLAIPVSSLN
SQYCVSAEGLVHVWGVTTTEKSKVCITIFNSSIKGSLWIPVVAALLLFLVLSLVFICFYIKKINPLKEKS
IILPKSLISVVRSATLETKEPKYVSLITSYQPFSLKEVCEPLSPATVPGMHTEDNPGKVEHTEELS
SITEVVTTEENIPDVVPGSHLTPIERESSPLSSNQSEPGSIALNSYHSRNCSES DHRNGFDTDSSCLE
SHSSLS DSEFPNNKGEIKTEGQELITVIKAPTSFGYDKPHVLVDLLVDDSGKESLIGYRPTEDSKEFS

SEQ ID NO:141

Importin a4

>GL2_91_2_M13F Direction: sense

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTTTC
TGCCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTTGTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACATCAC
AATTGAGAACAACTGGGTCTGCTCGTCCGTGCCAGTCACTATGTTGCCAACTGCTCTGAGGGCTGCTGTTTGAA
CTTTGACTTCCTGATGGCTCAGAAGGGGCACAAGAAAGGGCACAACCTCCTGAATTC AATAACCATCTGTTATCT
GTTTATTACCTTCCATCTGTCAAAGTTATGACAGAGCCCAAAACAAGTGTCTTACAAGAAATGTTTATATCTGGA
ATGGGTAATATGAAGGACAACATAAAAGGC

SEQ ID NO:142

>GL2_91_1_M13R Direction: sense

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTTTC
TGCCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTTGTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACATGCTTCCTTATTTATCTTCTCTTTAGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACATCA
CAATTTGAGGAACAACCTGGGTCTGACTCGTCCGTGCCAGTCACTATGTTGCCAACTGCATCTGAGGGCCTGCTG
TTTGAAACTTTGACTTCCTGATGGCTCAGAAGGGGCACAAGAAAGGGCNACAACTCCTGGAATCNCAATAAAC
AATCTGTATCTGTTCAATAACCTCCCATCTGTTGCAAGGTANCTGAACACGGGAGGCCCAAAACAGGTGGT
CCTACAAGGAAATGGTGAACAAACATGGAAATGGGAATAGGANGGACCACCACATAAAGG

SEQ ID NO:143

>GL2_91_3_M13R Direction: sense

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACCTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACGAGGTACTCAACCTGATCTTTTC
TGCCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTTGTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAACGAGATTTGGGAAGTGTGACAGGACATCA
CAATTGAGAACAACCTGGGTCTGCTCGTCCGTGCCAGTCACTATGTTGCCAACTGCTCTGAGGGCTGCTGTTTGT
AACTTTGACTTCCTGATGGCTCAGCAAGGGGCACAAGAAAGGGCACAACCTCCCTGAAAATCCAATAAACCAA
TCTGTAATTTCTGGTTCACATTTACCTTCCAATCTTGGTTCAAAGGTATGACAGAAGCCCCAAAACAGGTGTTCT
ACCAAGAAATTTGTTACATAATCTGAATGGGAATANTGACNNGGACACACATTAAAGCCGCAAAAACCANACANA
CAAACACAGAC

SEQ ID NO:144

>GL2_202_1_M13R Direction: anti-sense

CTTTATGTGTCCTCATATACCATAACAGATATAAACATTCTTGTAGACACTGTTTGGGCTCTGTGCATCTTGACAG
ATGGAGGTAATGAACAGATACAGATGGTTATTGATTCAGAGATTGTGCCCTTCTTGTATGCCCTTCTTTGGGGA
AAANCCCCAACTCCACGGGGGAGAAGCGTCCNAACAAAGNGTTCCCCACAAAACAAGCACCACAACGCGGCCG
AAGGACACCGCAGTTCCAACNGGAAAAAGAGAGGCCACAACACACGGGAGCATAATATNTGAGGGGGGGGCC

AAGAAAACACCCGCAACTTAAAANGCGCNTGGGGAAGAGCCATTAGGTGGGNNCAACCGCCCCGGGAAAAGCCGC
GGAAAAGGGCCCAANGGAAAAACACCCACCCCANCCCCAANAACACGGGGGGGAGAATGCATCACGGGGCGAG
ATCAATACCAGATTTACCCAAAAACATTCACAACG

5 SEQ ID NO:145

>GL2_202_1_M13F Direction: sense

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACTTGAG
AATCTTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGGTTTAACAAGGTACTCAACCTGATCT
TTTCTGCCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTGTGTTCCAAAGTCCCCCTTAGCAAGG
10 CTGATGAATTATCATAGGAATTAATCCAG

SEQ ID NO:146

>GL2_66_F10_G3F1 Direction: N/A

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAANCACCTGAACCACTTGAG
15 AATCTTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGGGACTCAACTGATCTTTTC
TGGCACTTATTGGTAAAGTTGCTGATTGGCCAAGGCAGCTTCTTTTGTGTTCCAAAGTTCCCTTAGCAAGCTGA
TGAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGGNACCTGTTGCAGGGTTGACCTGCTGGATAATGT
TTGGGAAGGAAACACACTGGGTTCCTTAATTTATCTTATCTCTATAGGGAGTGATAAGAGATATATGGGAAAGT
20 TGTTAACAGGACATTACAAATTTGATGAACAACCTGGGTCTGATACGTCNCAGNTGGGCCACNCGCAACGCAAA
TAAGTTTTGGGCCCCAACCAGGGGGGCCACGAAAAAGAGGACGCAGCCACGTTGGNTTGGAGAACCATCTTGA
AACANTACCCTCNGGAATAGAGCGTCCCAANAGGGGGCGGACCCAAGGAANAAAGGGGGACCAAAGTACCCTGG
AAATCCACACATAAAACCATACTGTAATACTCGTGTGCCACGCTGTTAATACCCANTTCACCAACAATCCACTG
GGGTACACACAGGATNANTGAAAGCACACGGAAGAGAGCCGCCAACAAACCAGNGGGGGTGCGTNTTNGCCAAG
25 CAACCACANGGGTGCGCTGAAGTAGCAATAACCAGGANAANTGGGGGGGACGAGCAACTTNGTAAAGGGTGAACG

SEQ ID NO:147

>GL2_91_1_M13F Direction: anti-sense

CTTTATGTGTCCTCATATACCATACAGATATAAACATTCTTGTAGACACTGTTTGGGCTCTGTCTACTTGACAG
ATGGAGGTAATGAACAGATACAGATGGTTATTGATTAGGAGTTGTGCCCTTTCTTGTGCCCTTCTGAGCCATC
30 AGGAAGTCAAAGTTCAAACAGCAGCCCTCAGAGCAGTTGGCAACATAGTGACTGGCACCGACGAGCAGACCCAGG
TTGTTCTCAATTGTGATGTCTGTCTCACACTTCCCAAATCTCTTATCACACCCAAAAGAGAAGATAAATAAGGAAG
CAGTAGTGGTTCCCTTCCAACATAACAGCAGGCAANCAGCAACAAGTTCAAGCTGTAATAGATGCTGGATTAATT
CCTATGATAATTTATCAGCNTTGCTAAGNGGGGACATATTGGAACACAAAAAGAAGCTGCATATGGGGCAAC
35 AATCAGGCAANAC

SEQ ID NO:148

>GL2_91_2_M13R Direction: anti-sense

CTTTATGTGTCCTCATATACCATACAGATATAAACATTCTTGTAGACACTGTTTGGGCTCTGTCTACTTGACAG
ATGGAGGTAATGAACAGATACAGATGGTTATTGATTAGGAGTTGTGCCCTTTCTTGTGCCCTTCTGAGCCATC
40 AGGAAGTCAAAGTTCAAACAGCAGCCCTCAGAGCAGTTGGCAACATAGTGACTGGCACCGACGAGCAGACCCAGG
TTGTTCTCAATTGTGATGTCTGTCTCACACTTCCCAAATCTCTTATCACACCCAAAAGAGAAGATAAATAAGGAAG
CAGTGTGGTTCCCTTCCAACATAACAGCAGGCAACCAGCAACAAGTTCAAGCTGTAATAGATGCTGGATTAATT
CTATGATAATTCATCAGCTTGCTAAGGGGGACTTTGGAACACAAAAAGAAGCTGCTTGGGCAATCAGCAACTTAA
45 CAATAAGTGGCAAGAAAAGATCAGGTTGAGTACCTTGTAACAGCAGAATTGTAAATACCACCGTTCTGTAAATTT

SEQ ID NO:149

>GL2_91_3_M13F Direction: anti-sense

CTTTATGTGTCCTCATATACCATACAGATATAAACATTCTTGTAGACACTGTTTGGGCTCTGTCTACTTGACAG
ATGGAGGTAATGAACAGATACAGATGGTTATTGATTAGGAGTTGTGCCCTTTCTTGTGCCCTTCTGAGCCATC
50 AGGAAGTCAAAGTTCAAACAGCAGCCCTCAGAGCAGTTGGCAACATAGTGACTGGCACCGACGAGCAGACCCAGG
TTGTTCTCAATTGTGATGTCTGTCTCACACTTCCCAAATCTCTTATCACACCCAAAAGAGAAGATAAATAAGGAAG
CAGTGTGGTTCCCTTCCAACATAACAGCAGGCAACCAGCAACAAGTTCAAGCTGTAATAGATGCTGGATTAATT
CTATGATAATTCATCAGCTTGCTAAGAGGGGACTTTGGAACACAAAAAGAAGCTGCTTGGGCAATCAGCAAACTT
AACAAATAAAGTGGCAGAAAAGATCAGGTTGAGTACCTCGTACAGCAGAATTGTAAATACCACCGATACTGTTAACT
55 TNTACCTGTGAGTGAACAGATCCTCAAGTGGATCANAGAGGGACCTAGAATGGGTCTTAAAAAAAACAATNTC
TGGATAAATTTNGGGCCGGGAGGACATGAAAAGCAAAGGCAACAAATCAAGGACACGGAACGAGAAACCAAGCANA
CACATAGGAAGACCACCCGNTGAGCCAACCCGGGACTATGAGGAGGGGCGTCCCTCCATGGANACAGGAGCAGC
GACCCAAGNCCAAAAAAGGGGCGAATACAGTAGAACAAGAGNAGNAACAACACCATAACAAGAGAGAANAACACC
60 GACAGCCA

SEQ ID NO:150

>GL2_66_F07_G3F1 Direction: N/A

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACTTGAG
AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTTTC
5 TGCCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTGTTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACATCAC
AATTGAGAACAACCTGGGTCTGCTCGTCCGTGCCAGTCACTATGTTGCCAACTGCTCTGAGGGCTGCTGTTTGAA
10 CTTTGACTTCCTGATGGCTCAGAAGGGGCACAAGAAAGGGCACAACCTCCTGAATCAATAACCATCTGTATCTGTT
CATTACCTCCATCTGTCAAGTATGACAGAGCC

SEQ ID NO:151

>GL2_66_F08_G3F1 Direction: N/A

CTATTGTGCTTGCTTCATCACCGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACTTGAG
15 AATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTTTC
TACCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTGAT
GAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTGTTGCTGGTTGCCTGCTGTTATGTTGGAAA
GGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACATCAC
AATTGAGAACAACCTGGGTCTGCTCGTCCGTGCCAGTCACTATGTTGCCAACTGCTCTGAGGGCTGCTGTTTGAA
20 CTTTGACTTCCTGATGGCTCAGAAGGGGCACAAGAAAGGGCACAACCTCCTGAATCAATAACCATCTGTATCTGTT
CATTACCTCCATCTGTCAAGTATGACAGAAGCCCAAACAGCTGTCTACAAGAATGTTTATATCTGTATGGTATAT
TGAAGGACACCATAAAG

SEQ ID NO:152

>GL2_66_F09_G3F1 Direction: N/A

CTATTGTGCTTGCTTCATCACCGGGCCATTATCAGAATGTTTTTTAGACCATCTAGAACCACCTGAACCACTTG
AGAATCTTTCACTGACAGTAAATTACAGAACGGTGGTATTACATTCTGCTGTACAAGGTACTCAACCTGATCTTT
TCTGCCACTTATTGTTAAGTTGCTGATTGCCCAAGCAGCTTCTTTTTGTGTTCCAAAGTCCCCCTTAGCAAGCTG
30 ATGAATTATCATAGGAATTAATCCAGCATCTATTACAGCTTGAACCTGGTTGCTGGTTGCCTGCTGTTATGTTGG
AAAGGAACCACACTGCTTCCTTATTTATCTTCTCTTTTGGGTGTGATAAGAGATTTGGGAAGTGTGACAGGACAT
CACAATTGAGAACAACCTGGGTCTGCTCGTCCGTGCCAGTCACTATGTTGCCAACTGCTCTGANGGCTGCTGTTTG
AACTTTGACTTCCTGATGGCTCAAAGGGGCACAAGAAAGGGCACAACCTCCTGAATCAATAACCATCTGTATCTGT
GTCATTACCTCCATCTGTCAAGTATGACAGAGCCCAAACAGTGTCTACACAGCAATGTTCTATATCTCGTATGGN
35 GATATGAGGGACACCTNAAAGCCG

SEQ ID NO:153

>gi|4504898|ref|NM_002267.1| Homo sapiens karyopherin alpha 3 (importin
alpha 4) (KPNA3), mRNA

AATTCGTGGTTCCAGAATCGATAGGGCTCCAAGATTGCGCCGCCGCCGCCGCCGAGCCGCAGGAGTAGCC
40 GCCGCCGAGCCGCGCGCAGCATGGCCGAGAACCCAGCTTGGAGAACCACCGCATCAAGAGCTTCAAGA
ACAAGGGCCGCGATGTGGAAACAATGCGAAGACATAGAAATGAAGTGACAGTGGAACCTGCGGAAGAACAA
AAGAGATGAACACTTATTGAAAAAGAGAAATGTTCCCAAGAAGAAAGTCTAGAAGATTAGATGTTGAT
GCTGATTTTAAAGCACAAAATGTAACCTTAGAAGCTATATTGCAGAATGCCACAAGTGATAACCCAGTGG
TCCAATTGAGTGCTGTCCAGGCAGCAAGAAAACCTGTTATCCAGTGACCAGAATCCACCGATTGATGACTT
45 AATAAAATCTGGGATTTTACCAATTCTAGTCAAATGTCTAGAAAGGGATGATAATCCTTCATTACAGTTT
GAAGCTGCTTGGGCATTAACATAAGCATCAGGAACCTCTGCACAGACTCAAGCTGTTGTGCAGTCTA
ATGCAGTACCTCTTTTTCTGAGACTTCTTCGTTCCACCACATCAGAATGTTTGTGAACAAGCAGTATGGGC
TTTGGGAAACATTATAGGTGATGGTCCTCAATGTAGAGATTATGTCATATCACTGGGAGTTGTCAAACCT
CTTCTGTCCTTCATCAGTCCCTCCATCCCATCACTTCCTTCGGAACGTCACATGGGTCATTGTCAATC
50 TCTGCAGGAATAAGGATCCCCACCGCTATGGAGACAGTTTCAAGGATTTTGGCAGCTTTATGTGTCCT
CATATACCATAACAGATATAAACATTCTGTAGACACTGTTTGGGCTCTGTCACTTGACAGATGGAGGT
AATGAACAGATACAGATGGTTATTGATTAGGAGTTGTGCCCTTCTGTGCCCCCTCTGAGCCATCAGG
AAGTCAAAGTTCAAACAGCAGCCCTCAGAGCAGTTGGCAACATAGTGACTGGCACCGACGAGCAGACCCA
GGTTGTTCTCAATTGTGATGTCCTGTACACTTCCCAAATCTCTTATCACACCCAAAAGAGAAGATAAAT
55 AAGGAAGCAGTGTGGTTCTTTTCCAACATAACAGCAGGCAACCAGCAACAAGTTCAAGCTGTAATAGATG
CTGGATTAATTCCTATGATAATTCATCAGCTTGCTAAGGGGGACTTTGGAACACAAAAGAGCTGCTTG
GGCAATCAGCAACTTAACAATAAGTGGCAGAAAAGATCAGGTTGAGTACCTTGTACAGCAGAATGTAATA
CCACCGTTCTGTAATTTACTGTGAGTGAAGATTCTCAAGTGGTTTCAAGTGGTTCTAGATGGTCTAAAAA
ACATTCTGATAATGGCCGGTGATGAAGCAAGCACAATAGCTGAAATAATAGAGGAATGTGGAGGTTTGGAA
60 GAAAATTGAAGTTTTACAGCAACATGAAAATGAAGACATATATAAATTAGCATTGAAATCATAGATCAG

TATTTCTCTGGTGATGATATTGATGAAGATCCCTGCCTCATTCCTGAAGCAACACAAGGAGGTACCTACA
ATTTTGATCCAACAGCCAACCTTCAAACAAAAGAATTTAATTTTAAATTCAGTTGAGTGCAGCATCTTT
CCCACATTCAATATGAAGCACCACCAGATGGCTACCAAATGATAAGAACAACAGCAACAAAAGGCTCCAA
AACACACATGCCTCTTTGTTTTGATGCTTCTAAAGAAAGCCATGTCTCAGTCACTTTGCAGTTGCCAAAA
5 GTCATATCACATGGACTGTAAATGCATATGCATGATTTCTAAACTGTTTTAGAACTCTCCTTAACAAT
CTCAACTACCTATTTTTCCCTGTTCCCTGGTGCCACAGGCTGACAACTGCAGTCTCCAGTTTAGAATAA
ATATTCCATAGTGGTGACATGTCAGTGCCTGCTGATACTCTTTGGAAAATGGTGCGCTGTGGATCAAG
ACACTTTGGTATGATGCATATACAAGTTGGAAGACTAAAGAGGTGCAATGTGATCTGAGCCTCCATCATT
10 GTCTCCACAAACATATTTTCATATTCCTTATGTGGAAGAATAGATTTTAAAGTACAAGCCAAATGATTT
TCATTGGTGGAAGTACACAAAAAAGTAACTTAAAAACAAGAACTTGTTATTGAATAAACAGATAA
GTTTT

SEQ ID NO:154

>gi|4504899|ref|NP_002258.1| karyopherin alpha 3; importin alpha 4 [Homo
sapiens]

MAENPSLENHRIKSFKNKGRDVETMRRHRNEVTVELRKNKRDEHLLKKRNVPQEESESDVDADFKAQN
VTLEAILQNASDNPVQLSAVQAARKLLSSDQNPPIDDLKSGILPILVKLERDDNPSLQFEAAWALT
NIASGTSAQTAQVQSNAPVPLFLRLLRSPHQNVCEQAVWALGNIIGDGPQCRDYVISLGVVKPLLSFISP
SIPITFLRNVTWVIVNLCRNKDPPTMETVQEILPALCVLIYHTDINILVDTVWALSYLETDGGNEQIQMV
20 IDSGVVPFLVPLLSHQEVKQVTAALRAVGNIVTGTDEQTQVVLNCDVLSHFNNLLSHPKEKINKEAVWFL
SNITAGNQQQVQAVIDAGLIPMIIHQAKGDFGTQKEAAWAISNLTISGRKDQVEYLVQQNVIPPCNLL
SVKDSQVVQVVLVDGLKNILIMAGDEASTIAEIIIECGGLEKIEVLQQHENEIDYKLAFEIIDQYFSGDDI
DEDPCLIPEATQGGTYNFDPTANLQTKENF

SEQ ID NO:155

Lysosomal pepstatin-insensitive protease (CLN2)

>GL3_21A_2_M13F Direction: N/A

CCATTTCAATACTATGTGGTCGTTACAATGCTAGAGGTAGTGACAGGGGGCGCAATGCAAGGGAGGAAGGGCGT
TAACATCTGCCACCTACTTCCAGGTGCCAAGCACTGTTATCAACATTATTCCACTTTATTCCCTGGGTGATTAT
30 GAAAGGCCAGGTATTGAGTATTCACACTTNACAGACGAGGAAAACAAGCGCTCAGGGNAGAATAAGCGTTACTTG
ANCCAGGTCATACAATACGTTCCACTAGAGTCCANTTATTTCTAGGAAACCACAGGAGTTTCCAAAACAGGGGTG
TTTGGTGTNAGGAAACAATCNTATGGGGAGATATTTTTCCAAGCGCAATTACCACAACATTATAAAGTANGCCT
CCAGGGGGGAAAATCAAAACCATTCCACGAAAAGAAAGGTTNGAACATTCTGGAGAGCATTGAAGGATCTTTGCG
CAAAGAAATTCCTTGGGAAAAATTTACCTTGGGCAAGGTATGTTATCAAGAGGGGTTGGGTAAAGGGGGGNACC
35 GGGAGAACAAGCGTTTGAAGCGCA

SEQ ID NO:156

>GL3_21A_4_M13F Direction: N/A

CCATTTCAATACTATGTGGTCGTTACAATGCTAGAGGTAGGCACAGGGGGCGCAATGCAAGGGAGGAAGGGCGT
40 AACAATTCCTGGCGCACGCTAACTTTCCAGGTGGCCAAGGCCACTGGTTATCAACCAGTTATTCCACGTTTTATT
TCCCTGGGTTTGAATTTACTGGAAAAAGGGGGCCAAGGGGGTTAAATTGGAGTATTCACTTTTATACAGACG
AGGGAAACAGGCCTCAGGGAGATAAGCTTACTTGACCCAAGTCTCTCGTCCTTAGGTCCATATCCAGGGAAACCC
AAAGGGAATTTTCCAAAACAGG

SEQ ID NO:157

>GL3_21A_1_M13F Direction: N/A

CCATTTCAATACTATGTGGTCGTTACAATGCTAGAGGTAGGCACAGGGGGCGCAATGCAAGGGAGGAAGGGCGT
AACATCTGCCACCTACTTCCAGGTGCCAAGCACTGTTATCAACATTATTCCACTTTATTCCCTGGTGATTATGAA
AGGCAGGTATTGATATTCACACTTAACAGACGAGGAAACAGCCTCAGGGAGATCAAGCTTACTTGACCCAGTCTC
50 TCTCCTAGTTCCATATCAGAACCAAGATTCAAACAGTTTGGTTTAGAAAATCTAGGATTTTTCAGCCATACCAA
AATAAAGTAGCCTCAGGGAATCAAAACATTACGAAAGAAGGTGACTTCTGAACTGAGTCTTGCAAGAATTCTGG
AAATTAACCTGGCAGTTGTATCAGGGGTGGTAAGGGGACGGAA

SEQ ID NO:158

>GL3_21A_2_M13R Direction: anti-sense

CCACTTGGATGAAAACCCCTTCAAGGATTACTGGATAGAATTCAGGCTTTCCCCTCTAGCCCCCAATCATAGCTCA
CAAACCTTCCTTGCTATTTGTTCTTAAGTAAAAAATCATTTTTCCTCCTCCCTCCCCAAACCCCAAGGAACTCTC
5 ACTCTTGCTCAAGCTGTTCCGTCCCCCTTACCACCCCTGATACAACAGGCTTAATTTCCAGAATTCTTGCAAG
ACTCAGTTTCAAGTACCTTCTTTCGGTGAATGTTTGGATTCCCTGAGGCTACTTTATTTTGGTATGGCTGAAA
AATCCTAGATTTTCTAAACAAAACCTGTTTGAATCTTGGTTCTGATATGGACTAGGAGAGAGACTG

SEQ ID NO:159

>GL3_21A_3_M13F Direction: N/A

CCATTTCAATACTATGTGGTTCGTTACAATGCTAGAGGTAGGCACAGGGGGCGCAATGCAAGGGAGGAAGGGCGTT
AACATCTGCCACCTACTTCCAGGTGCCAAGCACTGTTATCAACATTATTCCACTTTATTCCCTGGTGATTATGAA
AGGCAGGTATTGATATTTCACTTAACAGACGAGGAAACAGCCCTCAGGGAGATAAGCTTACTTGACCCAGTCT
15 CTCTTCCTAGTCCATATCAGAACCAAGATTCAAACAGGTTTGGTTTAGAAAATCTA

SEQ ID NO:160

>GL3_21A_3_M13R Direction: anti-sense

CCACTTGGATGAAAACCCCTTCAAGGATTACTGGATAGAATTCAGGCTTTCCCCTCTAGCCCCCAATCATAGCTCA
CAAAGCCTTCCTTGCTATTTGTTCTTAAGTAAAAAATCATTTTTCCTCCTCCCTCCCCAAACCCCAAGGAACTCT
20 CACTCTTGCTCAAGCTGTTCCGTCCCCCTTACCACCCCTGATACAACAGGCTTAATTTCCAGAATTCTTGCAA
GACTCAGTTTCAAGTACCTTCTTTCGTGAATGTTTGGATTCCCTGAGGCTACTTTATTTTGGTATGGCTGAAA
AATCCTAGATTTTCTAAACAAAACCTGTTTGAATCTTGGTTCTGATATGGACTAGGAGAGA

SEQ ID NO:161

>GL3_21A_4_M13R Direction: anti-sense

CCACTTGGATGAAAACCCCTTCAAGGATTACTGGATAGAATTCAGGCTTTCCCCTCTAGCCCCCAAGTCATAGCTC
ACAAAGCCTTCCTTGCTATTTGTTCTTAAGTAAAAAATCATTTTTCCTCCTCCCTCCCCAAACCCCAAGGGA
CTCCTCTTGCTCAAGCTGTTCCGTTCGNCCTTACCACCCCTGATACAACAGGCTTAATTTCCAGAATTCT
TTGCAAGACTCAGTTTCAAGTACCTTCTTTCGTGAATGTTTGGATTCCCTGAGGCTACTTTATTTTGGTATGG
30 CTGAAAATCTAGATTTTCTAAACAAAACCTGTTTGAATCTTGGTTCTGATATGGACTAGGAGAGAGACTGGGT
CAAGTAAGCTTATCTCCCTGAGGCTGTTTCCT

SEQ ID NO:162

>GL3_21A_PCR_G3F1 Direction: N/A

CCATTTCAATACTATGTGGTTCGTTACAATGCTAGAGGTAGGCACAGGGGGCGCAATGCAAGGGAGGAAGGGCGTT
AACATCTGCCACCTACTTCCAGGTGCCAAGCACTGTTATCAACATTATTCCACTTTATTCCCTGGTGATTATGA
AAGGCAGGTATTGATATTTCACTTAACAGACGAGGAAACAGCCCTCAGGGAGATAAGCTTACTTGACCCAGTCTC
TCTCCTAGTCCATATCAGAACCAAGATTCAAACAGGTTTGTGTTAGAAAATCTAGGATTTTTCAGCCATACCAAA
ATAAAGTAGCTCAGGGAATCAAAACATTCACGAAAGAAGGTGACTTCTGAACAGTCTTGCAAGAAATCTGGA
40 AATTAACCTGGCAGTTGTATCAGGGGTGGTAAGGGGACGGAACAGCTTGAGCAAGAGTGAGAGTTTCTTGGGGT
TGGGGAGGGAGGAGGAAAATGATTTTCTTAAAGAACAAATAGCAAGGAAGGTTTGTGAGCTAT

SEQ ID NO:163

>gi|5597012|ref|NM_000391.2| Homo sapiens ceroid-lipofuscinosis, neuronal
2, late infantile (Jansky-Bielschowsky disease) (CLN2), mRNA

ACATGACAGCAGATCCGCGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCCTAGGGCTCTTTGCCCCCAT
CCTCTCTGGCAAATGCAGTTACAGCCCCGAGCCCGACGAGCGGAGGACGCTGCCCCAGGCTGGGTGTCC
CTGGGCCGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTTGCCCTGAGACAGCAGAATGTGGAAGAC
TCTCGGAGCTGGTCAGGCTGTGTCGATCCCAGCTCTCCTCAATACGGAATAACCTGACCCTAGAGAA
50 TGTGGCTGATCTGGTGAGGCCATCCCCACTGACCCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGA
GCCCAGAAGTGCCATTCTGTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGC
TGCTGCTCCCTGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAACCCATGTTGTAAGGTCCCC
ACATCCCTACCAGCTTCCACAGGCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGTTTTCCTC
CCAACATCATCCCTGAGGCAACGTCTCTGAGCCGAGGTGACAGGGACTGTAGGCCTGCATCTGGGGGTAA
CCCCCTCTGTGATCCGTAAGCGATACAACCTTGACCTCACAAAGACGTGGGCTCTGGCACCAGCAATAACAG
55 CCAAGCCTGTGCCAGTTTCTGGAGCAGTATTTCCATGACTCAGACCTGGCTCAGTTCATGCGCCTCTTC
GGTGGCAACTTTGCACATCAGGCATCAGTAGCCCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCCGGGA
TTGAGGCCAGTCTAGATGTGAGTACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAG
CCCTGGCCGGCAGGAGGACAGGAGCCCTTCTGTCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTG
60 CCACATGTGCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA

5 ACACGTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCCTCAGGTGACAGTGGGGCCGG
 GTGTTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAGCCCCATGTCAACACA
 GTGGGAGGCACATCCTTCCAGGAACCTTTCTCATCACAAATGAAATTGTTGACTATATCAGTGGTGGTG
 GCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAGGAAGCTGTAACGAAGTTCTTGAGCTCTAGCCC
 10 CCACCTGCCACCATCCAGTTACTTTCAATGCCAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTTCTGAT
 GGCTACTGGGTGGTCAGCAACAGAGTGGCCATTCCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTGT
 TTGGGGGGATCCTATCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAA
 CCCAAGGCTCTACCAGCAGCATGGGGCAGGACTCTTTGATGTAACCCGTGGCTGCCATGAGTCTGTCTG
 15 GATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAACAGGCTGGGGAACAC
 CCAACTTCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCTTTCTCTATCAGGAGAGATGGCTTGTG
 CCTGCCCCGAGCTGGCAGTTTCAGTCCCTTATTCTGCCCTGTTGGAAGCCCTGCTGAACCCCTCAACTAT
 TGACTGCTGCAGACAGCTTATCTCCCTAACCTGAAATGCGGTGAGCTTGACTTGACTCCCAACCCCTACC
 ATGCTCCATCATACTCAGGTCTCCCTACTCCTGCCTTAGATTCTCTCAATAAGATGCTGTAACTGATTTT
 20 TTTGAATGCCTCTCCCTCCGCATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAG
 ACTCTGTGCACTATTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTT
 ACTCTTTCTTACCTTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTTGCTTTATGGCC
 TTTCCATCATAGTTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTCTCTGACTACTCTTGT
 CTTCCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGCTCCATTTGTAGATTTTGTG
 25 TCTTCTCAGTTTACTCATTGTCCCTGGAACAAATCACTGACATCTACAACCATTACCATCTCACTAAAT
 AAGACTTTCTATCCAATAATGATTGATACCTCAAATGTAAGATGCGTGATACTCAACATTTTCATCGTCCA
 CCTTCCCAACCCCAACAAATTCATCTCGTTTCTTCTTGGTAAATGATGCTATGCTTTTCCAAACCAAGC
 CAGAAACCTGTGTCATCTTTTACCCCCACCTTCAATCAACAAGTCCCTCAATCAACAAGTCCCTAGTACTG
 CACATCTTAAATATATCTTTATCAGTCCACAAGTCCCTTCAATTATATTTCCCAAGTATATCTAGAACTT
 30 ATCCACTTATATCCCCACTGCTACTACCTTAGTTTAGGGCTATATTCTCTTGAAAAAAGTGTCTTACT
 TCCTGCCAATCCCCAAGTCATCTTCCAGAGTAAATGCAAATCCCATCAGGCCACTTGGATGAAAACCCCT
 TCAAGGATTACTGGATAGAATTCAGGCTTTCCCTCCAGCCCCCAATCATAGCTCACAAACCTTCTTGTG
 TATTTGTTCTTAAGTAAAAAATCATTTTCTCTCTCCCTCCCCCAACCCCAAGGAACCTCTACTCTTGTG
 CAAGCTGTTCCGTCCCCTTACCACCCCTGATACAACTGCCAGGTTAATTTCCAGAATTCTTGCAAGACTC
 35 AGTTCCAGAAGTCACCTTCTTCTGTAATGTTTGTATCCCTGAGGCTACTTTATTTTGGTATGGCTGAAA
 AATCCTAGATTTTCTAAACAAACCTGTTTGAATCTTGGTCTGATATGGACTAGGAGAGAGACTGGGTC
 AAGTAAGCTTATCTCCCTGAGGCTGTTTCTCTGCTCTGTTAAGTGTGAATATCAATACCTGCTTTTCAATA
 TCACCAGGAATAAAGTGAATAATGTTGATAACAGTGCCTTGGCACCTGGAAGTAGGTGGCAGATGTTAA
 CGCCCTTCTCCCTTGCAGTGCAGCCCCCTGTGCCTACCTCTAGCATTGTAACGACCACATAGTATTGAAA
 40 TGGCCAGTTTACTTGTCTGCCTTCTTCCAGACCGTTGGTGCCTAGAGGACTAGAATCGTGTCTCTATT
 TAACCTTGTGTTCCAGGTCTAGCTCAGGAGTTGGCAAATAAGAATTAAATGTCTGCTACACCGAAACA
 AA

SEQ ID NO:164

40 >gi|5729770|ref|NP_000382.3| ceroid-lipofuscinosis, neuronal 2, late
 infantile (Jansky-Bielschowsky disease) [Homo sapiens]
 MGLQACLLGLFALILSGKCSYSPEPDQRRITLPPGWVSLGRADPEEELSLTFALRQONVERLSELVQAVSD
 PSSPQYGYKYLLENVADLVRPSPLTLHTVQKWLAAAGAQKCHSVITQDFLTCWLSIRQAEILLPGAFFHH
 YVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRPEPQVTGTVGLHLGVTPSVIRKRYN
 45 LTSQDVSGTSSNNSQACAQFLEQYFHDSDLAQFMRLFPGNFAHQASVARVVGQGRGRAGIEASLDVQYL
 MSAGANISTWVYSSPGRHEGQEPFLQWLMLLSNESALPHVHTVSYGDDDSLSSAYIQRVNTELMKAAAR
 GLTLLFASGDSGAGCWSVSGRHQFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPS
 YQEEAVTKFLSSSPHLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINE
 50 HRILSGRPPLGLNPRLYQQHGAGLFDVTRGCHESECLDEEVEGQGFCSGPGWDPVTGWGTPNFPALLKTL
 LNP

SEQ ID NO:165

Novel protein disulfide isomerase
 Novel (disulfide isomerase-like)
 55 CGGACCAACACAGTATTGAGTCAACTGTGACCTTAAGATCAGAGGAACGTCAATACTGCCACAAGGCCACCTTTC
 CAGAACTCGTGGGCAGGTAAACTATGCTTTGGATGTGCTTTCTTTACCAAATCACTCAACTCAGGAGCCACAA
 ATAGTCCAGCAATTTCAATTTCCCTCAACGCTATTTTAGTCTCAAAGGAAACCATGTAAATTTTCATCAAGAGAAGG
 TCAAAGGGGATATATCGCCACTGAAAATGTTTACACAGTGACCATGAGTTACACATTTACTTAGAGAACTTAAC
 TTAATAAAGAATCTGTAGAGTGTGTTGGCTTGGAAAACACACACAAAGAAGATACCTCACGCTTAGTATGTTT
 60 TGCTTTTCTGAACAGCCACCAGTGGGAACCCAGTGGCCTCTGTGGGACTGAACTCCTAAACGCAGGGTGCAGGAGC
 TGGGCAGGAGAGGTGACCTCAACTGTGTTCTTAAAGTTCGTCTTTTCGCTTGGCTCAGGACAAAGCGGTGTAACG

AGTCAAAGTCTCTGCCTCCACTGTGCTCACTGACTTTCTTCCCTCCTCGGAAAAGCAATAACGTGGGGTAGCCTC
GT

SEQ ID NO:166

5 Microtubule-associated protein 4 (MAP4)
>GL1_19_HIGH_3_G3F1 Direction: sense
CCACCTCCATTTCTGGAGGCAGACATACGTTCTTGATGAGAACTACTTCTGTTTCTGGAGGTGGAGTCACATCCT
TGCCCAGAGCCATTTCTGTTTCTGATAGTG

10 SEQ ID NO:167

>GL1_19_HIGH_3_G3R1 Direction: anti-sense
CACTATCAGAAACAGAAATGGCTCTGGGCAAGGATGTGACTCCACCTCCAGAAACAGAAGTAGTTCTCATCAAGA
ACGTATGTCTGCCTCCAGAAATGGAGGTGG

15 SEQ ID NO:168

>GL1_19_LOW_2_G3F1 Direction: sense
CCACCTCCATTTCTGGAGGCAGACATACGTTCTTGATGAGAACTACTTCTGTTTCTGGAGGTGGAGTCANATCCT
TGCCCAGAGCCATTTCTGTTTCTGATAGTG

20 SEQ ID NO:169

>gi|14195631|ref|NM_002375.2| Homo sapiens microtubule-associated protein 4
(MAP4), transcript variant 1, mRNA
TGCGACCGCCTCCCTGCGCCCCGCCCTCCGGCTAGCTCGCTGGCTCCCGGCTCCTCCCGACGTCTCCTA
CCTCCTCACGGCTCTTCCCGGCGCTCTCCTGGCTCCCTTCTGCCCCAGCTCCGTCTCGGCGGCGGGC
25 AGTTGCAGTGGTGCAGAAATGGCTGACCTCAGTCTTGAGATGCATTAACAGAACCATCTCCAGACATTGA
GGGAGAGATAAAGCGGGACTTCATTGCCACACTAGAGGCAGAGGCCCTTTGATGATGTTGTGGGAGAACT
GTTGGAGAAAACAGACATATTCCTCTCCTGGATGTTGATGAGAAAACCGGGAACCTCAGAGTCAAAGAAGA
AACCGTGCTCAGAAACTAGCCAGATTGAAGATATCCATCTTCTAAACCAACACTCCTAGCCAATGTTGG
TCATGGAGTAGAAGGGAGCGATACTACAGGGTCTCCAATGAATTCCTGAAGAGAAAAATGGCCTACCAG
30 GAATACCCAAATAGCCAGAACTGGCCAGAAGATACCAACTTTTGTTCACCTGAGCAAGTGGTCGATC
CTATCCAGACTGATCCCTTTAAGATGTACCATGATGATGACCTGGCAGATTTGGTCTTCCCTCCAGTGC
GACAGCTGATACTTCAATATTTGACAGGACAAAATGATCCCTTGAAAGACAGTTACGGTATGTCTCCCTGC
AACACAGCTGTTGTACCTCAGGGGTGGTCTGTGGAAGCCTTAAACTCTCCACACTCAGAGTCCTTTGTTT
CCCCAGAGGCTGTTGCAGAACCTCCTCAGCCAACGGCAGTTCCCTTAGAGCTAGCCAAGGAGATAGAAAT
35 GGCATCAGAAGAGAGGCCACCAGCACAAGCATTGGAATAATGATGGGACTGAAGACTACTGACATGGCA
CCATCTAAAGAAAACAGAGATGGCCCTCGCCAAGGACATGGCACTAGCTACAAAACCGAGGTGGCATTGG
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SEQ ID NO:170

>gi|4505099|ref|NP_002366.1| microtubule-associated protein 4, isoform 1
 [Homo sapiens]
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 50 IASAQKQPAQKQIVSKKVSYSHIQSKCGSKDNIKHVPGGGNVQIQNKKVDISKVSSKCGSKANIKHKPG
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SEQ ID NO:171

>gi|14195625|ref|NM_030884.1| Homo sapiens microtubule-associated protein 4
 (MAP4), transcript variant 2, mRNA
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5 GACAGCTGATACTTCAATATTTGCAGGACAAAATGATCCCTTGAAAGACAGTTACGGTATGTCTCCCTGC
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10 CCATCTAAAGAAACAGAGATGGCCCTCGCCAAGGACATGGCCTAGCTACAAAACCGAGGTGGCATTGG
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50 AGGCTCGCCTTCCCTCTGCTTTGCGTGCCCGGGGAGCAGCAGCCCTGCCCCACACCTCCTCTCACTCC
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60 AGGCACACAAGGGGCCCTTGGAGCGTGGACTGGTGGTTTGGCCATTTTGTGTGTGTATGCTGCTTTTC
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SEQ ID NO:172

>gi|14195626|ref|NP_112146.1| microtubule-associated protein 4, isoform 2
[Homo sapiens]

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SEQ ID NO:173

>gi|14195627|ref|NM_030885.1| Homo sapiens microtubule-associated protein 4
(MAP4), transcript variant 3, mRNA

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 IIDNRVHCCFYFISPFHGLKPLDVAFMKAIHNKVNIIVPIAKADTLTLKERERLKKRILDEIEEHNKI
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 5 DGDGGALGHHV

SEQ ID NO:185

Novel (breast cancer antigen; tyrosine/serine/threonine kinase)

>G3_3_29_PCR_G3F1 Direction: N/A

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SEQ ID NO:186

>GL3_1.36_A2_M13F Direction: N/A

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 25 ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACCTCTGGCCTGAGTGACAGC
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SEQ ID NO:187

>GL3_1.36_A2_M13R Direction: anti-sense

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SEQ ID NO:188

>GL3_1.36_B2_M13F Direction: N/A

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 45 ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACCTCTGGCCTGAGTGNCAGC
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SEQ ID NO:189

>GL3_1.36_B2_M13R Direction: anti-sense

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 CCTGAGACTGGCTGCCCTCAAAATTGGTGTATGGGGGTGACAGGACGAAGCAATTCTGGGCAAAGCCTCTGAGGCAC
 GTCGCTTGATCTGGGGGAGAAGAGAGAGGTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA
 AGGAACCATGGCCTGGTGGCAGACGGGCTGTCCGAGCCAACCTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
 TTCGGAAGCGGGTAGTTTCTCTCATTCAAAAGGAGGGGAGAGAAAGCTG

SEQ ID NO:190

>GL3_1.36_B3_M13F Direction: anti-sense

60 CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTACCAGGCCAAAGATTCCACTGTGGT
 CCTGAGACTGGCTGCCCTCAAAATTGGTGTATGGGGGTGACAGGACGAAGCAATTCTGGGCAAAGCCTCTGAGGCAC
 GTCGCTTGATCTGGGGGAGAAGAGAGAGGTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA

AGGAACCATGGCCTGGTGGCAGACGGGCTGTCGGAGCCAACTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
TTCCGGAAGCGGGGTAGTTTCTCTCATTCAAAGGAGGGGAGAGAAAGCTGGCATCCGGGTTCGCTGAAGGCACT
GCTCCACAAAGTGGTGGAAAGTGGGGGAGAAAGTTTCGGTGGTAGGGGTGGGAGGGCGAGTCACCGTNGGAGGGCC
GGGGGGTGTGGTGGTCANGCTGTCACTCAGGCCAGAGTTGGNCACTGATCGCGAANGGCTCATGGTCAGNTCCT
5 CANCAGGGATGGTGTGCTGGTATCCAACAGGCAGGGCACTGTGCCGTTTCTCTNAGCAGCATCTGGGTGGCA
GGCATATCCTTAAAGGGACATGGCCGTTGGCCACTCACAGGCCTGT

SEQ ID NO:191

>GL3_1.36_B3_M13R Direction: sense

10 CAGGGGGTGTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCAT
GTCCCCCTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAAACTGAACGGCACAGTGGCCTGCCTGTTGGAT
15 ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACCTCTGGCCTGAGTGACAGC
CTGACCACCAG

SEQ ID NO:192

>GL3_1.36_B4_M13F Direction: anti-sense

20 CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGTATGGGGGTGACAGGACGAAGCAATTCGGGCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAAGAGAGAGGTGGGTGACAGATCCTGTNGCTCTGGGTCCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGANNAGCTGTATAGCCAAACNCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
TTCGGAAGCGGGTAGTTTCTCTCATTCAAAGGAGGGGAGAGAAAGCTGGCATCCGGGTTCGCTGAAGGCACT
25 GCTCCACAAAGTGGTGGAAAGTGGGGGAGAAAGTTTCGGTGGTAGGGGTGGGAGGGCGAGTCACCGTTGGAGGGCC
GGGGGGTGTGGTGGTCAGGCTGTCACTCANGCCAGAGTTGGCCACTGACCGCGAAGGGCTCATGGTCAGTTCCT
CANCAGGGATGGTGTGTA

SEQ ID NO:193

>GL3_1.36_B4_M13R Direction: sense

30 CAGGGGGTGTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCAT
35 GTCCCCCTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAAACTGAACGGCACAGTGGCCTGCCTGTTGGAT
ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACCTCTGGCCTGAGTGACAGC
CTGACCACCAGCACCCCC

SEQ ID NO:194

>GL3_10.04_PCR_G3F1 Direction: N/A

40 CAGGGGGTGTGAAGGCCCTCGACTACGTCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTNCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGNCAT
45 GTCCCCCTTAAGGATATGCCTGCCACCCATATGCTGCTAGAGAAACTGAACGGCACAGTGGCCTG

SEQ ID NO:195

>GL3_3.29_A_M13F Direction: N/A

50 CAGGGGGTGTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCAT
GTCCCCCTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAAACTGAACGGCACAGTGGCCTGCCTGTTGGAT
55 ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACCTCTGGCCTGAGTGACAGC
CTGACCACCAGCACCC

SEQ ID NO:196

>GL3_3.29_A_M13R Direction: anti-sense

60 CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTGTATGGGGGTGACAGGACGAAGCAATTCGGGCAAAGCCTCTGAGGCAC

GTTCGCTTGATCTGGGGGAGAAAGAGAGAGGTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGACGGGCTGTCTGGAGCCAACCTCCATGAGAGGAAGGAGCAGTGTCTTTCAGGGGC
TTCGGAAGCGGGGTAGTTTCTCTCATTTCAAAGGAGGGGAGAGAAAGCTGGCATCCGGGTTGCGCTGAAGGCACCT
GCTCCACAAAGTGGTGGAAAGTGGGGGGAGAAAGTTCCGTGGTAGGGGTGGGAGGGCGAGTACCGTTGGAGGGCC
5 GGGGGGTGCTGGTGGTCAGGCTGTCACTCAGGCCAGAGTTGGCCACTGAGCGCGAAGGGCTCATGGTCAGCTCCT
CAGCAGGGATGGTGTGTTATCCAACAGGCAGGGCACTGTGCCGTTTCAGTTTCTCTAGCAGCATCTGGGTGGCAG
GCATATCCTTAAAGGGGACATGGCCGTGGCCAGTTCACAGGCTGTGATTCCACACT

SEQ ID NO:197

>GL3_3.29_B_M13F Direction: N/A

CAGGGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGCTCTGGTTTGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCAT
15 GTCCCCCTTTAAGGATATGCCTGCCGCCAGATGCTGCTAGAGAACTGAACGGCACAGTGGCCTGCCTGTTGGAT
ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACCTCTGGCCTGAGTGACAGC
CTGACCACCAGCACCC

SEQ ID NO:198

>GL3_3.29_B_M13R Direction: anti-sense

CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTATGGGGGTGACAGGACGAAGCAATTCGGGCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAAGAGAGAGGTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGACGGGCTGTCTGGAGCCAACCTCCATGAGAGGAAGGAGCAGTGTCTTTTCAGGGGC
25 TTCGGAAGCGGGGTAGTTTCTCTCATTTCAAAGGAGGGGAGAGAAAGCTGGCATCCGGGTTGCGCTGAAGGCACCT
GCTCCACAAAGTGGTGGAAAGTGGGGGGAGAAAGTTCCGTTGGTA

SEQ ID NO:199

>GL3_3.29_C_M13F Direction: N/A

CAGGGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAAGCCAGCCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTCCAGCAG
AATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCAT
GTCCCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGGCCTGTTGGAT
35 ACCAGCACCATCCCTGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCAGTGGCCAACCTCTGGCCTGAGTGACAGC
CTGACCACCAGCACCC

SEQ ID NO:200

>GL3_3.29_C_M13R Direction: anti-sense

CAGAGGCTCAGAACTCCCAATCGTCCACCTCCAGCTCTTCCAGGTTTGTACCAGGCCAAAGATTCCACTGTGGT
CCTGAGACTGGCTGCCCTCAAATTTGGTATGGGGGTGACAGGACGAAGCAATTCGGGCAAAGCCTCTGAGGCAC
GTCGCTTGATCTGGGGGAGAAAGAGAGAGGTGGGTGACAGATCCTGTTGCTCTGGGTCCCAGGACACCATGGGGCA
AGGAACCATGGCCTGGTGGCAGACGGGCTGTCTGGAGCCAACCTCCATGAGAGGAAGGAGCAGTGTCTTTTCAGGGGC
45 TTCGGAAGCGGGGTAGTTTCTCTCATTTCAAAGGAGGGGAGAGAAAGCTGGCATCCGGGTTGCGCTGAAGGCACCT
GCTCCACAAAGTGGTGGAAAGTGGGGGGAGAAAGTTCCGTTGGTAGGGGTGGGAGGGCGAGTACCGTTGGAGGGCC
GGGGGGTGCTGGTGGTCAGGCTGTCACTCAGGCCAGAGTTGGCCACTGAGCGCGAAGGGCTCATGGTCAGCTCCT
CAGCAGGGATGGTGTGTTATCCAACAGGCAGGGCACTGTGCCGTTCA

SEQ ID NO:201

>GL3_3.29_D_M13F Direction: N/A

CAGGGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAANCCAGNCACATC
CTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGCAGCAACCTCAGCATGATAAGCCATGGGCAGCGG
CAGCNAAGTGGTCCANGANN

SEQ ID NO:202

>gi|20559344|ref|XM_044379.3| Homo sapiens similar to serologically defined
breast cancer antigen NY-BR-96 (LOC92335), mRNA

GCGGCGCGGCAGTAAACTGAGGAGGCGGAGCCAAGACGGTCGGGGCTGCTTGCTAACTCCAGGAACAGG
TTTAAGTTTTTGAAGTGAAGTAGGCCTACACAGTAGGAACCTCATGTCAATTTCTTGTAAGTAAACCAGAG
60 CGAATCAGGCGGTGGGTCTCGGAAAAGTTCATTGTTGAGGGCTTAAGAGATTTGGAACATTTGGAGAGC

AGCCTCCGGGTGACACTCGGAGAAAAACCAATGATGCGAGCTCAGAGTCAATAGCATCCTTCTCTAAACA
GGAGGTCATGAGTAGCTTTCTGCCAGAGGGAGGGTGTACGAGCTGCTCACTGTGATAGGCAAAGGATTT
GAGGACCTGATGACTGTGAATCTAGCAAGGTACAAACCAACAGGAGAGTACGTGACTGTACGGAGGATTA
ACCTAGAAGCTTGTTCATGAGATGGTAACATTCTTGCAGGGCGAGCTGCATGTCTCCAACTCTTCAA
5 CCATCCCAATATCGTGCCATATCGAGCCACTTTTATTGCAGACAATGAGCTGTGGGTTGTACATCATTC
ATGGCATAACGGTTCTGCAAAAGATCTCATCTGTACACACTTCATGGATGGCATGAATGAGCTGGCGATTG
CTTACATCCTGCAGGGGGTGTGTAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGT
CAAAGCCAGCCACATCCTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTTCGCGAGCAACCTCAGC
ATGATAAGCCATGGGCAGCGGCAGAGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGGTTCTGCCGT
10 GGCTCAGCCCCGAGGTCTCCAGCAGAATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGG
AATCACAGCCTGTGAAGTGGCCACGGCCATGTCCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTA
GAGAACTGAACGGCACAGTGCCTGCTGTGGATACCAGCACCATCCCCGCTGAGGAGCTGACCATGA
GCCCTTCGCGCTCAGTGGCCAACCTTGGCCTGAGTGACAGCCTGACCACCAGCACCCCCCGGCCCTCCAA
CGGTGACTCGCCCTCCACCCCTACCACCGAACCTTCTCCCCCACTTCCACCCTTTGTGGAGCAGTGC
15 CTTACAGCGCAACCCGGATGCCAGGCCAGTGCAGCACCCCTCCTGAACCACTCTTTCTTCAAGCAGATCA
AGCGACGTGCCTCAGAGGCTTTGCCCGAATTGCTTTCGTCTGTACCCCCATCACCAATTTTGAGGGCAG
CCAGTCTCAGGACCACAGTGGAACTTTTGGCCTGGTAACAAACCTGGAAGAGCTGGAGGTGGACGATTGG
GAGTTCTGAGCCTCTGCAAACTGTGCGCATTTCTCCAGCCAGGGATGCAGAGGCCACCCAGAGGCCCTTCC
TGAGGGCCGGCCACATTTCCCGCCCTCCTGGGCAGATTGGGTAGAAAGGACATTCTTCCAGGAAAGTTGAC
20 TGCTGACTGATTGGGAAAGAAAATCCTGGAGAGACACTTCACTGCTCCAAGGCTTTTGAGACACAAGGGA
ATCTCAACAACAGGGATCAGGAGGGTCCAAAGCCGACATTCCAGTCTGTGAGCTCAGGTGACCTCCT
CCGAGAAGAGAGATGCTGCTCTGGCCCTGGGAGCTGAATTCCAAGCCAGGGTTTGGCTCCTTAAACCC
GAGGACCGCCACCTCTTCCAGTGCTTTCGACCCAGCCTCATTCTATTTAACTTTGCTCTCAGATGCCTCA
GATGCTATAGGTGAGTGAAGGGCAAGTAGTAAGTGCCTGCCTCCCTCCCTCAGACCTCTCCCTCATA
25 ATTCCAGAGAAGGGCATTCTGTCTTTTAAAGCACAGACTAAGGCTGGAACAGTCCATCCTTATCCCTCT
TCTGGCTTGGGCCCTGACACCTAAGTCTTTCCACGGTTTATGTGTGTGCCTCATTCTTTCCACCAAG
AATCCATCTTAGCGCCTCCTGCCAGCTGCCCTGGTGCTTTCTCCAAGGGCCATCAGTGTCTTGCCCTAGCT
TGAGGGCTTAAGTCCTTATGCTGTGTAGTTTCGTTGTCAGAA

SEQ ID NO:203

>gi|14770985|ref|XP_044379.1| similar to serologically defined breast
cancer antigen NY-BR-96 [Homo sapiens]
MSFLVSKPERIRRWVSEKFIVEGLRDLLELFGEPQPPGDRRKTNDAASSEIASFSKQEVMSFLPEGGCYE
LLTVIGKGFEDLMTVNLARYKPTGEYVTVRRINLEACSNEVMVTFLOGLHVSCLFNHPNIVPYRATFIAD
35 NELWVVTSF MAYGSAKDLICTHFM DGMNELAIAYILQGV LKALDYIHHM GYVHRSVKASHILISVDGKVY
LSGLRSNLSMISHGQRQRVVHDFPKYSVKVLPWLSPEVLQQLQGYDAKS DIYSVGITACELANGHV PFK
DMPATQMLLEKLN GTVPCLLD TSTIPAEELTMSPSRSVANSGLSDSLTSTPRPSNGDSPSHPYHRTFSP
HFHHFVEQCLQRPNDARPSASTLLNHSFFKQIKRRASEALPELLRPVTPITNFEQSQSDHSGIFGLVTN
LEELEVD DWEF

SEQ ID NO:204

Novel (chromosome 1)

>GL2_46A_B12_G3F1 Direction: sense

ATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
45 TACCACCTGTTACTTTGACAACCTCTAGCTTCAGGGCTACCAGGACCATTGCAAACTTACACCCACAGAAAACT
CAAAGTCTCCAGAGGCATAAGCTCCAATCCCCCAGAGAGCTCGCACTAGCATTCTTCTCCCTTTCTAGTAGTACT
TTTATGGGGGGGAGTTATTCTTCCCCACAAAAGTGAGCGGCGACAATAAAAACAATGTTTCCCACAAAGAGTTTT
CCCCGGTTCTTCTCCAAAAATTNNGGGGGGGCCCCCGTTTNTCCCCCGGGCGACGGGGGCGGGNNGGGCCCCG
50 CCAAAACCACAANGNGGTGTGTTCCCTCTGAAAGCTCNNACAAAGAGGGGTGACCCCCCGGTTTGGGTGA
TGAATACCGCCCCGAAGATAGGNCGCCGAAAAAGAGCCAACCCNNGAAAAGAGAGATTTTTATATAGAGGAAGCA
AAAACGAAANGANAGCGTTTTTTTTTTTTTGTCCNGCCAACAACATGGGGGGCCCCCGTTTTATAAATAGAGTT
TTTTGTTTTTAAACAATCGACTTTTTTTTTTCCCCCGTGATTTAAAAAAGAAGGAAGGGTATTTATATTNTT
GGGGGNGCGTGATTATATAAATTATTTAGTGGGGTGCGGGGANGGAAAGAGNGAAGCTGTTTATCCCATCAAAA
TATTATTGTG

SEQ ID NO:205

>GL2-30-CON-TOPO Direction: sense

ATCTACATGAGGTCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
TACCACCTGTTACTTTGACAACCTCTAGCTTCAGGGCTACCAGGACCATTGCAAACTTACACCCACAGAAAACT
60 CAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTTG

TTTCCAGGAAAATCATCTCAATGCTCGGGCCACAGTCACAGTCCTGACCAGCACCATAGAAAATTTTCAGCCATTATT
CTAGTTGTATGGAGTCATTCAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACCT
TTGCTAATTTTTCCATAAATTGAAAGCCTT

5 SEQ ID NO:206

>GL2_46A_B07_G3F1 Direction: N/A

ATCTACATGAGGTCCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
TACCACCTGTTACTTTGACAACCTCTAGCTTCAGGGGGCTACCAGGACCATTGCAAAACTTACACCCACAGAAAA
CTCAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTT
10 GGTTCAGGAAAATCATCTCATGCTCGGGCCACAGTCACAGTCCTGACCAGCACCATAGAAAATTTTCAGCCATTA
TTCTAGTTGTATGGAGTCATTCAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTT
ACCTTTGCTAATTTTTT

SEQ ID NO:207

15 >GL2_46A_B08_G3F1 Direction: sense

ATCTACATGAGGTCCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
TACCACCTGTTACTTTGACAACCTCTAGCTTCAGGGGCTACCAGGACCATTGCAAAACTTACACCCACAGAAAACT
CAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTTGG
20 TTCCAGGAAAATCATCTCATGCTCGGGCCACAGTCACAGTCCTGACCAGCACCATAGAAAATTTTCAGCCATT

SEQ ID NO:208

>GL2_46A_B10_G3F1 Direction: sense

ATCTACATGAGGTCCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
TACCACCTGTTACTTTGACAACCTCTAGCTTCAGGGGCTACCAGGACCATTGCAAAACTTACACCCACAGAAAACT
25 TCAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTTGG
GTTTCAGGAAAATCATCTCATGCTCGGGCCACAGTCACAGTCCTGACCAGCACCATAGAAAATTTTCAGCCATTAT
TCTAGTTGTATGGAGTCATTCAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACCT
TTTGCTAATTTTTTCCATAAATTGAAAGCCTT

30 SEQ ID NO:209

>GL2_46A_B11_G3F1 Direction: N/A

AATCTACATGAGGTCCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAG
CTACCACCTGTTACTTTGACAACCTCTAGCTTCAGGGCTACCAGGACCATTGCAAAACTTACACCCACAGAAAACTCA
AAGTCTCCAGAAGCATAAGCTCCAACCCCCAGANAGCTCCAAGATTCTTCTCCTTCTAGTAGTACTTTTGGTTTC
35 CAGGAAAATCATCTCATGCTCGGGCCACAGTCACAGTCCTGACCAGCACCATAGAAAATTTTCAGCATTTCTTAGT
TGTATGTGAGTCCTTCAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACNTTGGT
AATTTTTCCCTAAATTGAAAGCCTTCCGCAGAAACCAGCACAGTGGTTAGATAGATAAA

SEQ ID NO:210

40 Clone 30 -Novel (Chromosome 1)>

ATCTACATGAGGTCCTGTAGATTGAGCAACTTTGGCTATTTGGGTAGCTGATCCACTGCCAAGCTGGCTCCCAGC
TACCACCTGTTACTTTGACAACCTCTAGCTTCAGGGGCTACCAGGACCATTGCAAAACTTACACCCACAGAAAACT
CAAAGTCTCCAGAGGCATAAGCTCCAACCCCCAGAGAGCTCCACAGCATTCTTCTCCTTCTAGTAGTACTTTTGG
TTTCCAGGAAAATCATCTCATGCTCGGGCCACAGTCACAGTCCTGACCAGCACCATAGAAAATTTTCAGCCATTATT
45 CTAGTTGTATGGAGTCATTCAAATACTAGTTCCGAAAGAAGTTTCAAAGGTCCAACGCCGAGCATCTTTTACCT
TTGCTAATTTTTTCCATAAATTGAAAGCCTT

SEQ ID NO:211

Novel (chromosome 3; h40)

50 >GL2_46B_C03_G3F1 Direction: N/A

GCGTCGCTCGGCGTTAGCCAAGGCCCGGGCGGCCACCCTCCGGGGGCACTAGGTCTGGGGCCGAGTGCCCCC
CCATAGGCACACAGAGNGAAAGCGCCAATGGGCGCTGGGTTTTTTTTTAAATTTCCGGGGCGGGGCGNAACCCCGG
AACACAACGGGCAAACCTGTACAATTTTTGTGGGGANCAACAACCGGGACACAANTTTTTGGGGNAATGGCGCCA
CAAAAAAANAACCAACGACGCGACGAAAGCGCGTGTTGTTGTCNGAATACTTTTTATAAAACCACCAATGG
55 GCGCCTCTCGCTTGTGCGCGCCCTTCTCCCCAANGGGGGCGGCGCTGTTTTTCCCCAACACGGGCGTGCGG
CCCCAAAAAATTTGTGGGCGCCCAAAGAAAAAATATTTTAATAAAACAGAGGCGGCCCCCAACACAGGCGGT
TNTGGGGGAACAGGAAACCAACACAACGACAACACGGCGCTGGCGGCAACAAGCAAACACGGGAGCAAACAAAC
ACGGGCGGAAAGAAACACACGGGCGAAACGACTTTTATAACAAACACTTTTGTGGGGCGCAAACAGCACACAC
ACAACCAAATGGGCGCCCCCCCCNCCGAGGGGGCCCAAAAGGNCGAAGAGAAAAAACACCCCCCCCCAAAA
60 AGAGAGCGCCCGCAAAACAACCAAAAAAAGGGGAGGAGTTTGGAGAGCAGGGCGAGANGTTTTTTTATATTA

AAACACGGGCNACGAAAACATCATTTTATAAATAGGGCAGGCAGAAAAACACGATTTATAATATTTCAACAGAAAA
CAGGGNTGGCCTCTGGGGGTTTGGTGTGTGTGCTTCCCNACCGGTGGTGCGCGTGTTCCTCCTGGTGNGGAA
AAAAGACACCTGTTTTATAAAAGAGGAGNGTATTNCCNCCTTTTTGTGGGTGCGAAAAACAGACGNGAGGCGGGA
NGATNTATCCCACTCTTTTGGTGGTGCAACAAGTGTTTTATATAGNATACCTG

SEQ ID NO:212

>GL2_46B_C01_G3F1 Direction: N/A

GCGTTGCTCGGCGTTAGCCAAGGGCCCGGGCGGCGCCACCCTCCGGGGGCACTAGGTCTGGGGCCGCAGTGCCCA
GNCACAGAGCAGCGTTTATCTGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCGGGC
TCANGGGTTCAGGCGAATGCAAATAAGCACGTGAAAAGGAAGAAGACGATAATGAAAAGCCGCAGAAACCAGCAC
AGTGGTTAGAT

SEQ ID NO:213

>GL2_46B_C02_G3F1 Direction: sense

CAAGCCGGTGACGCGTTGTCTAGTGTGCTGGGTCTGCGGGCGTTGCTTCGGCGTTAGCCAAGCCGGGCGGCGCCA
CCCTCCGGGGGGGGGGCCACTAGGTCTGGGGCCGCAGTGCCAGCACAGAGCAGCGTTTATCGGGACGAAGAAT
GAATTGGAAAGAATTGGAGCAAAAAGAGTTGATAACAGCGGCCTCAGGGGTTTCAGGCAATGCAAATAAGCAGTG
AAAAGGAAGAAGACGATAATGAAAAGCCGCAGAAACCAGCACAGTGGTTAGATAGATAAAGCGGGCGCTCGACTA
GTCTGAGGTCTGATA

SEQ ID NO:214

>GL2_46B_C04_G3F1 Direction: N/A

GCGTGCCTCGGCGTTAGCCAATGCCCGGGCGGCGCCACCCTCCGGGGGCACTAGGTCTTGGGGCCGCAGTGCCAGC
ACAGAGCAGCGTTTATCGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCTGGCCCTCA
GGGGGTTTCAGGCAATGCAAATAAGCAGTGAAAAGGAAGAAGAC

SEQ ID NO:215

>GL2_46B_C05_G3F1 Direction: sense

GCGTGCCTCGGCGTTAGCCAAGGCCCGGGCGGCGCCACCCTCCGGGGGCACTAGGTCTGGGGCCGCAGTGCCAG
CACAGAGCAGCGTTTATCGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCGGCTCAG
GGGTTTCAGGCAATGCAAATAAGCAGTGAAAAGGAAGAAGACGATAATGAAAAG

SEQ ID NO:216

>GL2_46B_C06_G3F1 Direction: sense

GCGTGCCTCGGCGTTAGCCAAGGCCCGGGCGGCGCCACCCTCCGGGGGCACTAGGTCTGGGGCCGCAGTGCCAG
CACAGAGCAGCGTTTATCGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCGGCTCA
GGGGTTTCAGGCAATGCAAATAAGCAGTGAAAAGGAAGAAGACGATAATGAAAAG

SEQ ID NO:217

>GL2_95_1_M13R Direction: anti-sense

CTTTTCATTATCGTCTTCTTCTTTTCACTGCTTATTTGCATTGCCTGAACCCTGAGGCCGCTGTAATCAACCTC
TTTTTGCTCCAATTCTTTCCATTCTTCTGCTCCGATAAACGCTGCTCTGTGCTGGGCACTGCGGCCCCAGACC
TAGTGCCCCCGGAGGTTGGCGCCGCGGCGCTCGGCTAACGCCGAGCGACGC

SEQ ID NO:218

Clone 95 -Novel (Chromosome 3/ H41)>

GCGTGCCTCGGCGTTAGCCAAGGCCCGGGCGGCGCCACCCTCCGGGGGCACTAGGTCTGGGGCCGCAGTGCCAG
CACAGAGCAGCGTTTATCGGGACGAAGATGAATGGAAAGAATTGGAGCAAAAAGAGGTTGATTACAGCGGCTCA
GGGGTTTCAGGCAATGCAAATAAGCAGTGAAAAGGAAGAAGACGATAATGAAAAG

SEQ ID NO:219

Novel (chromosome 17)

>GL2_147_1_M13F Direction: anti-sense

CTTGCCATTCCACTCCAGCCTGGGCAACGAGAGCGAAACTCTGTCTCAAAAAGAAAAGAAAAGAAAAGAAAACC
ACCTCCCAACAGGTTAAATAAATAATTAACATTTTGGTATGTACCCTTCCAGACATTTTCTATGCATCACATCA
ATAAATATATGATAGGATATTTTACATTTGATGTATCTGAAGATTAATTCAACAAATGTTTAGTGAGTAGGCTT
GTTGTAGGTGCTGGGAATTCAGCAGTGAACAAAACAAAGTCTCTGCCTCATGGAGCTCATATTTATAGTAGGGAAG
ACTGTCAATAAGCAATATACACATTGACTAAATGATAGATAATGCCAGTAATGTGGCAAGTTTTATGGAAAAAT
AAATCAGGATAAAAGGATAAGAGTGATATGGGGATTCTCTTAGTTAGGGTAGATAAGGAAGGCCCTCTTAGCTAAG

GAGGCACATAAATATCTGATCATCTAATGAGAGAAGGAGCAACATGGGATTCTAGAGGGAACTATCCTAGAAA
GA

SEQ ID NO:220

>GL2_147_2_M13F Direction: sense

CTGCTTCTCTTCTAGGATAGTTTCCCTCTAGAAATCCATGTTGCTCCTTCTCTCATTAAATGATCAGATATTTAT
GTGCCTCCTTAGCTAAGAGGCCTTCTTATCTACCCTAACTAAGAGAATCCCCATATCACTCTTATCCTTTTATC
CTGATTTATTTTTCCATAAACTTGCCACATTACTGGGCATTATCTATCATTTAGTAATGTGTATATTGCTTATT
GACAGTCTTCCCTACTATAATATGAGCTCCATGAGGCAGAGACTTGTGTTTGTTCACCTGCTGAATTCCCAGCACC
TACAACAAGCCTACTCACTAAACATTTGTTGAATTAATCTTCAGGATACATCAAATGTAAAAATATCCTATCATA
TATTTATTGATGTGATGCATAGGAAAATGTCTGGAAGGGTACATACCAAAATGTTAATTATTTATTTAACCTGGT
GGGAGGTGGATTATTTCTTTCTTTTCTTTCTTTTGGAGACCAGAGTTTCCGCATCTTCGTTGCCCCAGGCTGGG
AGTGGAATTTGGGCAAAGCCCGCAGAAACCCCAAGCAACAAGTGGGTTTAGATAGNATCAAAGCGGGCCGCTCGA
CTTAANTCCTTGAAGGTCTGATTACTCAACCTGACTTGTCAGAAA

SEQ ID NO:221

>GL2_147_2_M13R Direction: anti-sense

CTTGCCATTCCTACTCCAGCCTGGGCAACGAGAGCGAACTCTGTCTCAAAAAGAAAAGAAAAGGAAAGAAAAACC
ACCTCCCACCAGGTTAAATAAATAATTAACATTTTGGTATGTACCTTCCAGACATTTTCCTATGCATCACATCA
ATAAATATATGATAGGATATTTTACATTTGATGTATCCTGAAGATTAATTCAACAAATGTTTAGTGAGTAGGCTT
GTTGTAAAGTGCTGGGAATTCAGCAGTGAACAAAACAAAGTCTCTGCCTCATGGAGCTCATATTATAGTAGGGAA
GACTGTCAATAAGCAATATACACATTACTAAATGATAGATAATGCCCAGTAATGTGGCAAGTTTATGGAAAAAT
TAATCAGGATAAAGGATAAGAGTGATATGGGGATTCTCTTAATTAGGGTAGATNAGGAAGGGCTCTTTAGCTNAA
GGAAGCAACATAAATATCTGATCATTTTAAAANGGGAAGGAACGAAAAAGGGGAAAGCCAAAACACAAATGGGGG
ACAATTTATACCTTACGAAAAGGGGGGAAAAAACCATAAAATCCCTAAGGAAACANAAAAGCAAAAGCNCAAAGA
CCAGCAAAAACAA

SEQ ID NO:222

>GL2_147_3_M13F Direction: anti-sense

CTTGCCATTCCTACTCCAGCCTGGGCAACGAGAGCGAACTCTGTCTCAAAAAGAAAAGAAAAGGAAAGAAAAACC
ACCTCCCACCAGGTTAAATAAATAATTAACATTTTGGTATGTACCTTCCAGACATTTTCCTATGCATCACATCA
ATAAATATATGATAGGATATTTTACATTTGATGTATCCTGAAGATTAATTCAACAAATGTTTAGTGAGTAGGCTT
GTTGTAGGTGCTGGGAATTCAGCAGTGAACAAAACAAAGTCTCTGCCTCATGGAGCTCATATTATAGTAGGGAAG
ACTGTCAATAAGCAATATACACATTACTAAATGATAGATAATGCCCAGTAATGTGGCAAGTTTATATGGAAAAAT
AAATCAGGATAAAGGATAAGAGTGATATGGGGATTCTCT

SEQ ID NO:223

>GL2_147_3_M13R Direction: sense

CTGCTTCTCTTCTAGGATAGTTTCCCTCTAGAAATCCATGTTGCTCCTTCTCTCATTAAATGATCAGATATTTAT
GTGCCTCCTTAGCTAAGAGGCCTTCTTATCTACCCTAACTAAGAGAATCCCCATATCACTCTTATCCTTTTATC
CTGATTTATTTTTCCATAAACTTGCCACATTACTGGGCATTATCTATCATTTAGTAATGTGTATATTGCTTATT
GACAGTCTTCCCTACTATAATATGAGCTCCATGAGGCAGAGACTTGTGTTTGTTCACCTGCTGAATTCCCAGCACC
TACAACAAGCCTACTCACTAAACATTTGTTGAATTAATCTTCAGGATACATCAAATGTAAAAATATCCTATCATAT
ATTTATTGATGTGATGCATAGGAAAATGTCTGGAAGGGTACATACCAAAATGTTAATTATTTATTTAACCTGGTG
GGAGGTGGTTTTCTTTCTTTTCTTTTCTTTTGGAGACAGAGTTTACGCTCTCGTGTGCCCAGGCCTGGAGTGG
AATGGCAAGCCGCAGAANCCAGCACAGTGGTTANGATNAATTAAGCGGGCNAGTCCAATAAGTCTGAAGGCTGA
AACACACACACAGAGACGGTCAAAAGGGCGAAATNCGGCAAAATNCCATCCCCTGCGGGGCCGCATCAAAAAT
GNATNGAGAAGGGGACCAAATGGCCAAAGANGAGCGAT

SEQ ID NO:224

>GL2_147_4_M13F Direction: sense

CTGCTTCTCTTCTAGGATAGTTTCCCTCTAGAAATCCATGTTGCTCCTTCTCTCATTAAATGATCAGATATTTAT
GTGCCTCCTTAGCTAAGAGGCCTTCTTATCTACCCTAACTAAGAGAATCCCCATATCACTCTTATCCTTTTATC
CTGATTTATTTTTCCATAAACTTGCCACATTACTGGGCATTATCTATCATTTAGTAATGTGTATATTGCTTATT
GACAGTCTTCCCTACTATAAATTATGAGCTCCATGAGGCAGAGACTTGTGTTTGTTCACCTGCTGAATTCCCAGCAC
CTACAACAAGCCTACTCACTAAACATTTGTTGAATTAATCTTCAGGATACATCAAATGTAAAAATATCCTATCATA
TATTTATTGATGTGATGCATAGGAAAATGTCTGGAAGGGTACATACCAAAATGTTAATTATTTATTTAACCTGGT
GGGAGGTGGTAA

SEQ ID NO:225

>GL2_147_1_M13R Direction: sense

CTGCTTCTCTTCTAGGATAGTTTCCCTCTAGAAATCCATGTTGCTCCTTCTCTCATTAGATGATCAGATATTTAT
GTGCCTCCTTAGCTAAGAGGCCTTCCTTATCTACCCTAACTAAGAGAATCCCCATATCACTCTTATCCTTTTATC
5 CTGATTTATTTTCCATAAACTTGCCACATTACTGGGCATTATCTATCATTTAGTAATGTGTATATTGCTTATT
GACAGTCTTCCCTACTATAATATGAGCTCCATGAGGCAGAGACTTTGTTTTGTTCACTGCTGAATTCCCAGCACCC
TACAACAAGCCTACTCACTAAACATTTGTTGAATTAATCTTCAGGATACATCAAATGTAAAAATATCCTATCATAT
ATTTATTGATGTGATGCATAGGAAAATGTCTGGAAGGGTACATACCAAATGTTAATTATTTATTTAACCTGGTG
10 GGAGGTGGTTTTTCTTTCTTTTCTTTNCTTATTGAGACAGAGTTTCGCTCTCGTTGCCCCGGCTGGAAGTGGAA
TGGCAAGCCGGCAGGAACCCAAGACAACAAGGAGGTTAAGATCAGAATAAAAGACGGGGACCGCATCCAGAAAC

SEQ ID NO:226

>GL2_147_4_M13R Direction: anti-sense

CTTGCCATTCCACTCCAGCCTGGGCAACGAGAGCGAAACTCTGGTCTCAAAAAGAAAGGAAAAGGAAAAGAAAAC
15 CACCTCCCACCAGGGTTAAATAAATAAATTAACATTTTGGTATGTACCCTTCCAGGACATTTTCTATGCATCACA
TCAATAAATATATGATAGGATATTTACATTTGATGTATCCTGAAGATTAATTCAACAAATGTTTAGTGAGTAGG
CNTGTTAGTAGGTGCTGGGAATTCAGCAGTGAACAAAACAAAGTCTCTGCCTCATGGAGCTCATATTATAGTAGG
GAAGACTGTCAATAAGCAATATACACATTACTAAATGATAGATAATGCCAGTAATGTGGCAAGTTTTATGGAAA
AATNAATCAGGATAAAAGGATAAGAGTGATATGGGGATTCTNCTTAGATTAGGGTAGATAAAGGAANGCCTCTTA
20 GNCTNAAGAGGCCACATAAAACAAATCAATTCCTTGGGAAAATCCAANCTGNCTAAACGTAGACAGGGACAAGCA
ANAGGCGGACGG

SEQ ID NO:227

Clone 147 - Novel (Chromosome 17)>

CTGCTTCTCTTCTAGGATAGTTTCCCTCTAGAAATCCATGTTGCTCCTTCTCTCATTAAATGATCAGATATTTAT
25 GTGCCTCCTTAGCTAAGAGGCCTTCCTTATCTACCCTAACTAAGAGAATCCCCATATCACTCTTATCCTTTTATC
CTGATTTATTTTCCATAAACTTGCCACATTACTGGGCATTATCTATCATTTAGTAATGTGTATATTGCTTATT
GACAGTCTTCCCTACTATAATATGAGCTCCATGAGGCAGAGACTTTGTTTTGTTCACTGCTGAATTTCCAGCACCC
TACAACAAGCCTACTCACTAAACATTTGTTGAATTAATCTTCAGGATACATCAAATGTAAAAATATCCTATCATAT
30 ATTTATTGATGTGATGCATAGGAAAATGTCTGGAAGGGTACATACCAAATGTTAATTATTTATTTAACCTGGTG
GGAGGTGGTTTTTCTTTCTTTTCTTTTCTTTTGGAGACAGAGTTTCGCTCTCGTTGCCCAGGCTGGAGTGGAAAT
GGCAAG

SEQ ID NO:228

Novel (chromosome 8)

>GL1_41_2_G3F1 Direction: sense

GCTTGCAAAGGAGAGGCTGTGACTACCAAGGTCGTGTCAACAACCTGAATGGCTGAAATACCCAACTTGCCCATG
CAAATGGGCTTGGGTCTCTCCTGGCAGCCGCTTTGAAGGCTCTAGACTTATCTGTGAACCTCTTTTGGAGAGG
GTCTTTCCAAGTAGTGGTTTATTCTTTGACTCTCCTCATACCTTTTTTGGCAGAGAGTGAGAGTGAGAAGGGAGG
40 GCTAATGCCTGAGCTCCTGCCCTTTCTATGCAGTGAGGGTCAAGATCCTCAGCTAGTGTGTTGAGGGAAGTGGTGT
AACCTGGGTCTCTCATTTTCTACCATCCAAGTTGCC

SEQ ID NO:229

>GL1_41_2_G3R1 Direction: anti-sense

GGCAACTTGGATGGTAGAAAATGAGAGACCCAGGTTACACCAGGTTCCCTCAAACACTAGCTGAGGATCTTGACC
CTCACTGCNTAGAAAGGGCAGGAGCTCAGGCATTAGCCCTCCCTTCTCACTCTCACTCTCTGGCAAAAAGGTAT
GAGGAGAGTCAAAGAATAAACCACTAGTTGGAAAGACCCTCTCAAAAAGGAGTTCACAGATAAGTCTAGAGCCT
TCAAAGGCGGCTGCCAGGAGAGACCCAAGCCATTGCGATGGGCAAGTTTGGGTATTTAGCCATTCAAGTTGTTG
50 ACACGACTTGGTAGTCACAGCCTCTCCTTTGCAAGC

SEQ ID NO:230

>GL1_41_3_G3F1 Direction: sense

GCTTGCAAAGGAGAGGCTGTGACTACCAAGTCGTGTCAACAACCTGAATGGCTGAAATACCCAACTTGCCCATGC
AAATGGGCTTGGGTCTCTCCTGGCAGCCGCTTTGAAGGCTCTAGACTTATCTGTGAACCTCTTTTGGAGAGGG
55 TCTTTCCAAGTAGTGGTTTATTCTTTGACTCTCCTCATACCTTTTTTGGCAGAGAGTGAGAGTGAGAAGGGAGGG
CTAATGCCTGAGCTCCTGCCCTTTCTATGCAGTGAGGGTCAAGATCCTCAGCTAGTGTGTTGAGGGAAGTGGTGT
GCCTGGGTCTCTCATTTTCTACCATCCAAGTTGCC

SEQ ID NO:231

>GL1_41_3_G3R1 Direction: N/A

GGCAACTTGGATGGTAGAAAATGAGAGACCCAGGCTACACCAGNTTCCCTCAAACACTAGCTGAGGATCTTGACC
CTCACTGCATAGAAAGGGCAGGAGCTCAGGCATTAGCCCTCCCTTCTCACTCTCACTCTCTGGCAAAAAAGGTAT
GAGGAGAGTCAAANAATAAACCACTANTTGGANAGACCCCTCTCAANAAAGGAGTTACAGATAANTNTATAGCCT
TCAAAGGCGGCTGCCAGGAGAGAC

SEQ ID NO:232

Novel (chromosome 8)>

GCTTGCAAAGGAGAGGCTGTGACTACCAAGTCGTGTCAACAACCTGAATGGCTGAAATACCCAAACTTGCCCATGC
AAATGGGCTTGGGTCTCTCCTGGCAGCCGCCCTTTGAAGGCTCTAGACTTATCTGTGAACTCCTTTTTTGAGAGGG
TCTTTCCAACCTAGTGTTTATTCTTTGACTCTCCTCATACCTTTTTTTGCCAGAGAGTGAGAGTGAGAAGGGAGGG
CTAATGCCTGAGCTCCTGCCCTTTCTATGCAGTGAGGGTCAAGATCCTCAGCTAGTGTGTTGAGGGAACCTGGTGTA
ACCTGGGTCTCTCATTTTCTACCATCCAAGTTGCC

SEQ ID NO:233

Novel (chromosome 9)

>GL2-49-5M13R Direction: anti-sense

CTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCCTGGCGGAGGTCCGAGTCGGG
TTGGATGGCTGTGTCCGTCGCCATGTTTGTGTGGTGCTGGCCCCGTGGTCCCATGTTCTGGCAGCTTCTGGCTC
CAGCCTCAGCCTGTAGTGGGGTGTACGTGGTAGNAGTGCCTGAGCTGGGGGCCTGCAGTGGGGTAGGTCACTG
GTAGGAGTGCAGNTAGCATAGAAGTTANAAAGGTTACTAGTAGAGACTGGTCCCATACTTAGAGATGGGACACCA
TGACCTGATGGNTACNACCCTGACAGGCCGAGAAACAGACACACTGGAGCCACCGACTGACACAACGGGCCNT
GGGNACGGACGTCCAATNGCGTATGANTACCANGACAGTCAGGANCCCCAATGACCCGGAAGCAGGAAACGGGG
CAGAAAAANCAATAGCCAAGGAATAGTCACANGGTGCACANAACCTGNGCAGGGACCAGNAAACCAGAANGACC
AATGCACANTACATAAGAAGGGGGGGGGGCACNCCACAAAAGATATGCCGGGCGACGCCAGATAAGATAAGGGACT
AGGGAAGGAGTCCGGGNAAANATGTAACGAAAGAGTATCGAACC AATGGAGGGNCGCCGGGTACCCGNGCGNAAG
GACAAACAANAAGCAGGCATCCGGACTGGGAACCAATGGGGGGGAAAGAAGCAGCGCCCCCATGGGGANAGGGAT
GTAAANCCACAACAACACGTGTNAAACG

SEQ ID NO:234

>GL2-49-4M13F Direction: N/A

AATTGAANTTACACTCACTATAGGGCGAATTGGGCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGATGGAAT
ATCTGCAGAATTGCCCTTCTCTCGGCATGGACGAGCTGTACAAGGAGGAGGCCGCAAGGCCGGTGGCAGCGGTG
GCTCCAAGTGGTGGCCTTGGGGGTTCTTGCGGCTGCAGGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGC
CACAGAAACCCTCTAACCTCAGCACTGCACTCCACCACGAACACCCACGCAGGCCCTCAGGCAACCCGGCAACC
TTCCAAACCAACGGAACACCCACACAGGCTGAGGCTGGAGCCAGAAGCCGCCAGAACATGGGACCACAGGGCCA
GGCACCACACAAACATGGCGACGGACACAGCCAATCCAAACCCCGGAAAAACCGATTTCNCNGNGGGGGGAAAA
ACCGCCCCAGTTTTCCACCCCGGGAGAGCGCCCCAAAAGGGGGGGGGNACACCCACCCACNACCCCAAAGGGGN
CGCAGGGGCCAAACAGCAGAAANCCCCGAANTTCCCTTGCGGGGGGAATTGCGCCGCGCCCAAAGGGGAACNAGCA
AGGAAGGCCATTGCCGGTTGCCGGGCCCAAGCACCGCCAGGAACAGCGCGCAAGGCGAC

SEQ ID NO:235

>GL2-49-1M13F Direction: sense

CTGCAGGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCCTCTAACCTCAGCACTGCACTC
CACCACGACCACCCACGCAGGCCCTCAGCACCGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCC
AGAAGCTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGA
CTCGGACCTCCGCCAGGCCCCCAGCGCACAAACCATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:236

>GL2-49-1M13R Direction: anti-sense

GCTGGCCGCACGCAGCTCTTTTCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCCTGGCGGAGGTCCGAGTCGG
GTTGGATGGCTGTGTCCGTCGCCATGTTTGTGTGGTGCTGGCCCTGTGGTCCCATGTTCTGGCAGCTTCTGGCT
CCAGCCTCAGCCTGTGTGGGGTGTTCGTGCTGGAGTGCGGTGCTGAGGGCCTGCGTGGGGTGGTCTGTGGTGGAGT
GCAGTGCTGAGGTTAGAGGGTTTCTGTGGCTGTCCCTCTTAGGTGGGCACCTGCCTGTGGTCTCCCTGCAG

SEQ ID NO:237

>GL2-49-2M13F Direction: sense

CTGCAGGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCCTCTAACCTCAGCACTGCACTC
CACCACGACCACCCACGCAGGCCCTCAGCACCGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCC

AGAAGCTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGA
CTCGGACCTCCGCCAGGCCCCCAGCGCACAAACCATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:238

>GL2-49-2M13R Direction: N/A

CTGGCCGCACGCAGCTCTTTTCCCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGCGGAGGTCCGAGTCGGG
TTGGATGGCTGTGTCCGTCGCCATGTTTGTGTGGTGCCCTGGCCCTGTGGTCCCATGTTCTGGCAGCTTCTGGCTC
CAGCCTCAGCCTGTGTGGGGTGTTCGTGGTGGAGTGCGGTGCTGAGGGCCTGCGTGGGGTGGTCTGTGGTGGAGTG
CAGTGCTGAGGTTANAGGGTTTCTGTGGCTGTCCCTCTTAGGTGGGCACCTGCCTGTGGTCTCCCTGCAGCCGCA
AAACCCANCACTGGAGCCACCGCTG

SEQ ID NO:239

>GL2-49-4M13R Direction: N/A

CTGGCCGCACGCAGCTCTTTTCCCTGGGGATCCCAGATGGTTGTGCGCTGGGGGCTGGCGGAGGTCCGAGTCGGG
TTGGATGGCTGTGTCCGTCGCCATGTTTGTGTGGTGCCCTGGCCCTGTGGTCCCATGTTCTGGCGGCTTCTGGCTC
CAGCCTCAGCCTGTGTGGGGTGTTCGTGGTGGAGTGCGGTGCTGAGGGCCTGCGTGGGGTGGTCTGTGGTGGAGTG
CAGTGCTGAGGTTAGAGGGTTTCTGTGGCTGTCCCTCTTAGGTGGGCACCTGCCTGTGGTCTCCCTGCAG

SEQ ID NO:240

>GL2_72_G07_G3F1 Direction: N/A

CTGCAGGGAGACCCGCAGGCAGGTGCCACCTAAGGGGGACAGCTACAGAAACCTCTAACTCAGCACTGNACTC
CACCACGACACCCACGCAGGCCCTCAGCACCGCACTCCACCACGAACAACCCACACAGGCTGAGTGCTGGAGCC
AGAAGCTGGCAGAACATGGGACCACAGGGGCCAGGCACCACACAAACATGGCGACGGACACAGGCATNCAAACCG
ACTCGGACCTCCGCCAGGNCCTCAGCGCACAAACATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGGCAGCGCA
GAAACCAGCACAGTGTTAGATATGATTAAAGCGGGCGNGTCGANTAATCTGAGGTCTGATACTCACTGACTGTCTG
TAAGGGNGAATTTCGCGGGCGCGTAAATTCAATTCTGGCCCTATAGTGAGTCGTATTACAATTCACTGGGCGGCGTTT
TACAACGTCTGTGACTGGGAAAAACCTGNGCGTTATCCAACCTAATCTGNGCTTGGAGAATTTCCCTTTTGCAGA
CTGGGCGTAATAACGAAAAAGGNNCCGAA

SEQ ID NO:241

>GL2_72_G08_G3F1 Direction: sense

CTGCAGGGAGACACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCTCTAACCTCAGCACTGCACTCC
ACCACGACCACCCACGCAGGCCCTCAGCACCGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCCA
GAAGCTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGAC
TCGGACCTCCGCCAGGCCCCCAGCGCACAAACCATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:242

>GL2_72_G09_G3F1 Direction: sense

CTGCAGGAGACCGCAGGCAGGTGCCACCTAAGGGGGACAGCTACAGAAACCTCTAACCTCAGCACTGCACTCC
ACCACGAACACCCACGCAGGCCCTCAGCACCGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCCA
GAAGCTGGCAGAACATGGGACCACAGGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGA
CTCGGACCTCCGCCAGGCCCCCAGCGCACAAACCATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:243

>GL2_95_2B10_G3F1 Direction: sense

CTGCAGGAGACACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCTCTAACCTCAGCACTGCACTCCA
CCACGACCACCCACGCAGGCCCTCAGCACCGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCCAG
AAGCTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGGACACAGCCATCCAACCCGACT
CGGACCTCCGCCAGGCCCCCAGCGCACAAACCATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:244

>GL2_95_2B11_G3F1 Direction: sense

CCGCACTGGAGACACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCTCTAACCTCAGCACTGCACTC
CACCACGACACCCACGCAGGCCCTCAGCACCGCACTCCACCACGAAAAACCCACACAGGCGTGAGGCTGGAGCCAG
AAGCTGCCAGAACATGGGANACAGGGNCAGGCGACCACACAAACATGGCGACGTGACACAGGCATCCAACCCGA
CATCGGACTCCGACGGGCCCCAGCGCACAAACATACTGGGATCCCCACGAAAAGAGCTGCGTGCTGGGCAGNAG
CGCNAGAAACCAGCACAGCTGGTTAGAGTACAGATAAANACGGGCGCGTCGCACGTAAANCTGAAAAAGGTCGTG
AGTATAATCAACATGTANACTGNTT

SEQ ID NO:245

>GL2-49-5M13F Direction: sense

CTGCAGGGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCCCTCTAACCTCAGCACTGCACT
CCACCACGANCAACCCACGCAGGCCCCCAGCACCGCACTCCACCACGAAACACCCCAACACAGGCTGAGGCTGGA
GCCAGAAGCTGGCCAGAACATGGGACCAACGNGCGGNNCCCCAACGCNGGGCGGGCCAGAACGACCGAAAAGCG
AAACCCCAAAGAAGNNGCGCAAATTATGCAGACCAGGAAACAGATGAAAACAAACCAAGGCGACCAATACC
CCAAAANANCACCGCNCAGGAAAGCATACACGCGGGGAAACGCCCAGTTCCACCACAGGGGCCCCACAAGGAGGG
GACCCNCCACCNACGNGCAGGGGCACCGGCCAGCAGACAGCGAGAGCGCCGCGAAGTACCGATTAGGAGGCGGCG
AATACCCGACCACCAAAAAAGGGGGAAACACGAAAGAAAGCTGGGAAAACGGCCCGATTTTAGGACCACGGGAGT
TTGACCGCACGGGGAGACGCCCCCCCCAAAGGGACACCCCCAGAGGCACAAAAAGCAAGAAGACACCCCCCCCCAA
AGAGACCGCTCAAGACCCGAAAGAGGTTGGAGCGGCTTCCTTAACAGAGGAAGCTTAACNCGGCACAGTTNAAAC
GAAGGCGAGTGGGC

SEQ ID NO:246

>GL2_49_1_M13R Direction: anti-sense

CTGGCCGCACGCAGCTCTTTTCCTGGGGATCCAGATGGTTGTGCGCTGGGGGCTGGTGGAGGTCCGAGTCGGG
TTGGATGGCTGATGTCCGCCGCCATGATTTGATAGATGGATGCCTGGACCTGATGAGTCCCAATGATTCCTGGCA
GACATTCTGGACATCCAGCACATCAGACCTGATGATGGGGATGNTTCGATGGATG

SEQ ID NO:247

>GL2_49_2_M13R Direction: N/A

CTGGCCGCACGCAGCTCTTTTCCTGGGGATCCAGATGGTTGTGCGCTGGGGGCTGGCGGAGGTCCGAGTCGGG
TTGGATGGCTGGTTCGCGCAGTGGTGGTGCCTGGCCTGGGCTGTCTGGCAGCTTCTGGCTCCAGCCTCAGCCCTG
TGTGGGGCTGGTTCCGNTGGTGGAGTGGGGTGTGAAGGCCATGCGATGGAGAGTGGATCNAGGAAGGAGATGC
AGAAGCATAGAGAGTTACGAGGGTATCTAGTGGCTGTACCTCTATAGGTAGGGCACCATGACACTAGATGGTAC
TNCCTTGACAGAACGCAAGAAACACCAAGAAAAACCTGAGAGGCCAACCAGAAATGAC

SEQ ID NO:248

Clone 49 -Novel (Chromosome 9)>

CTGCAGGAGACCACAGGCAGGTGCCACCTAAGAGGGACAGCCACAGAAACCCCTCTAACCTCAGCACTGCACTCC
ACCACGACCACCCACGCAGGCCCTCAGCAGCGCACTCCACCACGAACACCCACACAGGCTGAGGCTGGAGCCA
GAAGCTGCCAGAACATGGGACCACAGGGCCAGGCACCACACAAACATGGCGACGACACAGCCATCCAACCCGAC
TCGGACCTCCGCCAGGCCCCAGCGCACACCATCTGGGATCCCCAGGAAAAGAGCTGCGTGCGGCCAG

SEQ ID NO:249

Novel (clone 1/226)

>GL2_1_3_M13F Direction: anti-sense

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTATATTGGGGGGAGG
GAGTAGAAAAGCAAGCCCCCTATACTGGGCCCTATTAGTGGCAGCTTCTTGTTCATAGGATTAAGGAAGACTCT
GAGGAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTG
AAGTGTGAAGGCCCTCATAACCTCCATCTTGCTCAGGACTATAGTCTTGAAACCTNNGGGCGGAGAAAAGCGC
CAACATTTTCATNCCCTGCATACATAAGGGAGAAAGGAGACAGGACAACGATAAGTGAAGAGAGAACAGAACGAAG
AAAAGAAGCGGANAAACGGCCCCAGACAATAGTAAGGGCGAANGAATGGGCAGAAAGNCTTGCAANCGTNCCCGGG
GCAATACAATCCCTTGAACACAAGANCCAGGGCANNCCGGGACCACGCAAGAAAACCAAGAAACACAT

SEQ ID NO:250

>GL2_81B_E02_G3F1 Direction: N/A

GCCCGAGCCGGACTGGTCAGGATGATCACCGGACGCGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCT
CTTCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGTGAATGAAAGTGGCGCTTTC
TCCGGGCCCAGGGTCCAGGACATAGTCTGAGTGCAAGATGGAGGGTATGAGGGGGCTTCACACTTCACTTCATC
CTTTTAACCATTAATAACAAAGCGAACTACANCTGGATTTTCCAAACAAATTTTATTTCCCTCAGAGTCTTCCCT
TAATCCTATGGAACAAGAAGCTGGCACTGAATAGTGGGCCAGTATAGGGGCTTGCCTTTCTANATCCCTTCCCC
CAATATTAATAATATATGACTTTTAAAAAAGGGGAGGGGAGGGGAGGGGAGGGGAGGGGAGGGGAGGGGAGGGG
CCAGACAGTTGGTTAGATAGATAAAGCGGCGCGTCTGACTANTCTGAGGTCTGATACTCACTGACTGTGCTAAGG
CGAATTGCTTTTAAACCTGCAGGACTAGTCCCTTTATGAGGGTTAATTCTGAGCTTGGCGTAATCAT

SEQ ID NO:251

>GL2-96-1M13R Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTCGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCCTCC

5
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACGTTCACTTCAGTCCCT
TCTACCCATCACAACATACAAGGCAACTACACCTGGATTTTTCCAAACAACTTTTATTTCCTCAGAGTCTTCCTT
AATCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAAT
ATAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

SEQ ID NO:252

>GL2-96-3M13F Direction: sense

10
GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACTTCATCCCTTC
TACCCATCACAACATACAAGCAACTACACCTGGATTTTTCCAAACAACTTTTATTTCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGAC

15 SEQ ID NO:253

>GL2-96-3M13R Direction: N/A

20
ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTAAAAAGTCTATATTTTTTATATTGGGGGGAGGG
AGTAGAAAAGCAAGCCCTATACTGGGCCCTATTCACTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCTG
AGGAAATAAAAGTTGTTTGAAAAATCCAGGTGTAGTTGCTTNTGNTATGTTGTGATG

SEQ ID NO:254

>GL2-96-4M13F Direction: anti-sense

25
ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTAAAAAGTCTATATTTTTTATATTGGGGGGAGGGAGTAG
AAAAGCAAGCCCTATACTGGGCCCTATTCACTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCTGAGGAA
ATAAAAGTTGTTTGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAAGTGT
GAAGGCCCTCATACCCTCCATCTTGCTTCAGACTATGTCTTGGAACCTGGGGCGGAGAAAGCGCCACTTTTCAT
TCCTGCTTCTTGGGATTGTTGACGGCCACGTAGTGATAGAGAACGACAAGCAAGAAGAGCGACACGCCCAGCATG
TTGGCGAAGATGGCGAGCTGCACGTCCGTGATCATCTGACCAGTCCGGCTCGGCCCGCAGAAACCAGCACACTG
GAGCCACCGCTGCCACCGGCCTT

30 SEQ ID NO:255

>GL2-96-5M13F Direction: sense

35
GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACTTCATCCCTTC
TACCCATCACAACATACAAGCAACTACACCTGGATTTTTCCAAACAACTTTTATTTCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGTCCGCAAAACCCAGCAC
AGTGGTTAGATAGATAAAGC

40 SEQ ID NO:256

>GL2-96-5M13R Direction: N/A

45
ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTAAAAAGTCTATATTTTTTATATTGGGGGGAGGGA
GTAGAAAAGCAAGCCCTATACTGGGCCCTATTCACTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCTGA
GGAAATAAAAGTTGTTTGAAAAATCCAGGTGTAGTTGCATATAAGTATGTTGTGATA

SEQ ID NO:257

>GL2_1_1_M13R Direction: sense

50
GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACTTCATCCCTTC
TACCCATCACAACATACAAGCAACTACACCTGGATTTTTCCAAACAACTTTTATTTCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGCGCCGATCGCGATCTAGAACTAGT

55 SEQ ID NO:258

>GL2_1_2_M13F Direction: sense

60
GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAAGGGCCTTCACACTTCACTTCATCCCTTC

TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACTTTTATTTTCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAATACTAGACTTATT

5 SEQ ID NO:259

>GL2_1_2_M13R Direction: anti-sense

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTTATATTGGGGGGAGG
GAGTAGAAAAGCAAGCCCTATACTGGGCCCTATTCAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCT
10 GAGGAAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTG
AAGTGTGAAGGCCCTTCATACCCTCCATCTTGCCTCAGACTATGTACCTGGAACCCTGGGGCNGAGAAAGCGCCA
CNTTCATTCTGCTTCTAGGGATCGNNAGACGGACACGATAGNTGACTAGAGAACGACAAGCAAGAA

SEQ ID NO:260

>GL2_226_1_1_M13F Direction: sense

15 GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCTCT
TCTTGCTTGTGCTTCTCTATCACCACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCCTTCACACTTCACTTCATCCCTTC
TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACTTTTATTTTCCTCAGAGTCTTCCTAAT
20 CCTCATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

SEQ ID NO:261

>GL2_226_1_1_M13R Direction: anti-sense

25 ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTTATATTGGGGGGAGGGA
GTAGAAAAGCAAGCCCTATACTGGGCCCTATTCAGTGGCAGCTTCTTGTTCCATAGGATTAGGAAGACTCTGAG
GAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAAG
TGTCAGGGCCCTCATACCCTCCATCTTGCCTCAGACTATGTCCTGGAACCCTGGGGCGGAGAAAGCGCCNCTTT
CATTCCTGCTTCTTGGGATTGTTGACGGCCACGTGGTGATAGAGAACGACAAGCAAGAAGAGCGANACGCCACG
30 ATGTTGGCGAAGATGGCGAGCTGCACGTCCGTGATCATCCTGACCAGTCCAGGCTCGGC

SEQ ID NO:262

>GL2_226_1_2_M13F Direction: sense

35 GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCCTTCACACTTCACTTCATCCCTTC
TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACTTTTATTTTCCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

40 SEQ ID NO:263

>GL2_226_1_2_M13R Direction: anti-sense

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTTATATTGGGGGGAGGGA
GTAGAAAAGCAAGCCCTATACTGGGCCCTATTCAGTGGCAGCTTCTTGTTCCATAGGATTAAGGAAGACTCTGA
45 GGAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAA
GTGTGAAGGCCCTCATACCCTCCATCTTGCCTCAGACTATGTCCTGGAACCCTGGGGCGGAGAAAGCGCCACTT
TCATTCTGCTTCTTGGGATTGTTGACGGCCACGTAGTGATAGAGAACGACCAGCAAGAAGAGCGACACGCCACCA
GCATGTTGGCGAAGATGGCGAGCTGCACGTCCGTGATCATCCTGACCAGGTCCGGCATCGG

SEQ ID NO:264

>GL2_226_1_3_M13F Direction: sense

50 GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCCTTCACACTTCACTTCATCCCTTC
TACCCATCACAAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACTTTTATTTTCCTCAGAGTCTTCCTTAA
55 TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAACTAGT

SEQ ID NO:265

>GL2_226_1_4_M13F Direction: sense

5 GCGGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCGTCGCCAACATGCTGGGCGTGTGCTCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATA
TAAAAATATAGACTTTTAAAAAAGGGCGCGCTCGCGATCTAGAACTAGT

10 SEQ ID NO:266

>GL2_81B_E01_G3F1 Direction: sense

15 GCGGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCTT
CTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAGGTGGCGCTTTCTCCG
CCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTTCATCCCTTCT
ATCCATCACAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGNCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATA
TNAATATAGACTTTTAAAAAAGGGCGCGCTCGCGATCTAGAACTAGT

20 SEQ ID NO:267

>GL2_81B_E05_G3F1 Direction: N/A

25 GCGGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCTT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GNCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGGCACTGAATAGTGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATA
TNAATATAGACTTTTAAAAAAGGGGNGCGGTGCGATCTAGAACTAGTCCGNNAGAAACCAGCA
CAGTGGTTAGATAGATAAAGCGGGCGGTGCGACTANTCTGAGGTCTGATACTCACTGACT

30 SEQ ID NO:268

>GL2_81B_E06_G3F1 Direction: sense

35 GCGGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCTT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGGCGCGCTCGCGATCTAGAACTAGTCCGNAGAACCCAG
CACAGTGGTTAGATAGATAAAGCGGCCGCTCGACTAGTCTGAGGTCTGATACTCACTGACTGTGTAAGGGCGAA
TTCGTTTAAACCTGCAGGACTAGTCCCTTTATGAGGGTTAAATTCTGAGCTTGGCGTAATCATGGTCAT

40 SEQ ID NO:269

>GL2_1_3_M13R Direction: sense

45 GCGGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCTT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGCCACTGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAAA
TATAAAATATAGACTTTTAAACAAACACAACAACAACAAAAAGGGCGCCAGCTCGGCGATCTAGAACTAGT
CCGGCAAGAACCCAGNAACAGGGGTTAGATA

50 SEQ ID NO:270

>GL2_81B_E04_G3F1 Direction: N/A

55 GCGGAGCCGGACTGGTCAGGATGATCACGGACGCGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCTT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAAGTGGCGCTTTCTCC
GCCCCAGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCTTCACACTTCACCTTCATCCCTT
CTANCCATCACAACATACAAAGCAACTACACCTGGATTTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
ATCCTATGGAACAAGAAGCTGGCACTGAATAGGGCCAGTATANGGGCTTGCGTTTTCTACTCCCTCCCCCAAT
ATAAAATATAGACTTTTAAAAAATNAAGGGNGCGCTCGCGATACTAGAACTAGT

SEQ ID NO:271

>GL2_226_1_3_M13R Direction: anti-sense

CTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTATATTGGGGGGAGGGAG
TAGAAAAGCAAGCCCCTATACTGGGCCCCTATTAGTGGCAGCTTCTTGTTCATAGGATTAAGGAAGACTCTGAG
GAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAAG
TGTGAAGGCCCCCTCATACCCTCCATCTTGCCTCAGACTATGTCTTGGAACCCCTGGGGCGGAGAAAGCGCCACTGT
TCATTCTGCTNTCTTGGGATTGTTTCGACGGNCACGTAGATGATAGAGAACGACAAGCAAGAAGAGCGAANACGC
CCAGCATGTAAGGCGAAGATGGCGAGCTGCACGTCCGTGATCATCTTGACCAGTCCGGCTCGGA

SEQ ID NO:272

>GL2_226_1_4_M13R Direction: anti-sense

ACTAGTTCTAGATCGCGAGCGGCGCCCTTTTTTTTTTTTTTTTAAAAAGTCTATATTTTTATATTGGGGGGAGGGGA
GTAGAAAAGCAAGCCCCTATACTGGGCCCCTATTAGTGGCAGCTTCTTGTTCATAGGATTAAGGAAGACTCTGA
GGAAATAAAAGTTGTTTGGAAAAATCCAGGTGTAGTTGCTTTGTATGTTGTGATGGGTAGAAGGGATGAAGTGAAG
GTGTGAAGGCCCCCTCATACCCTCCATCTTGCCTCAGACTATGTCTTGGAACCCCTGGGGCGGAGAAAGCGCCACTT
TCATTCTGCTTCTTGGGATTGTTGACGGCCACGTAGTGATAGCGAACGACAAGCAAGAAGAGCGACACGCCCAG
CATGTTGGCGACGATGGCGAGCTGCACGTCCGTGATCATCTTGACCAGTCCGGCTCGGCCCCGAAGAAGAGGAGACA
ACACTGGAGCCACCGTGGCACCAGGCTTGGCGGCTACCTCCTGTACAAGCTCGGTCCATGCCGAGAGAAGGGCG
AAATACTGCAGATATCCATCAACAACCTGGCGGGCCGATCCGAGCATGCATCTAGAAGGGCCAAATACGCCATATA
GGNGAGTCGGAATAACAATTACCTGGCCGGCGATCCAAACGTCGTGACTGGAAAAAACCGGGGGATNACCCAA
AAAAGTTAAATCGGCCNGAAGGACANAACCCACGATTAGGCAANAGNGCGAAAAATAACNAAAA

SEQ ID NO:273

>GL2_81B_E03_G3F1 Direction: sense

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAGGTGGCGCTTTCTCC
GCCCCAGGGGTTCCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCCTTCACACTTCACCTTCATCCCTT
CTACCCATCACAACATACAAAGCAACTACACCTGGATTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTA
ATCCATATGGAACAAGAAGCTGCCACTGGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATA
TAAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAAGTAGT

SEQ ID NO:274

Clone 1/226 - Novel (Clone1/226) >

GCCGAGCCGGACTGGTCAGGATGATCACGGACGTGCAGCTCGCCATCTTCGCCAACATGCTGGGCGTGTGCTCT
TCTTGCTTGTGCTTCTCTATCACTACGTGGCCGTCAACAATCCCAAGAAGCAGGAATGAAGGTGGCGCTTTCTCC
GCCCCAGGGTTCAGGACATAGTCTGAGGCAAGATGGAGGGTATGAGGGGCCCTTCACACTTCACCTTCATCCCTTC
TACCCATCACAACATACAAAGCAACTACACCTGGATTTTCCAAACAACCTTTATTTCTCAGAGTCTTCCTTAA
TCCTATGGAACAAGAAGCTGCCACTGGAATAGGGCCAGTATAGGGGCTTGCTTTTCTACTCCCTCCCCCAATAT
AAAAATATAGACTTTTAAAAAAGGGCGCCGCTCGCGATCTAGAAGTAGT

SEQ ID NO:275

Novel (FLJ10688)

>GL2_51_C08_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGA
AGCCACACTTGAAGTTAGCACGCGTTAGAGTCAAAATGGCATAGTACTGTCATGGAGTGTCTTGGAGGTGGATC
GAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAAT
GGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGC
AAATACTACTTTG

SEQ ID NO:276

>GL2_51_C10_G3F1 Direction: sense

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCAGAAGCTGCCAGCACATCTCTGCCTCAG
AAGCCACACTTGAAGTTAGCACGCGTTAGAGTCAAAATGGCATAGTACTGTCATGGAGTGTCTTGGAGGTGGAT
CGAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACA
TGGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGC
AAATACTACTTTG

SEQ ID NO:277

>GL2_51_C11_G3F1 Direction: N/A

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGA
AGCCACACTTGAAGTTAGCACGCGTTTCAGGGGTCAAAATGGCATAGTACTGTTCATGGAGTGTCTTGGAGGTGGAT
CGAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
TGGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGC
AAATACTACGTTTG

SEQ ID NO:278

>GL2_59_E07_G3F1 Direction: sense

CACCAGCACCTTACAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGAAA
CCACACTTGAAGTTAGCACGCGTTTCAGAGTCAAAACTGGCATAGTACTGTTCATGGAGTGTCTTGGAGGTGGATCG
AAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAAATG
GAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGCAA
ATACTACTTTG

SEQ ID NO:279

>GL2_59_E08_G3F1 Direction: sense

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAG
AAACCACACTTGAAGTTAGCACGCGTTTCAGAGTCAAAATGGCATAGTACTGTTCATGGAGTGTCTTGGAGGTGGAT
CGAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAA
TGGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGC
AAATACTACTTTG

SEQ ID NO:280

>GL2_59_E09_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGAA
GCCACACTTGAAGTTAGCACGCGTTTCAGAGTCAAAATGGCATAGTACTGTTCATGGAGTGTCTTGGAGGTGGATCG
AAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAAATG
GAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGCAA
ATACTACTTTG

SEQ ID NO:281

>GL2_59_E10_G3F1 Direction: sense

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGA
AGCCACACTTGAAGTTAGCACGCGTTTCAGAGTCAAAATGGCATAGTACTGTTCATGGAGTGTCTTGGAGGTGGATC
GAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAAAT
GGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGCA
ATACTACTTTG

SEQ ID NO:282

>GL2_59_E11_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGA
AACCACACTTGAAGTTAGCACGCGTTTCAGAGTCAAAATGGCATAGTACTGTTCATGGAGTGTCTTGGAGGTGGATC
GAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAAAT
GGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGCA
ATACTACTTTG

SEQ ID NO:283

>GL2_59_E12_G3F1 Direction: sense

CACCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGAA
GCCACACTTGAAGTTAGCACGCGTTTCAGAGTCAAAATGGCATAGTACTGTTCATGGAGTGTCTTGGAGGTGGATCG
AAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAAATG
GAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCACCAGTTTGTATCTGGTAGCAA
ATACTACTTTG

SEQ ID NO:284

>GL2_51_C09_G3F1 Direction: N/A

CACCAGCACCTTACCAGAAGCTCCACAACCACAGGCGTCTGGCCCCCAAGAACAAACAGGGGCCCTTTGTGGTCCG
TNCCCCACAAAAGGGGGCCCCCTTATAAACACCCATAAAATTTTTTACCCCTTTTNTCCCCCTTGGGGTGTCCCC
CCCCCCTTTTTTCCCCAAAAAAGGGGNCCCCAAACCAAGGGGGCCCCCCCCCTTTAAAAACCCATAAAACCCC
CCTTTTTTTTTTTTTTNGGGGGCCCCCAACCCAAAC

SEQ ID NO:285

Novel (FLJ10688) >

CACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCAGAAGCTGCCAGCACATCTCTGCCTCAGA
AGCCACACTTGAAGTTAGCAGCGTTTACAGAGTCAAATGGCATAGTACTGTCATGGAGTGTCTGGAGGTGGATC
GAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTACCATGAGGAACCCAGTGCCACTGTGCCCTCACAAT
GGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGCCCATGGCATGTACTCTCAGCCAGTTTGTATCTGGTAGCA
AATACTACTTTG

SEQ ID NO:286

>gi|8922591|ref|NM_018179.1| Homo sapiens hypothetical protein FLJ10688
(FLJ10688), mRNA

ATCTAAACAAGAAAGTAGTGAGAGTTTGCCAAAAGAAGCCTTTCTGGTCTCTCTGATGAAGAGGATATT
TCGGGTGAAAAAGATGAGTCTGAAGTTATATCGCAAAATGAAACGTGCTCTCCAGCAGAAGTAGAAAGTA
ATGAAAAAGGACAACAGACCTGAGGAAGAAGAGCAAGTAATACATGAAGATGATGAAAGACCTTCTGAGAA
AAATGAATTTTCTAGACGAAAACGTTCTAAATCAGAAGACATGGACAATGTACAGTCTAAACGTCGTGCA
TATATGGAAGAAGAATATGAGGCAGAATTTCAAGTAAAGATTACAGCCAAAGGAGACATTAACCAGAAAC
TTCAAAAGGTTATACAGTGGTTGCTGGAAGAAAAATTGTGTGCGCTGCAGTGTGCTGTATTTGATAAGAC
TTTGGCAGAAATTGAAAACACGAGTGGAAAAGATTGAATGTAACAAGAGGCATAAAACAGTTCTCACTGAA
CTACAGGCCAAGATAGCCAGGTAAACCAAACGCTTTGAAGCAGCCAAAGAAGATCTTAAGAAAAGACATG
AACATCCACCCAACCCACAGTATCACCAGGAAAAACTGTAAATGATGTCAACAGCAATAATAACATGTC
TTACAGAAATGCAGGCACAGTGAGACAGATGCTGGAGTCCAAAAGAAATGTAAGCGAGAGTGCACCACCA
TCCTTTCAAACCTCCTGTGAATACAGTATCTTCAACCAATCTTGTCACTCCTCCAGCAGTTGTGAGTAGTC
AACCTAAATTGACAGACTCCAGTGAATTCGGGTTCCCTCACAGCAACGTCAGTTCTTCTGCACCCAATAC
AGCTACTGTAGTTGCTACTACTCAGGTGCCTAGTGGAAATCCCCAGCCTACAATCTCTTTACAGCCTTTG
CCAGTGATTTTGCATGTACCTGTTGCAGTATCCTCCCAGCCTCAGCTTCTACAGAGCCATCCAGGGACTT
TGGTGACTAATCAACCATCTGGCAATGTTGAATTCATTTCTGTGCAAAGCCACCTACAGTGAGTGGTCT
TACCAAAAATCCAGTATCCTTGCCATCCTTGCCAAATCCCACTAAACCAACCAACGTTCTTCTGTGCCC
AGTCCTAGTATTCAAAGGAACCTACTGCCAGTGCTGCACCATTGGGAACAACACTTGCTGTGCAGGCTG
TTCCAACAGCACACTCTATTGTACAAGCCACAAGGACTTCTTTACCCACAGTGGGGCCCATCAGGACTCTA
TAGTCCATCAACTAATCGAGGTCTATACAGATGAAAATTCGAATTTCTGCATTTAGTACTTTCGTCTGCT
GCAGAACGAAACAGCAATACCACCCCAAGAATTGAAAACAGACAAAACAAATAGATGCTTCTGTCA
GTAAGAAAGCAGCTGATAGCACATCAGTGTGGAAGGCCACTGGCAGTGATTCAAGTGGTGTCAATTGA
TCTCACAATGGATGATGAAGAGAGTGGAGCTTCAAGACCCCCAAAAAACTAAATCACACTCCTGTATCA
ACCATGAGTTCTTCTCAGCCTGTGTACGACCATTGCAACCCATACAACCAGCACCGCCTCTTCAACCAT
CTGGGGTGCCAACAAGTGGACCATCTCAGACCACCATACACTTACTACCTACAGCTCCAACCTACCGTGAA
TGTAACACATCGTCCAGTAACTCAGGTGACCACAAGACTCCCTGTACCAAGAGCTCCTGCAAACCACAG
GTGGTTTATACAACCTCTTCTGCAACCACAGCTCAGGCTCCCTTGCGAGGAACGTGTATGCAGGCTCCTG
CTGTTTCGGCAGGTCAATCCCCAAAATAGTGTTACAGTTCAGAGTGCCCTCAAACAACCACATATGTTGTAAA
CAATGGACTAACCCTGGGATCAACAGGACCTCAGCTCAGTGTCATCACCAGCACCAAGTGACATACT
GAGCCCCCAGCCCCGTGCACCCAGCACCTTACCAGAAGCTCCACAACCACAGCGTCTGCCCCAGAAG
CTGCCAGCACATCTCTGCCTCAGAAGCCACACTTGAAGTTAGCACGCGTTCAGAGTCAAAATGGCATAGT
ACTGTCATGGGGTGTCTTGGAGGTGGATCGAAGCTGTGCCACTGTTGATAGCTACCATCTCTATGCTTAC
CATGAGGAACCCAGTGCCACTGTGCCCTCACAATGGAAAAAGATTGGGGAAGTCAAGGCACTTCCCTTGC
CCATGGCATGTACTCTCAGCCAGTTTGTATCTGGTAGCAATACTACTTTGTCAGTACGAGCCAAGGATAT
TTATGGACGTTTGGGCCTTTCTGTGATCCTCAGTCAACAGATGTGATCTCTTCTACCCAGAGCAGTTAA
ACCTTGAGGCCTTTATATTTTCTCTTTTAAATTTCCACCTTTTGGTCTTGTTTTAACTTGTGTCATG
ATACCCCATGTAAAATCCACCTTGTGCAAGATTTCTTGGACAGATGTGTGTATACACTACATTTGTTTAT
AACCAGAAGCAAAATAAATCAGCCCAAAAGCT

SEQ ID NO:287

>gi|8922592|ref|NP_060649.1| hypothetical protein FLJ10688; likely ortholog of mouse activating transcription factor 7 interacting protein [Homo sapiens]

5 MDNVQSKRRRYMEEYEAEFQVKITAKGDINQKLQKVIQWLLKEKLCALQCAVFDKTLAELKTRVEKIEC
NKRHKTVLTELQAKIARLTKRFEAAKEDLKKRHEHPPNPPVSPGKTVNDVNSNNMSYRNAGTVRQML
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10 PQPTISLQPLPVILHVPVAVSSQPQLLQSHPGTLVTNQPSGNVEFISVQSPPTVSGLTKNPVSLPLPNP
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VHHRPPQVHTEPPRPVHPAPLPEAPQORLPPEAASTSLPQKPHLKLARVQSQNGIVLSWGVLEVDRSCA
15 TVDSYHLIYAYHEEPSATVPSQWKKIGEVKALPLPMACLTLTQFVSGSKYYFAVRAKDIYGRFGFPFCDPQST
DVISSTQSS

SEQ ID NO:288

Novel (KIAA0217)

>G3_4_03_PCR_G3F1 Direction: N/A

20 TCTTGCGGCAGGGTCAAAACAACATCATGGTACAACCTTCTGGTAACATGTCAGTGGGCAACAAAGTGTATGTTTT
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GTTACTTGCTTGCACTGCATCAGAACCAAGGTTTCTGGGGTGGCCCCCTGCAGTTCACTCCGCCAGGAGATCAAA
AAGGATGCGCTCTCTACATTCTTAAATGCCACAGTCCCTACCAACGGCTTAGTTGAAGCACAGCTCCCATCA
GCATTATTCCCTGGCGCGCCAGCACTGCCTCTACGAGGCCACACCTGCCTCTGCCAAGGCCACTGGCCCTCAT
25 TCATCTTCGGGGACGTTCTAGAGATATGCACTTACAG

SEQ ID NO:289

>GL3_4.03_A_M13F Direction: anti-sense

30 CTGTAAGTGCATATCTCTAGAACGTCCCCGAGATGAATGAGGGCCAGTGGCCTTGGCAGAGGCAGGTGTGGCCT
CGTAGAGGCAGTGCTGGCCGCGCCAGGGCATCAGTGCTGATGTGGGAGCTGTGCTTCCACCTAAGCCGTTGGTAG
GGGACTGTGGCATTAAAGAATGTAGAGAGCGCATCCTTTTGTATCTCCTGGGCGGAGTGAACCTGCAGGGGCCAC
CCCAGAAACCTTGGTTCTGATGCACTGCAAGCAAGTAACCAGCTTCTCACTCCAGTTTCAAGTGGCTATTATGTA
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35 AAGTTGTACCATGATGTTGTTTGTACCCCTG

SEQ ID NO:290

>GL3_4.03_A_M13R Direction: sense

40 CAGGGGTCAAACAACATCATGGTACAACCTTCTGGTAACATGTCAGTGGGCAACAAAGTGTATGTTTTTCATGTAG
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SEQ ID NO:291

>GL3_4.03_B_M13F Direction: sense

45 CAGGGGTCAAACAACATCATGGTACAACCTTCTGGTAACATGTCAGTGGGCAACAAAGTGTATGTTTTTCATGTAG
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CTTGCACTGCATCAGAACCAAGGTTTCTGGGGTGGCCCCCTGCAGGTTCACTCCGCCAGGAGATCAAAAAGGATG
50 CGCTCTCTACATTCTTAAATGCCACAGTCCCTACCAACGGCTTAGGTGGAAGCACAGCTCCCATCATCAGCACTG
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SEQ ID NO:292

>GL3_4.03_B_M13R Direction: anti-sense

55 CTGTAAGTGCATATCTCTAGAACGTCCCCGAGATGAATGAGGGCCAGTGGCCTTGGCAGAGGCAGGTGTGGCCT
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CCAGAAACCTTGGTTCTGATGCACTGCAAGCAAGTAACCAGCTTCTCACTCCAGTTTCAAGTGGCTATTATGTA

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SEQ ID NO:293

>GL3_4.03_C_M13F Direction: anti-sense

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GGGACTGTGGCATTAAAGAATGTAGAGAGCGCATCCTTTTTGATCTCCTGGGCGGAGTGAACCTGCAGGGGCCAC
CCCAGAAACCTTGGTTCTGATGCACTGCAAGCAAGTAACCAGCTTCTCACTCCAGTTTCAAGTGGCTATTATGTA
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SEQ ID NO:294

>GL3_4.03_C_M13R Direction: sense

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SEQ ID NO:295

>GL3_4.03_D_M13F Direction: anti-sense

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GGGACTGTGGCATTAAAGAATGTAGAGAGCGCATCCTTTTTGATCTCCTGGGCGGAGTGAACCTGCAGGGGCCAC
CCCAGAAACCTTGGTTCTGATGCACTGCAAGCAAGTAACCAGCTTCTCACTCCAGTTTCAAGTGGCTATTGTGTA
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SEQ ID NO:296

>GL3_4.03_D_M13R Direction: sense

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CGCTCTCTACATTCTTAAATGCCACAGTCCCCTACCAACGGCTTAGGTGGAAGCACAGCTCCACATCAGCACTG
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SEQ ID NO:297

>gi|22051279|ref|XM_040265.5| Homo sapiens KIAA0217 protein (KIAA0217),
mRNA

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TCGCTCTGGGTCCCTCAGAATATGACTCTCTGCCTGAAAATAGCGAGACAGGAGGAAATGAGTCTCAACC
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5 CTACCGGAAGAAAAGGGAGGAGAAGTTTACAAGCAGCCAGACACAGTCTCCAACGCCACCAAAGCCTCCG
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15 GCGGCCGGCGGGGGGGCCGGCCCTCGCCCTCGGCCATGGGGAAGCGTCTCAGCCGAGAGCAGAGCACTCCC
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20 AGAAAAAGCATTATCTTAACAAATGGTATTTTTTATTAAGCCTCCATGTGGCTCTGAATGCAAGCTAT
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25 TGGCTATTATGTAATATAAATTCAAAGCACATTGTGAATAGAACCTACATGAAAACATACACTTTGTGTGC
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30 TGTGGTTTTTCCCCCTCTTGGCTGGTGGAGGATAAAGTTCCTGCTCTTTTACCTCCAAGACGAGGCCCT
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35 CAGAGTTACTCAGTTACTGCGTGGATCTCCTGTGCTAGTTTTACTGAGTAAGCATACTGTAGTACAAGA
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45 AAGAACATGGGGATTTTTTTTTGTAGTTGTCTAGTTCACTGACCAAAAAAAAAAAAAAAAAATCAGAAATAAT
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50 GCAGCGCGTGCATTAGCCAGTCGCCACTGGAGGGCTCTGCTGCCCTCCGGTCAATACACTGTAGTTACTG
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CAGCGATGAGAGTGGCTTTTACATCTTTTTTTTTTTTTTAAAGTTAACACCCCTCCTTTACCCCCAGCAGTATC
55 TCAGGTTATAGAATCAGAGATGCAGCAGTGACAAATGGCATTTTAACTTGTAATAATCGTGTGATGATGCT
TATCATTTTGAAATAGAAAGATAAAAACCTGGTCCCGTTTACCAGACATGAATTTCAAGTGGAGTCGTC
GTTCTCTGAGAGTGAGTGTCTTGACATTTTACCCAGGCCCTCCTGTCTCATCATCACCCGGCTGTCACTG
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TGTATCCGGGCGACGGGTAGTGGTGGTGCATGCCTGTCTGTGTGCCCCGCTGGCGAGCTGTAGTTGCGGC
60 TTGCGTGCCTCGCGGCCACTACAGGGCTGCAGACAATCGAGGCGAGGGCGCTGGCCGCCAGCAGCTCAC
AGCGCGGGGTCATGTGTCGCTCCTCGAGGGTTTCGTTTTTGTCTGCTTCATTAAGACTGGAATCAAG

CTTACATGTAACTATTGGTAATTTAAGTTTCCTTTTGTGTCATTCAGTGTAAACTGTCTAATTTGAAA
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SEQ ID NO:298

5 >gi|20543999|ref|XP_040265.4| similar to no similarities to reported gene
products [Homo sapiens]
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EASSAADGVSAWEEVAGHHADRGPDQSDANGDGDQGHENAALPDQESDPADMNALALGPSEYDSL PEN
SETGGNESQPDSDQEDPREVLKKTLEFCLSRENLASDMYLISQMDSDQYVPITTVANLDHIKKLSTDVDLI
10 VEVLRLSLPLVQVDEKGEKVRPNQNCIVILREISESTPVEVIEALFKGDNLPKFINCEFAYNDNWFITFE
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QQFPLYSLITPQTSATHSYLDPPLVTPFPNTGFIGFTSPAFKPAASPLTSLRQYPPRSRNPSKSHLRH
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15 LGRGRKNSFGYRKREEKFTSSQTSPTPPKPPSPSFELGLSSFPPLPGAAGNLKTEDLFENRLSSLIIG
PSKERTLSADASVNTLPVVVSREPSVPASCAVSATYERSPSPAHL PDDPKVAEKQRETHSVDR LPSALTA
TACKSVQVNGAATELRKPSYAEICQRTSKEPPSSPLQPQKEQKPNTV GCGKEEKKLAEP AERYREPPALK
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SEQ ID NO:299

20 Novel (KIAA1583)
>GL2_89_2B04_G3F1 Direction: N/A
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25 TTCCACCTGCAGTGCGAGCCGCCCAGCCACTCCCGACTGGCGCTATGCCTCGATCACCGCTCTTGCTCCCAAGTG
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30 TTACAAATTCAGTGGCGCGGTTTTTACAAANGTCGTGACTGGGAAAACCTGGCGTTACCCA ACTTAATCGCTTGA
GGAATCCCCCTTTTCGAGTGGGGTATAGGAGAAGGCGACGAATGCCTCCAACAGTGGGCAGCNAAGTACGACGGT
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GGATTG

35 SEQ ID NO:300

>GL2_202_3_M13F Direction: anti-sense
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AGAGCGTCTCCCCTGCGGTCCACTTGGGAGCAAGAGCGGTGATCGAGGCATAGCGCCAGTCGGGAGTGGGCTGGG
40 GCGGCTCGCTGCAGGGTGGAAAGGGCCTGACCCCAAGAGGGGCGGATGTCTGCGTTTTGAGAAACAGGAGCTGCT
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SEQ ID NO:301

>GL2_202_3_M13R Direction: sense
45 ACTGCAGGTGGCAGCCACGGGGCGGCGCGCTCGGCCTCATCTGACGCCTCTGCAGCGGGTCCCGCAGCCT
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CAGCTCTGTCCCCGGCGGCTCCTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATTGCCCCCTCTTGGGGT
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50 SEQ ID NO:302

>GL2_89_2B01_G3F1 Direction: sense
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55 TCAGTGCGCCTTCCACCTGCAGTGCGAGCCTGGCCAGACCACTCCCGACTGGCGCTATGCCTCGATCACCGGTC
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CTGAGCTCTGGTGTCTATCTTAGGCTCTGAGGGTCTG CAGAAACAGGCACCAAGTGGTTAGATAGATAAAGCTGG
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SEQ ID NO:303

>GL2_89_2B02_G3F1 Direction: sense

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5 CTCTGTCCTCCCGCGGCTCCTAATCACCAGCAGCTCCTGTTTCTCAAACGCAGACATCCGCCCTCTTGGGGTCAGG
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SEQ ID NO:304

>GL2_89_2B03_G3F1 Direction: sense

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15 GGCCCCGACCGATCGCCTCCCAACAGTGCGCAGCTATACGTACGGGAGTAAGGGTNCACCTATNAAGAAANAGCGAC
CGCCGGTGGGCGNCAACCACAGGGACAANAATGGACGCACGANCAACGAACGTACCCAGAACAAGAACTAGTCA
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SEQ ID NO:305

>GL2_89_2B05_G3F1 Direction: N/A

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25 AAGTGGACCGCAGGGGAGACGCTCTCTTACGGGGACCCTGGGGGCGCTCACTCTCTGAAGGGCCTGGAAGCTAGA
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SEQ ID NO:306

>GL2_89_2B06_G3F1 Direction: N/A

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ACCGCGAGGNGTCTGGTTCCCGGCGGGGTCCCTAAGTNACCAGCAGAGNGTCTGTTTCTCAAACGCAGACAT
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35 GGGGCGCGGTAATTGTCTTCTCGAATCTAAACAGCGGTCC

SEQ ID NO:307

clone 89 -Novel (KIAA1583)>

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40 TCGGGGAGGCCGGGACTGGCCGTCAGCGCTGAACGGGCCAGCCTGCCAGGGGCCAGCTGCTGGAGACCCGCAGC
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45 TCATCTTAGGCTCTGAGGGT

SEQ ID NO:308

>gi|10047240|dbj|AB046803.1| Homo sapiens mRNA for KIAA1583 protein,
partial cds

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SEQ ID NO:309

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SEQ ID NO:310

Novel (KIAA1814)

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SEQ ID NO:311

>GL2_75_2_M13R Direction: anti-sense

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SEQ ID NO:312

>GL2_75_3_M13R Direction: anti-sense

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SEQ ID NO:313

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SEQ ID NO:314

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SEQ ID NO:315

>GL2_81A_D11_G3F1 Direction: N/A

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SEQ ID NO:316

>GL2_81A_D12_G3F1 Direction: sense

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SEQ ID NO:317

5 Clone 75 -Novel (KIAA1814)>
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SEQ ID NO:318

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SEQ ID NO:319>gi|22053032|ref|XP_046822.3| similar to FLJ00192 protein
[Homo sapiens]

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SEQ ID NO:320

Novel (maps to chromosome 4)

Novel (Chromosome 4) >

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 AGGTTCTAATAATTTTTTATTTAATAATTAGATCTATTAGATTTTATTCATAACTGTGGTAGTTGAAGTACCTTC
 TAAGCTGAGTTTCAGATTTGAGAATAAACCTTGGGGTATCATTACAGAAAATTTTGTCTCAATCTGCTTTGTATTT
 25 GAAAGATATGAGATTTCTGAATTATATATCTTACAGACTAGTCCCCAAAAGAATACGTGTTTCTTACCTTTAAT
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SEQ ID NO:321

Novel peroxidase-like/ melanoma antigen

>GL2-86-4M13F Direction: sense

CGACCTGGCCAGCCACCGCGGCCTGCTGCGGCAGGGCATCGTGACGCGTCCGGGAAGCCGCTGCTCCCCTTCGC
 30 CACCGGGCCGCCACGGAGTGATGCGGGACGAGAACGAGAGCCCCATCCCCTGCTTCTGGCCGGGGACCAACCG
 CGCCAACGAGCAGCTGGGCCTGACCAGCATGCACACGCTGTGGTTCCGCGAGCACAACCGCATTGCCACGGAGCT
 GCTCAAGCTGAACCCGCACTGGGACGGCGACACCATCTACTATGAGACCAGGAAGATCGTGGGTGCGGAGATCCA
 GCACATCACCTACCAGCACTGGCTCCCGAAGATCCTGGGGGAGGTGGGCATGAGGACGCTGGGAGAGTACCACGG
 35 CTACGACCCCGGCATCAATGCTGGCATCTTCAACGCCTTCGCCACCGCGGCCTTCAGGTTTGGCCACACGCTTGT
 CAACCCACTGCTTTACCGCTGGACGAGAACTTCCAGCCCATTGCACAAGATCACCTCCCCCTTCACAAAGCTTT
 CTCTCTCCCCTTCGGATTG

SEQ ID NO:322

>GL2_93_2B08_G3F1 Direction: sense

CGACCTGGCCAGCCACCGCGGCCTGCTGCGGCAGGGCATCGTGACGCGTCCGGGAAGCCGCTGCTCCCCTTCGC
 40 CACCGGGCCGCCACGGAGTGATGCGGGACGAGAACGAGAGCCCCATCCCCTGCTTCTGGCCGGGGACCAACCG
 CGCCAACGAGCAGCTGGGCCTGACCAGCATGCACACGCTGTGGTTCCGCGAGCACAACCGCATTGCCACGGAGCT
 GCTCAAGCTGAACCCGCACTGGGACGGCGACACCATCTACTATGAGACCAGGAAGATCGTGGGTGCGGAGATCCA
 45 GCACATCACCTACCAGCACTGGCTCCCGAAGATCCTGGGGGAGGTGGGCATGAGGACGCTGGGAGAGTACCACGG
 CTACGACCCCGGCATCAATGCTGGCATCTTCAACGCCTTCGCCACCGC

SEQ ID NO:323

Novel peroxidase-like/ melanoma antigen>

CGACCTGGCCAGCCACCGCGGCCTGCTGCGGCAGGGCATCGTGACGCGTCCGGGAAGCCGCTGCTCCCCTTCGC
 50 CACCGGGCCGCCACGGAGTGATGCGGGACGAGAACGAGAGCCCCATCCCCTGCTTCTGGCCGGGGACCAACCG
 CGCCAACGAGCAGCTGGGCCTGACCAGCATGCACACGCTGTGGTTCCGCGAGCACAACCGCATTGCCACGGAGCT
 GCTCAAGCTGAACCCGCACTGGGACGGCGACACCATCTACTATGAGACCAGGAAGATCGTGGGTGCGGAGATCCA
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 55 CTACGACCCCGGCATCAATGCTGGCATCTTCAACGCCTTCGCCACCGCGGCCTTCAGGTTTGGCCACACGCTTGT
 CAACCCACTGCTTTACCGGCTGGACGAGAACTTCCAGCCCATGACACAAGATCACCTCCCCCTTCACAAAGCTTT
 CTCTCTCCCCTTCGGATTGTGAATGAGGGCGGCATCGATCCGCTTCTCAGGGGGCTGTTCCGGGGTGGCGGGGAA
 AATGCGTGTGCCCTCGCAGCTGCTGAACACGGAGCTCACGGAGCGGCTGTTCTCCATGGCACACACGGTGGCTCT
 GGACCTGGCGGCCATCAACATCCAGCGGGGCGGGACACGGGATCCACCCCTACCACGACTACAGGTCTACTG
 60 CAATCTATCGCGGCACACACGTTTCGAGGACCTGAAAAATGAGATTAAAAACCTGAGATCCGG

SEQ ID NO:324

>gi|20533845|ref|XM_056455.2| Homo sapiens Melanoma associated gene (D2S448), mRNA

5 AGCCGGCCGTGGTGGCTCCGTGCGTCCGAGCGTCCGTCCGCGCCGTGCGCCATGGCCAAAGCGCTCCAGGG
GCCCCGGGCGCCGCTGCCTGTTGGCGCTCGTGCTGTTCTGCGCCTGGGGGACGCTGGCCGTGGTGGCCCA
GAAGCCGGGCGCAGGGTGTCCGAGCCGCTGCCTGTGCTTCCGCACCACCGTGCCTGTCATGTCATCTGCTG
CTGGAGGCCGTGCCCCCGTGGCGCCGACACCTCCATCCTAGATCTTCGCTTTAACAGAATCAGAGAGA
TCCAACCTGGGGCATTTCAGGCGGCTGAGGAACTTGAACACATTGCTTCTCAATAATAATCAGATCAAGAG
10 GATACCTAGTGGAGCATTTGAAGACTTGGAAAATTTAAATATCTCTATCTGTACAAGAATGAGATCCAG
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15 AGGCAGCGGCCATCTGTGAATATCCCAGACGCATCCAGGGACGCTCAGTGCCAACCATCACCCCGGAAGA
GCTGAACTGTGAAAGGCCCCCGGATCACCTCCGAGCCCCAGGACGCAGATGTGACCTCGGGGAACACCGTG
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GCATGAAGACAGATTCCCGCCTAACTTGTGAGCATGGGACCCTGATGATCCAGAACACACAGGAGAC
AGACCAGGTATCTACCAGTGCATGGCAAAGAAGCTGGCCGGAGAGGTGAAGACGCAAGAGGTGACCCCTC
20 AGGTACTTCGGGTCTCCAGCTCGACCCACTTTTGTAAATCCAGCCACAGAATACAGAGGTGCTGGTTGGGG
AGAGCGTTCACGCTGGAGTGCAGCGCCACAGGCCACCCCGCGCGGATCTCCTGGACGAGAGGTGACCG
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CAGGGGACAGCGGAGTAGTATGCGTGCTCTGCGACCAACAACATTGACAGCGTCCATGCCACCGCTTTCA
TCATCGTCCAGGCTCTTCTCAGTTCACTGTGACGCCTCAGGACAGAGTCGTTATTGAGGGCCAGACCGT
25 GGATTTCCAGTGTGAAGCCAAGGGCAACCCGCGCCCGTTCATCGCCTGGACCAAGGGAGGGAGCCAGCTC
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35 GTTCCGATATCCGAGGGATCCTTACACAGTTGAACAGGCACGGGCGGGAGAAATCTTTGAACGGACATTG
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CAACTGCTCGGACATGTGCTTCCACCAGAAGTACCGGACGCACGACGGCACCTGTAACAACCTGCAGCAC
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40 CACCTGATCGGGACGGAGACCGTCAACCCGAGCAGTTCACCCACATGCTGATGAGTGGGGCCAG
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45 GGAGCACGGAGCATGAGGCCCGCAGCATCCGCGACCTGGCCAGCCACCGCGCCTGCTGCGGCAGGGCAT
CGTGACGCGTCCGGGAAGCCGCTGCTCCCTTCGCCACCGGGCCGCCCCAGGAGTGCATGCGGGACGAG
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50 TGGCTCCCGAAGATCCTGGGGGAGGTGGGCATGAGGACGCTGGGAGAGTACCACGGCTACGACCCCGGCA
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55 GGCTCTGGACCTGGCGGCCATCAACATCCAGCGGGGCGGGACCACGGGATCCACCCCTACCACGACTAC
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60 AGACGTGCTGGCCAGGATCCTATGCGACAACCGGGACAACATCACCCGGGTGCAGAGCGACGTGTTTCAG
GGTGGCGGAGTTCCTCACGGCTACGGCAGCTGTGACGAGATCCCCAGGGTAGACCTCCGGGTGTGGCAG

5 GACTGCTGTGAAGACTGTAGGACCAGGGGGCAGTTCAATGCCTTTTCTATCATTTCGAGGCAGACGGT
CTCTTGAGTTCAGCTACCAGGAGGACAAGCCGACCAAGAAAACAAGACCACGGAAAAATACCCAGTGTG
GAGACAGGGGGAACATCTCAGCAACAGCACCTCAGCCTTCAGCACACGCTCAGATGCATCTGGGACAAAT
GACTTCAGAGAGTTTGTCTTGAAATGCAGAAAGACCATCAGACCTCAGAACACAGATAAAGAACTTG
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10 GTGCTGTTACAGAAGGCAGTGCAGGAGGCTTCCAACCAGAGCATCTGCGGAGAAGGAGGCACAGCAGGTG
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15 CCATCACAAGCTATGTTTAAAAAGAAAATTGGTGTGTTGGCAAACGGAACAGAACCTTTGATGAGAGCGTT
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25 CTCATGGTCTCTCTTTAATTGACCAAAACCTTCCATTTTCTCTAAATACAAAGCGATCTGTGTTCTGAG
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30 CACAACCCGTGTTCCAGGTGCACATCTCCCAAGGAGACACCCAGACCTTCCAGCACGGGCCGGCCAAG
TTGCTGCGGCGGAGGCAGCATTTTCAGCTGTGAGGAAGGTTCATTGGATTTCATGTGTTTATCTGTAAAAAT
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TGTGTAAGTTTCGTCTAAAGCTGATGGTTATGTAAGTTGCTCAGGCACTCAGATGACAGCAGATTCTGGG
35 TTCTGGGAGTGTCTGTGCTCTTACATGCCCTGGAGGCCCTCATGGTCTCAGTGTGAGGCGGCACACCT
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GCTGACTGTGATTTACCAAAAAAATTCTGTAATTCAAACCAAAATGTCTGCGGAATCACCAGTTTGATA
CTCTCTGTAATCAGAACAGTGGGCAGTGCCTGGGTGAACGTGTCTAGCAGCCACTGTGCGGGATCGCTGT
AACAGGAGTGAATGTACATATTTATTTACTTTTCTAACTGCTCCAACAGCCAAATGCCTTTTTTATGAC
40 CATTGTATTTCAGTTTATTACCAAGAAATGTTTGACATTTGTAATGATGCCTTTCAGTTCAAATAAATGG
GTCACATTTTCAAATGG

SEQ ID NO:325

>gi|20533846|ref|XP_056455.2| similar to Peroxidasin [Homo sapiens]
45 MAKRSRGPGRCLLALVLFCAWGLAVVAQKPGAGCPSRCLCFRTTVRCMHLLLEAVPAVAPQTSILDRL
FNRIREIQPGAFRRRLRNLTLLNNNQIKRIPSGAFEDLENLKYLYLYKNEIQSIDRQAFKGLASLEQLY
LHFNQIETLDPDSFQHLPLKLERLFLHNNRITHLVPGTFNHLESMKRLRLDSNTLHCDCEILWLADLLKTY
AESGNAQAAAICEYPRRIQGRSVATITPEELNCERPRITSEPQDADVTSGNTVYFTCRABGNPKPEIWL
RNNNELSMKTD SRLNLLDDGTLMIQNTQETDQGIYQCMKNVAGEVKTQEVTLRYFGSPARPTFVIQPN
50 TEVLVGESVTECSATGPPPRISWTRGDRTPLPVDPVNITPSGGLYIQNVVQGSDEYACSATNNIDS
VHATAFIIVQALPQFTVTPQDRVVEGQTVFQCEAKGNPPPIAWTKGGSQLSVDRRLHLVLSGTLRIS
GVALHDQGGYECQAVNIIGSQKVVAHLTVQPRVTPVFASIPSDTTVEVGANVQLPCSSQGEPEPAITWNK
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AIATVDRAINSTRTHLFDSDRPRSPNDLLALFRYPRDPYTVEQARAGEIFERTLQLIQEHVQHGLMVDLNG
55 TSYHYNDLVSPQYLNLIANLSGCTAHRRVNCSMDMCFHQKYRTHDGTENNLOHPMWGASLTAERLLKSV
YENGFNTPRGINPHRLYNGHALPMPRLVSTLLIGTETVTPDEQFTHMLMQWGQFLDHDLDSTVVALSQAR
FSDGQHCSNVCSNDPPCFVSMIPPNDSDRARSARGCMFFVRSSPVCSSGMTSLLMNSVYPREQINQLTSYI
DASNVYSGSTEHEARSIRDLASHRGLLRQGIQVRSQKPLLPFATGPPTECMRDENESPIPCFLAGDHRANE
QLGLTSMHTLWFREHNRATIELLKLNPWDGDTIYYETRKIVGAEIQHITYQHWLPKILGEVGMRTLGEY
60 HGYDPGINAGIFNAFATAFRFGHTLVNPLLYRLDENFQPIAQDHLPLHKAFSSPFRIVNEGGIDPLLRG
LFGVAGKMRVPSQLLNTLTERLFSMAHTVALDLAAINIQGRDHGIPPYHDYRVYCNLSAHTFEDLKN

EIKNPEIREKLKRLYGSTLNIDLFPALVVEDLVPGSRLGPTLMCLLSTQFKRLRDGDRWLWYENPGVFSPA
QLTQIKQTSLARILCDNADNITRVQSDVFRVAEFPHGYGSCDEIPVDLRVWQDCCEDCRTGQFNAFSY
HFRGRRSLEFSYQEDKPTKKTRPKIPSVGRQGEHLNSTSAFSTRSDASGTNDFREBVLQMKTITDLR
TQIKKLESRLSTTECV DAGGESHANNTKWKKDACTICECKDGQVTCFVEACPPATCAVPVNIPGACCPVC
LQKRAEEKP

SEQ ID NO:326

Novel WD40/SOCS box protein

>GL2_81_2_M13F Direction: anti-sense

GGCTTGTAACCTTGCCACGGTGGCAGATGACAGACTCCTCAGGATCTGGGCCCTGGAAGTGAAGAACTCCCAGTTGC
ATATTGCATCCTATNACCAATGGGCTTTGCTGCACATTTTTTCCACATGGTGGAGTCATTGCCACAGGGACAAGA
GATGGCCACNTCCAGTTCTGGACAGCTCCTAGGGTCTGTCTCACTGAAGGCACTTATGCCGGAAGCCCTTCG
AAGTTTCCTAACAACTTACCAAGTCCTAGCACTGCCTATCCCCAAGAAAATGAAAGAGTTCTCTCACATACAGGAC
TTTGTTTAAAGCAACACCAGCATCTTGCTGCTTTCTTTGGTGAGCAGGTAAATCGTCCTGTCAAGGGAGTTGCTGGAA
TAATGGGGCCAAACATCTGGTCTTGCAATTGAAATAGCACTTTCTTTGGGATTGTGAATAGAAATGTAGCAAAACCAG
ATTCCAGTGTACTAGTCATGGATCTTTCTCTCCCTGGCATGTGAAAGTCAGCTTAGAGGAAGAGATCCACTTGCA
CCGGCACAGAGCCGCGGAGAACCCAGCGACACTGGGAGCACGGTGGCAACGGCCCTGGCGGCTCTCTGTACAGCT
CGTCANGCCGAGAGAAGGCCAAAATNCGGGAACCTGATGGAATCGCCCTTAGTGAGGGTATCCAGAACTGGCAA
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CAACACACAAAAGCGCACANCCATCACAGA

SEQ ID NO:327

>GL2_81_3_M13R Direction: anti-sense

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GGCCACGTCCAGTTCTGGACAGCTCCTAGGGTCTGTCTCACTGAAGCACTTATGCCGGAAGCCCTTCGAAGT
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SEQ ID NO:328

>GL2_81_2_M13R Direction: sense

CGGNTCTGTTGCCGTGCAAGTGGAAATCATCTTACCTCTAAGACATGACTTTTACATGCCAGGGGAGAGAAAGATC
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GACTTAGGTAAGTTGTTTCAGGAAACTTCGCAAGGGCTTTCCGGCATAAGTGCTATCAGTGAGGACAGGACCCTAG
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GCAAAGCCCATTTGGTCATAAGAACAAAATGCAATCGGGAGTTNCCAGGTCCAGGGGGCCGAGATCCTGAGGGAGG
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ATNAGAATCAAGCGGGCCGGTCCGANACTAGCCTTCGCAGGGGTCTGAAATACTCACCAAAGGNCGGCAAATA
AGGGGGGGGCACATTTCGTTTCAAAACCTCGCCCCGAAAAGACNCCTAGGATGAANGGCTACAAATGACCAGCGTGA
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SEQ ID NO:329

Novel WD40/SOCS box protein>

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ACCAGATGTTTGGCCCATTTATCCAGCAACTCCCTTTGACAGGACGATTTACCCTGCTACCAAGAAGCACAGA
TGTGGTGTGCTTAAAAAAGTCTGTATGTGAGGAACTCTTTCACTTTTCTTGGGGATTGGCAGTGCTAGGACTTG
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GAACTGGACGTGGCCATCTCTTGTCCTGTGGCAATGACTCCACCATGTGGAATAATGTGCAGCAAAGCCCAT
GGTCATAGGAGCAATGCAATGGGAGTTTTCAGTTCCAGGGCCAGATCCTGAGGAGTCTGTCTATCTGCCACCGT
GGCAAGGTACAAGCCCCCG

SEQ ID NO:330

>gi|20149658|ref|NM_018639.2| Homo sapiens CS box-containing WD protein
(LOC55884), mRNA

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GGCCGGAGAGGAACCGCTGCTGCTGGCCGAACCTCAAGCCCGGGCGCCCCACCAGTTTGATTGGAAGTCC
AGCTGTGAAACCTGGAGCGTCGCTTCTCCCCAGATGGCTCCTGGTTTGCTTGGTCTCAAGGACACTGCA

TCGTCAAAC TGATCCCCTGGCCGTTGGAGGAGCAGTTCATCCCTAAAGGGTTTGAAGCCAAAAGCCGAAG
TAGCAAAAATGAGACGAAAGGGCGGGGCAGCCCAAAAGAGAAGACGCTGGACTGTGGTCAGATTGTCTGG
GGGCTGGCCCTTCAGCCCGTGGCCCTTCCCCACCCAGCAGGAAGCTCTGGGCACGCCACCACCCCAAGTGC
CCGATGTCTCTTGCCTGGTTCTTGTCTACGGGACTCAACGATGGGCAGATCAAGATCTGGGAGGTGCAGAC
5 AGGGCTCCTGCTTTTGAATCTTTCCGGCCACCAAGATGTCGTGAGAGATCTGAGCTTCACACCCAGTGGC
AGTTTGATTGTTTGGTCTCCGCGTCACGGGATAAGACTCTTCGCATCTGGGACCTGAATAAACACGGTAAAC
AGATTCAAGTGTATCGGGCCACCTGCAGTGGGTTTACTGCTGTTCCATCTCCCCAGACTGCAGCATGCT
GTGCTCTGCAGCTGGAGAGAAGTCGGTCTTCTATGGAGCATGAGGTCTACACGTTAATTCGGAAGCTA
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10 ACGATACCAATGTGATTATGTGGGACCCCTACACCGCGCAAAGGCTGAGGTCACTCCACCACACCCAGGT
TGACCCCGCCATGGATGACAGTGACGTCCACATTAGCTCAGTGAATCTGTGTGCTTCTCTCCAGAAGGC
TTGTACCTTGCCACGGTGGCAGATGACAGACTCCTCAGGATCTGGGCCCTGGAACCTGAAAACCTCCCATG
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15 GCCCTTCGAAGTTTCTTAACAACCTTACCAAGTCCTAGCACTGCCAATCCCCAAGAAAATGAAAAGATTCC
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AGGGAGTTGCTGGAATAATGGGCCAAACATCTGGTCTTGCAATGAAATAGCATTTCTTTGGGATTGTGAA
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20 GCAAGTGTGAACTCTTCTGCTTGTGTTTGTGATTCAAAGTGCAGTTACTGATGTTGTTTTGATTATGCAAC
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AGTTGCTTCGATGTTGGCAAGTGCTTTCTTCTGGGCTCCCTTCTGACCTGCAGGACAGTTTTCCTGG
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25 GATCCAGACACTATTACTGGCTTTTTTTTTTTTTTAAACAATGGTGTGCATGTGCAGGAAATGACAAATTT
GTATGTCAGATTATACAAGGATGTATTCTTAAACCGCATGACTATTAGATGGCTACTGAGTTATCAGTG
GCCATTTATTAGCATCATATTTATTTGTATTTTCTCAACAGATGTTAAGGTACAACCTGTGTTTTCTCGA
TTATCTAAAACCATAGTACTTAAATTGAACAGTTGCAAAGATGCTTAATTGTGTAAAGAATTGGTGTA
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30 CTGGTTTCAACTCTACTGCGAAACAAAAATAGCTCCTTAAAGTACTGTTCTCTCTTCAGTGGCATGTAGT
TATCTAATCAAGACACCTCATTCAAACAAACCTGCCTTAGGAAAATTTAATATATTTTAAATTATTTTA
AAAGAAATACAACATCTTATTCTTTAGCTTTCTTAATCGGTGCTTTATGGAGGCCAGTGTAACGTTACAT
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ATGAGAGGCTTTTCATTGAAGAAAAGAAAAAACACAGTTAAAAA
35 AAAAAAAAAAAAAAAAAA

SEQ ID NO:331

>gi|8923881|ref|NP_061109.1| CS box-containing WD protein [Homo sapiens]
MEAGEEPLLLAELKPRPHQFDWKSSCETWSVAFSPDGSWFAWSQGHCIKLIWPWPLEEQFIPKGFPEAKS
40 RSSKNETKGRGSPKEKTLDCGQIVWGLAFSPWPSPSRKLWARHHPQVPDVSCLVLATGLNDGQIKIWEV
QTGLLLNLNLSGHQDVVRDLSTFPGSLILVSASRDKTLRIWDLNKHGKQIQVLSGHLQWVYCCSISPDCS
MLCSAAGEKSVFLWSMRSYTLIRKLEGHQSSVVSCDFSPDSALLVTASYDNTVIMWDPYTGERLRLSLHHT
QVDPAMDDSDVHISSLRSVCFSPGELYLATVADDRLLRIWALELKTPIAFAPMTNGLCCTFFPHGGVIAT
GTRDGHVQFWTAPRVLSSLKHLCKALRSFLTTYQVLALPIPKMKKEFLTYRTF
45

SEQ ID NO:332

Numb-like

>GL3_16A_3_M13R Direction: anti-sense
CGTCTGCCTGCCACTGGTGCAGGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGCAGGGCTCTTGNCC
50 GGTAAAACCTTGTTTCATGGTGCAGCGACCCGCTCTGGCTCCGTGTCAGGGTTTCTTGGGGGGCCCCGGGGCCCC
CACAAGGGGGACTGGGGGGCAGGGTGCCGGTTCAAGGGCCCCCTTCCTTTGTTACAGGCTTCGGTCCAATGCNG
AGAAGGAAAGGGGCGAAATTCNCTGCAGAATA

SEQ ID NO:333

>GL3_16A_4_M13R Direction: anti-sense
CGTCTGCCTGCCACTGGTGCAGGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGCAGGCTCTGCCGTA
ACTTGTTTCATGGTTGCCCGCCCCGCTCTGGCTCCGTGTCAGGTTTCTGGAGGCCACCGTTGCCATCGGGCCAT
GGGCGGGCCTTCCTTCCCTTTGTTACCAGGCCTTCCGGTTCCCAATAGCCCGGGAAGGAAGAAAACGGGGGCGG
AAATTTCTTGGCCAGGAGTTATTTCCNATTTCAAACAACTTGGGCCGGGGGACCCGGAGTTTCCGGAAAGCNC
60 ATATTTGNCAAATTCATAAGGAGAAGGGGGGGGGCCCCCAAAAATTTTCGGGCAGCCCCCTTTAATTTANGGT

TTGAGAAAGGATTTCCGGGTAATTTTACACCAAAATTTTCAACTTTGTGGGGCGCCAGGATACAGAGGATAT
TAAAAACACAAAAACGGCGGGGTANCAGGGGTNTGGGNCCTTTGGGGGGGAGAGAAGAAAAACCCGCCCCCT
TTTTGTGGGCCGNGGNTTTTATAACGCCCCCCCCGANAAAAATCCTTTTATAAAATTTCCATGCGAGCCGCGCTT
TTTTTTNGGNGTGAGAGAGGGACAGGAGCACAAATATTTTCCCCCGCCCTNTTTATTTTTTTACCGAGGGCG
5 CCCCANAGGCGTTATTGGGGACGCGGCCGTTTACAAAATAATAATGACGCTGCGAGAAAAATAGAGAAAAG
GGTGGCCCCCCCCCTGCGGAGAANAACCCGCGNGGNAGATATTACTTGGCAGGGAGCGCCCCCTTTTAT

SEQ ID NO:334

>GL3_39L_1_M13R Direction: anti-sense

CGTCTGCCTGCCACTGGTGCGGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGAGGCTCTGCCGTA
ACTTGTTCATGGTGCCCGCCCCCGTCTGGCTCCGTCCGTGCAGGTTTTCTGGGGGCCCCGGGGCCCCCAACAAGGG
GGGGCCTTGGGGGGGCCAGGGTTGCCGGAAGCCCAAGGCAACACTTGGNGAAAGCCCAACCGGNTAGGCACAA
CCGGGGCCACTTATNGGCGANGGAGCCATNACACATTCCTTTTGGTTACCCAAGGGCANATCCGGATCCCCAAT
TTGCACCCGGANATGGAAAGCAAAAGGGGGCGCCGGAATAATTTCTTTGCCCGAGGATTAATTTCCCCAAATT
15 CCAAACACACCCTGTGGTGGCACGGNGACCACGGAATTCGAAAGGCCNATTTTGGCCCATATTCTTTTAGGG
AAAGGGGGGGCCCCCCCCAAAAGAATTTTGTTCNGGCCCCCATATATAAA

SEQ ID NO:335

>GL3_16A_2_M13R Direction: anti-sense

CGTCTGCCTGCCACTGGTGCGTGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGAGGCTCTGCCGT
TAAACTTGTTTCATTGGTGCCCGCCCCGTTCTTGGCCTCCGTCCCTTGCAGGTTTTCTGGGGGCCCCGGNGGGGGCCC
CCAAACAAGGGGTGGCTTTGGAAGCCCCAACCGGTTGCCAACNCGGACACTATGGGGGGACCTTTCACATTCC
TTTTGTTACAGGCTTCGGTTCACAATTGGCCCCAAGGAAAGAAAAGGGGGCGCGGAAATTTCTTGTGCCAAGG
ATTTTATTCCCCAATTTTCAAGCGACCGTTGGGCCGGGGACCCCGGACTCCGAAGCCATTGGCAATTCATNAG
25 GGAAAGGGNGCCCCCAAAATTTTCGCGGACCTATAAATAAGATTGAGCAGACTCGGGTAATTTATAACAAATTT
TACCACAACGCGTTGTTGGGGACCCCCGGGTATACTGCAGGTTATTTATTATAACCANAAAAGGCGGTGATATTC
CANGTAGTTGTGGAACCTGTTGTGGNGGGGAAACAAAAAAAACAACACCCCCCCCCCTTTTGGGGGTANGGC
CGGGTGATTTTATAACAACCCCCCAGCCAAAAAGAAGCCGCTTTTNTAANAAG

SEQ ID NO:336

>GL3_39L_3_M13F Direction: N/A

CGAGGAGGCTCGCGCGCTGCATCCCGCACCATCCCCAGCCCCAGAAACCTGCAGGACGGAGCCAGACGGGGT
GGGCACCATGAACAAGTTACGGCAGAGCCTGCGGCGGAGGAAGCCAGCCTACGTGCCCCAGGGCCGTGCGCCCCG
AACCAGTGGCAGGCAGACG

SEQ ID NO:337

>GL3_39L_3_M13R Direction: anti-sense

CGTCTGCCTGCCACTGGTGCGGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGAGGCTCTGCCGGT
AACTTGTTTCATGGTGCCACCCCGTCTGGCTCCGTCCGTGCAGGTTTTCTGGGGGCTGGGGGATGGTGCGGGATGCA
40 ACGCGCGCGAGCTTCCTCG

SEQ ID NO:338

>GL3_16A_1_M13F Direction: anti-sense

CGTCTGCCTGCCACTGGTGCGGGCGCGACGCCTCGGGCACGTAGGCTGGCTTCCTCCGCCGAGGCTCTGCCGTA
45 ACTTGTTCATGGTGCCCGCCCCGTCTGGCTCCGTCCGTGCAGGTTTTCTGGGGGATGGTGCGGGATGCACGCGCGCG
AGCCTCCTCG

SEQ ID NO:339

>GL3_16A_1_M13R Direction: sense

CGAGGAGGCTCGCGCGCTGCATCCCGNACCATCCCCAGAAACCTGCAGGACGGAGCCAGACGGGGCGGGCACC
50 ATGAACAAGTTACGGCAGAGCCTGCGGCGGAGGAAGCCAGCCTACGTGCCCCAGGCGTCGCGCCCCGACCAGTGGC
AGGCAGACG

SEQ ID NO:340

>gi|10863898|ref|NM_004756.1| Homo sapiens numb homolog (Drosophila)-like (NUMBL), mRNA

ATGTCCCGCAGCGCGGCGGCCAGCGGCGGACCCCGAGGCGCTGAGCGGCACCTGCCCCAGCCCCCTGTG
GGGCCCCGGGGCCCCCAGAAACCTGCAGGACGGAGCCAGACGGGGCGGGCACCATGAACAAGTTACGGCA
GAGCCTGCGGCGGAGGAAGCCAGCCTACGTGCCCCAGGCGTCGCGCCCCGACCAAGTGGCAGGACAGAG
60 GACGCGGTGCGGAAGGGCACGTGCAGCTTCCCGGTGAGGTACCTGGGTACGTGGAGGTAGAGGAGTCCC



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25 SEQ ID NO:341

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SEO ID NO:342

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SEO ID NO:343

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SEQ ID NO:344

55

SEQ ID NO:345

>GL1_43_3_6_M13R Direction: anti-sense

GCCAAGCAGACATCCACCTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCCGGCCACAGACCTGTACCAG
GTGCCCCCAGGGGCGCTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACAT
CTACCAGGTCCCCCGTCCATGGACACACGCAGCTGGGAGGGCACGAAGCCCCCGGCAAAGGTGGTGGTGCCAC
CCGCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCCGC

SEQ ID NO:346

>GL1_43_4_4_M13F Direction: sense

CGCGGGATGTCTACTCGTCCCTGCTCCGGCTGGGCGGCCTCGTATACATAGCCCTGCCCCACGCGGGTGGGCACC
ACCACCTTTGCCGGGGGCTTCGTGCCCTCCCAGCTGCGTGTGTCCATGGACGGGGGGACCTGGTAGATGTCATGC
CCCATCCCCGGCAGAAAGTGGCACCTGGTAAATATCCTGGGCAGGGCCTCCAGGCCCTGGGGGCACCTGGTACAGG
TCTGTGGCCGGGCTGGGAAACGGGTGATGGGGTGTCTGCTTCGAGAAGGTGGATGTCTGCTTGGC

SEQ ID NO:347

>GL1_43_4_4_M13R Direction: anti-sense

GCCAAGCAGACATCCACCTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCCGGCCACAGACCTGTACCAG
GTGCCCCCAGGGGACCTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACAT
CTACCAGGTCCCCCGATCCATGGACACACGCAGCTGGGAGGGCACGAAGCCCCCGGCAAAGGTGGTGGTGCCCA
CCGCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCCGC

SEQ ID NO:348

>GL1_43_4_6_M13F Direction: sense

CGCGGGATGTCTACTCGTCCCTGCTCCGGCTGGGCGGCCTCGTATACATAGCCCTGCCCCACGCGGGTGGGCACC
ACCACCTTTGCCGGGGGCTTCGTGCCCTCCCAGCTGCGTGTGTCCATGGACGGGGGGACCTGGTAGATGTCATGC
CCCATCCCCGGCAGAAAGTGGCACCTGGTAAATATCCTGGGCAGGGCCTCCAGGCCCTGGGGGCACCTGGTACAGG
TCTGTGGCCGGGCTGGGAAACGGGTGATGGGGTGTCTGCTTCGAGAAGGTGGATGTCTGCTTGGC

SEQ ID NO:349

>GL1_43_4_6_M13R Direction: anti-sense

GCCAAGCAGACATCCACCTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCCGGCCACAGACCTGTACCAG
GTGCCCCCAGGGNCTTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACAT
CTACCAGGTCCCCCGATCCATGGACACACGCAGCTGGGAGGGCACGAAGCCCCCGGCAAAGGTGGTGGTGCCCA
CCGCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCCGC

SEQ ID NO:350

>GL1_43_LOW_3_G3F1 Direction: sense

GCGGGATGTCTACTCGTCCCTGCTCCGGCTGGGCGGCCTCGTATACATAGCCCTGCCCCACGCGGGTGGGCACCA
CCACCTTTGCCGGGGGCTTCGTGCCCTCCCAGCTGCGTGTGTCCATGGACGGGGGGACCTGGTAGATGTCATGCC
CCATCCCCGGCAGAAAGTGGCACCTGGTAAATATCCTGGGCAGGGCCTCCAGGCCCTGGGGGCACCTGGTACAGGT
CTGTGGCCGGGCTGGGAAACGGGTGATGGGGTGTCTGCTTCGAGAAGGTGGATGTCTGCTTGGC

SEQ ID NO:351

>gi|7656923|ref|NM_014567.1| Homo sapiens breast cancer anti-estrogen
resistance 1 (BCAR1), mRNA

GAGGCGGCAGCTGCGCGGCGGCACCGGGCGGCTGCGGCGCGCTCGGAGCCCCGAGGCACGCGGCCCGGG
CAGCTCGGTGTGCGCCCCGCGAGAGCCGGGCCCCAGGCCCGCCGGACACCATGAACCACCTGAACGTGC
TGGCCAAAGCGCTCTATGACAATGTGGCCGAGTCCCCGGATGAGCTCTCCTTCCGCAAGGGTGACATCAT
GACGGTGTGAGCAGGACACGCGAGGGCCTGGACGGCTGGTGGCTCTGCTCGCTGCATGGGCGCCAGGGC
ATCGTGCCTGGGAACCGCTCAAGATCTTGGTGGGCATGTATGATAAGAAGCCAGCAGGGCCTGGCTCCG
GCCCTCCCGCCACCCCGGCCAGCCTCAGCCTGGCCTCCATGCCCCAGCGCCTCCGGCCTCCAGTACAC
GCCCATGCTCCCCAACACCTACCAGCCCCAGCCAGACAGCGTCTACCTGGTGGCCACTCCAGCAAGGCT
CAGCAAGGCCTCTACCAAGTCCCGGGTCCCAGCCCTCAGTTCCAGTCTCCCCAGCCAAGCAGACATCCA
CCTTCTCGAAGCAGACACCCCATCACCCGTTTCCCAGCCCCGGCCACAGACCTGTACCAGGTGCCCCCAGG
GCCTGGAGGCCCTGCCAGGATATTTACCAGGTGCCACCTTCTGCCGGGATGGGGCATGACATCTACCAG
GTCCCCCGTCCATGGACACACGCAGCTGGGAGGGCACGAAGCCCCCGGCAAAGGTGGTGGTGCCACCC
GCGTGGGGCAGGGCTATGTATACGAGGCCGCCAGCCGGAGCAGGACGAGTACGACATCCCCGCGACACCT
GCTGGCCCCGGGGCCACAGGACATCTATGATGTGCCCCGGTTCCGGGGCTGCTTCCCAGCCAGTATGGC
CAGGAGGTGTATGACACACCCCATGGCTGTCAAGGTCCCAATGGCCGAGACCCGTTGCTGGAGGTGT
ATGACGTGCCCCCAGTGTGGAGAAGGGCCTGCCACCGTCCAACCACCACGCAGTCTACGACGTTCTCTCC

ATCGGTGAGCAAGGATGTGCCCGATGGCCCACTGCTGCGTGAGGAGACCTACGATGTGCCCCCGCCTTC
 GCCAAGGCCAAGCCCTTTGACCCGGCCCGCACCCCACTGGTACTGGCTGCGCCCCCTCCAGACTCCCCGC
 CGGCCGAGGACGTGTATGACGTGCCGCCCCCGGCTCCTGACCTCTACGACGTGCCCCCTGGCTTGCGGCG
 5 GCCTGGCCCGGGCACCTGTACGATGTGCCCCGTGAACGGGTGCTTCTCTGAGGTGGCTGATGGTGGC
 GTGGTTCGACAGTGGTGTGTATGCGGTGCCCTCCCCAGCTGAACGTGAAGCCCCGGCAGAGGGCAAGCGCC
 TGTGCGCCTCCAGCACCGGCAGCACACGCAGCAGCCAGTCTGCGTCTCTCTGGAGGTGGCAGGGCCGGG
 CCGGGAACCCCTGGAGCTGGAAGTTGCTGTGGAGGCCCTGGCACGGCTGCAGCAGGGTGTGAGCGCCACC
 GTTGCCACCTTCTGGACCTGGCAGGCAGCGCCGGTGCAGCTGGGAGCTGGCGTAGCCCCCTCTGAGCCAC
 10 AGGAGCCGCTGGTGCAGGACCTGCAGGCTGCTGTGGCCGCTGTCCAGAGTGCCGTCCACGAGCTGTTGGA
 GTTTGCCCCGAGCGCGGTGGGCAATGCTGCCACACATCTGACCGTGCCCTGCATGCCAAGCTTAGCCGG
 CAGCTGCAGAAGATGGAGGACGTGCACCAGACGCTGGTGGCACATGGTCAGGCCCTCGACGCTGGCCGGG
 GAGGCTCTGGAGCCACCCTTGAGGACCTGGACCGGCTGGTGGCCTGCTCGCGGGCTGTGCCCCGAGGACGC
 CAAGCAGCTGGCTCCTTCTGTCACGGCAATGCCCTACTGCTCTTACAGACGGACCAAGGCCACTGCCCCG
 15 GGGCCTGAGGGGGGTGGCACCCCTGCACCCCAACCCCACTGACAAGACCAGCAGCATCCAGTCACGACCC
 TGCCCTCACCCCTAAGTTACCTCCCAGGACTCACCAGATGGGCAGTACGAGAACAGCGAGGGGGGCTG
 GATGGAGGACTATGACTACGTCCACCTACAGGGGAAGGAGGAGTTTGAGAAGACCAGAAGGAGCTGCTG
 GAAAAGGGCAGCATCACGCGGCAGGGCAAGAGCCAGCTGGAGTTGCAGCAGCTGAAGCAGTTTGAACGAC
 TGGAACAGGAGGTGTACGGCCCATAGACCAGACCTGGCCAACTGGACGCCAGCCCAACCCCTGGCCCC
 20 GGGGCGAACAGGCGGCCTGGGGCCCTCGGACCGGCAGCTGCTGCTCTTCTACCTGGAGCAGTGTGAGGCC
 AACCTGACCACACTGACCAACGCCGTGGACGCTTCTTTACCGCCGTGGCCACCAACCAGCCGCCCAAGA
 TCTTTGTGGCGCACAGCAAGTTTCGTATCCTCAGCGCCCAAGCTGGTGTTCATCGGGGACACACTGTC
 ACGGCAGGCCAAGGCTGCTGACGTGCGCAGCCAGGTGACCCACTACAGCAACCTGCTGTGCGACCTCCTG
 CGCGCATCGTGGCCACCACCAAGCCGCTGCCCTTGACGTACCCATCGCCTTCCGCGGCCAGGACATGG
 25 TGGAGAGGGTCAAGGAGCTGGGCCACAGCAGCCAGTTCGCCCGCTCCTAGGCCAGCTGGCAGCCGC
 CTGAGGGTGGTGACCCAGGAGGGAGGCAGGGGAGGGGTGCGCGGTCCAGCTCCCTGGCTCCCATGTC
 AAGAGTCGCTGTGCCACAGGCTTAGGGACAGGACCCAGCTCTGCGTCGGTCTGGTGGCCTGGATGCCC
 AGGAATCTGTATATATTTATGGCCGGGCAGGGTGTGGGGCCATGCCCTCCTCAGGAGCCGAAGCCAGGGG
 CCGCAGTGGCCTTCCCCAGCATGCACCACGGGCCCGGTTGGGTACCAGACGGGGCTGGAGTGTGAGGG
 30 TCCTGCAGCCTGCAGGACCTCGTGCCACCCCGAGGGCTGAGCCTGGTCCCACGAGGGGTGCCGTGTCCCT
 GACAGGGCCAGTGCAGTTTGGTGTGTCTCCGCTTACCAGGAGAAGAACCTGAAGAACTATTTTCGTT
 ATTGGTTTTCCAATCATTGACTAAGAGTCTCCATTTAAATAAAGTTTTTAAAGGAA

SEQ ID NO:352

>gi|7656924|ref|NP_055382.1| breast cancer anti-estrogen resistance 1; Crk-
 35 associated substrate p130Cas [Homo sapiens]
 MNHLNLAKALYDNVAESPDELSFRKGDIMTVLEQDTQGLDGGWLC SLHGRQGI VPGNRLKILVGM YDKK
 PAGPGSGPPATPAQPQPLHAPAPPASQYTFMLPNTYQPPQDSVYLVPTPSKAQQGLYQVPGSPQFQSP
 PAKQTSSTFSKQTPHHPFSPATDLYQVPPGPGGPAQDIYQVPPSAGMGHDIYQVPPSMDTRSWEGTKPPA
 40 KVVVPTRVGQGYVYEAQAPEQDEYDIPRHL LAPGPQDIYDVPPVRG LLSQYQGEVYDTPPM AVKGPNGR
 DPLLEVYDVPPSVEKGLPPSNHHAVYDVPPSVSKDVPDGP LLREETYDVPPAFAKAKPFDPARTPLVLAA
 PPPDSPPAEDVDVPPAPDLYDVPPGLRRPGPGTLYDVPRERVLPEVADGGVVD SGVYAVPPPAEREA
 PAEGKRLSASSSTRSSQASSLEVAGPGREPLELEVAVEALARLQQGV SATVAHLLDLAGSAGATGSW
 RSPSEPQEP LVDLQA AVAVQSAVHELLEFARS AVGNAAHTSDRALHAKLSRQLQK MEDVHQT LVAHGQ
 45 ALDAGRGGSGATLEDLDR LVACSRAPVEDAKQLASFLHGNASLLFRRTKATAPGPEGGGTLHPNPTDKTS
 SIQSRPLPSPPKFTSQDSPDQYENSEGGWMEDYDVHLQKKEFEKTQKELLEKGSITRQKSQLELQQ
 LKQFERLEQEVS RPIDHDLANWTPAQPLAPGRTGGLGPSDRQLLLFYLEQCEANLTTLTNAVD AFFTAVA
 TNQPPKIFVAH SKFVILSAHKL VFIGDTLSRQAKAADVRSQVTHYSNLLCDLLRGIVATT KAAALQYPS
 50 SAAQDMVERVKELGHSTQQFRRVLGQLAAA

SEQ ID NO:353

perlecan
 >GL2_37_B06_G3F1 Direction: N/A
 ACCGCTCCTCTCCCGAGGGCACACAACCAACCAAACTGGTGCTCTGAAACAGCGCCAGTGTCCAGTTCTCTGAGG
 55 AGCACTGGGTCCATGAGGTCTTGGNCGGGCGGTGCAGCTGCCTGGAGCTGCTGGAGTGTGCGTGGAAGANACTG
 TNGAGTGGCGTGGNTCATTCAAGAACNGGTGTTCCGGANGAAAACCAGAACAAGGTGGGTAGATANGGAATAAA
 AGGGGGGCGGATCGAATAAATCTTGAAGGGTCTTGAANTNAATCGTNCCAACTTTGGAACACTTGGTCCCGGG
 TTTTCAACAGTGGTGGGCGAACATTTTTTCTAGCAGTGGGACCCGGCGGTTAAATAATTTCTATAAATATACT
 GGGCCNGTAATAAATAGATTGGAAGNGTTCACGAGTAATTTTAAACACAACATTTCCAACCATTTGTGGGNGCCG
 60 AGCGACCGAGAGTAATANTTAAGAAAAACGGGTACCGTTGGAAACCCCGTTTGGTGGGTGGAANAGTAAAAACA
 AGACCCATTTATGAGGACGCGGTTNTATNTAACCAGCCCCAAGAANACAGGTTTAAAAAAGTTTCATGGCGACC
 CAGCTTNTTGGTTCGAAGTTNTGAAGACAAAGAATTTTNGNGACCGNGCATTAATTTATTAATTGAGGACGGA

AAAAGAGGATTGTGTNCGGACACAGGCGTTAAAAAATTAAATTACCGCGNATAAAAGATGAAAATAGTTGGTGC
GCCGAGGNCGAAAACGCTCGGAAAGTATTCTCNGGCAGCGCCNGTTTTTTATACCCGCAAAAAACGAAAGAGTAG
ATAATTGTGCTAGCCGGTCGTCAANTAGATGACGAACTAAAATATNATAANTATGGGGTTAACACGCTGTGGGTG
AGTAAGAGAGGAATTTAAAAAACAGGGTGTGGTTTATACATAAACATTATATTTTTTATAATAGCGAATGANAGG
5 TAAAAGAGACCCGCGCNGGAGATAATATCTAGTGGGTACCAGATTGGTGAATAATAGGTACTGGGGTAAATTTGTT

SEQ ID NO:354

>GL2_37_B01_G3F1 Direction: N/A

ACCGCTCCTCTCCCGAGGGCACACACCCACCCAACTGGTGCTCTGAACCAGCGCCAGGTCCAGTTCTCTGAGGA
10 GCACTGGGTCCATGAGTCTGGNCGGCCGGTGACGCGCGGAGCTGCTGCAGGTGCTGCAGAGCCTGGAGTGGCG
TGCTCATCCAGAACTGTGTTCTGCGAGAAACCAGCACAGTGGTTAGATATGATAAAGCGGGCGCTCTGACTAAAT
CTGAGGTCTTGATACTCACTGACTGTGCTAAGGGNGGAATTCTGCGGCCGCGTAAATTCAAATTTGCCCCATAN
GTGAGTCCGTATTACAATTCACCTGGGGCGTCGTTTTACAACAGTCTGTGACTGGGAAAAAACCTGGCGTTACCC
ACACATTAATCTGCCCTTGACGCGACATTCCCTTTCTGCCAGACTGGNCGTAATAGCGAAGAGGGGCCGCGACAC
15 GATCTGCCCTTCCCAACAGTTGCGCAGAGCTATACGGTACAGGGGGANGATGTTAAAGCGGNTGTTACAAACGTA
TNTAAAAGAGGTAAAGAAAAGAACCAGGAGGTGTGTAATAATNACGGAGGCNCTTANGGTGTATTGGTGCGCGGC
GATTTGTTTNCCTAACGGCAAGNTTGGGAATACAATTTAAATTATTGAAACAAAGNGTGACNCGATGTGTGGTG
TGGAANAGGAATATAGGGGTGT

SEQ ID NO:355

>GL2_37_B02_G3F1 Direction: sense

ACCGCTCCTCTCCCGAGGGCACACACCCACCCAACTGGTGCTCTGAACCAGCGCCAGGTCCAGTTCTCTGAGG
AGCACTGGGTCCATGAGTCTGGCCGGCCGGTGACGCGCGGAGCTGCTGCAGGTGCTGCAGAGCCTGGAGGCCG
25 TGCTCATCCAGACCGTGT

SEQ ID NO:356

>GL2-86-1M13F Direction: sense

CTGGTGGGGATGGGGACCGCTGCCAGGGGTGAGCTGCCTTTTGCTCCACAGCCGACACTAAAGACAATTCCCA
ATCCTGAGTGGGTGGCAGAGACTCCTGCGATGCCCGTCTCAGGTAGCTGTGGGGCACCAGCCACAAGCCGAGGT
30 TGGCTCTCCTAGGAGTGAGAACTGCCCAAGGGCTGCAGAAACAGGCCACCCAGCTCTATCTGGGGGCTCCATCGG
TGGGTAGGGGGACAGTGGGGGCGATTCTGGGGCCACCCAGCCACTGTTCTGACCCCAAGTCTTGGTGACTTTCT
GAGGTGCCCACTCCCATCCAACCTGCCTTGCTGGCCAGCCTTGTGGCTTTGCCAGCTGTGTGTGTGAGGGTGGC
ATGCCACCTCCAGTCCAGCCAGGGCGGTA

SEQ ID NO:357

>GL2-86-2M13F Direction: sense

CTGGTGGGGATGGGGACCGCTGCCAGGGGTGAGCTGCCTTTTGCTCCACAGCCGGCACTAAAGACAATTCCCA
TCCTGAGTGGGTGGCAGAGACTCCTGCGATGCCCGTCTCANGTAGCTGTGGGGCACCAGCCACAAGCCGAGGTT
GGNTCTCCTAGGAGTGAGAACTGCCCAAGGGCTGCAGAAACAGGCCACCCAGCTCTATCTGGGGGCTCCAATCGG
40 TGGGTAGGGGGACAGTGGGGGCGATTCTGGGGCCACCCAGCACTGTTCTGAAACCAAGTCTTGGTGACTTTCTG
AGGTGCCCACTCCCATCCAACCTGGCTTGCTGGNAGCCTTGTGGCTTTGNCCAGCTGTGTGTGTGAGGGTGGCA
TGCCCANCTCCAGTCCAGCCAGGGCGGTAGCAGCAAAGCGTGGCATCGACTCGGNNTTTCTACAAAAAATTCA
TAAATAATATTCACTAATAATATACTCGGAACATTTGTGGGGCTTGGGGGCGTTGGCCCCGGGGAAAGTCCAGTG
TTGGGGGGCAAGGCCAGGTTGGCCCTANACGAAGGGGGGCCAGGGGCCGTTGTGTTTGGGGCCCCGGGCCCTGGGG
45 CGCNGGTGCTTGACAGGGC

SEQ ID NO:358

>GL2-86-3M13F Direction: sense

CTGGTGGGGATGGGGACCGCTGCCAGGGGTGAGCTGCCTTTTGCTCCACAGCCGGCACTAAAGACAATTCCCA
50 ATCCTGAGTGGGTGGCAGAGACTCCTGCGATGCCCGTCTCAGGTAGCTGTGGGGCACCAGCCACAAGCCGAGGT
TGGCTCTCCTAGGAGTGAGAACTGCCCAAGGGCTGCAGAAACAGGCCACCCAGCTCTATCTGGGGGCTCCATCGG
TGGGTAGGGGGACAGTGGGGGCGATTCTGGGGCCACCCAGCCACTGTTCTGACCCCAAGTCTTGGTGACTTTCT
GAGGTGCCCACTCCCATCCAACCTGCCTTGCTGGCCAGCCTTGTGGCTTTGCCAGCTGTGTGTGTGAGGGTGGC
ATGCCACCTCCAGTCCAGCCAGGGCGGTAGCAGCAAAGCGTGGCATCGCCTCGGTTTCTTACAAAAAATTCATA
55 ATAATATTAATAATAATAATACTCGACATTGTGCGGGCTG

SEQ ID NO:359

>GL2-86-5M13F Direction: sense

CTGGTGGGGATGGGGACCGCTGCCAGGGGTGAGCTGCCTTTTGCTCCACAGCCGGCACTAAAGACAATTCCCA
60 ATCCTGAGTGGGTGGCAGAGACTCCTGCGATGCCCGTCTCAGGTAGCTGTGGGGCACCAGCCACAAGCCGAGGT

TGGCTCTCCTAGGAGTGAGAACTGCCCAAGGGCTGCAGAAACAGGCCACCCAGCTCTATCTGGGGGCTCCATCGG
TGGGTAGGGGACAGTGGGGGAGTTCTGGGCCCACCCAGCCACTGTNCCTGACCCCAAGTCTGGTGACTTTCT
GAGGTGCCCACTCCACATCCAACCTGCCTTGCTGGNCAGCCTTGNTGGCATAATGCCCAGNCTGATAGATGCGTG
AGGGNGGACATGCCACCTACCAGTACCAGACCCAGGGCGGATAGGCAGCAAAGNACGTGGCATCGCCTCGG

SEQ ID NO:360

>GL2-86-1M13R Direction: N/A

CTGGTCAGCGGCCGGTCCCCAGGTCCCAACGTGGCAGTCAACGCCAAGGGCAGCGTCTACATCGGCGGAGCCCCCT
GACGTGGCCACGCTGACCGGGGGCAGATTCTCCTCGGGCATCACAGGCTGTGTCAAGAACCTGGTGCTGCACTCG
GCCCCACCCGGCGCCCCGCCCCACAGCCCCCTGGACCTGCAGACCGGCCAGGCCGGGGGCAACACACGCCCCCTG
CCCCTCGTAGGCACCTGCCTGCCCCACACGGACTCCCGGGCCACGCCCCAGCCCGACAATGTCGAGTATATTATT
ATTAATATTATTATGAA

SEQ ID NO:361

>GL2-86-2M13R Direction: N/A

CTGGTCAGCGGCCGGTCCCCAGGTCCCAACGTGGCAGTCAACGCCAAGGGCAGCGTCTACATCGGCGGAGCCCCCT
GACGTGGCCACGCTGACCGGGGGCAGATTCTCCTCGGGCATCACAGGCTGTGTCAAGAACCTGGTGCTGCACTCG
GCCCCACCCGGCGCCCCGCCCCACAA

SEQ ID NO:362

>GL2-86-3M13R Direction: N/A

TTGGTCAGCGGCCGGTCCCCAGGTCCCAACGTGGCAGTCAACGCCAAGGGCAGCGTCTACATCGGCGGAGCCCCCT
GACGTGGCCACGCTGACCGGGGGCAGATTCTCCTCGGGCATCACAGGCTGTGTCAAGAACCTGGTGCTGCACTCG
GCCCCACCCGGCGCCCCGCCCCACAGCCCCCTGGACCTGCAGACCGCGCCCAGGCCGGGGGCAACACACGCCCC
TGCCCCCTCGTAGGCACCTGCCTGCCCCACACGGACTCCCGGGCCACGCCCCAGCCCGACAATGTCGAGTATATTATTA
TTATTAATATTATTATGAATTTTNNGTAAAGAAACCGAGGCGATGCCACGCTTANGCTGCTACCGCCCTGGGCTGG
ACTGGAGGTGGGCATGCCACC

SEQ ID NO:363

>GL2-88-5M13R Direction: anti-sense

CTGGTCAGCGGCCGGTCCCCAGGTCCCAACGTGGCAGTCAACGCCAAGGGCAGCGTCTACATCGGCGGAGCCCCCT
GACGTGGCCACGCTGACCGGGGGCAGATTCTCCTCGGGCATCACAGGCTGTGTCAAGAACCTGGTGCTGCACTCG
GCCCCACCCGGCGCCCCGCCCCACAGCCCCCTGGACCTGCAGACCGCGCCCAGGCCGGGGGCAACACACGCCCCCT
GCCCCCTCGTAGGCACCTGCCTGCCCCACACGGACTCCCGGGCCACGCCCCAGCCGACAATGTCGAGTATATTATT
ATTAATATTATTATGAATTTTGTAAAGAAACCGAGGCGATGCCACGCTTTGCTGCTACCGGCCTGGGGCTGGA
CTGGAGGTGGGCATGCCAACACCATCACGGCACAACAGCTGGCAAAGGCCAACAAGGGCCCTTGGGCCAGGCAAG
GGCACAGGTTGGGACTGGGAGTGGGGCACCCTCANGAAAGGTCACCCAGGGAATATGGGGGGGTNCCAGAGGAA
ACCACAGGTAGGGGACTGGGGGTTTNGGGGGCCCCCAGGAAAACCTTGGGGCGCCCAAAANATNGNTACCACC
ACCATAAACACACAAGCCCAGAANTGTGAAAACCCCCAACCCAGAGAAAANTAGCAGAGCCATCGAGGAAAGCACC
CCAAGATACACAGCANNACCCCATGAGAA

SEQ ID NO:364

>GL2_93_2B09_G3F1 Direction: N/A

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SEQ ID NO:365

>gi|7427516|ref|NM_005529.2| Homo sapiens heparan sulfate proteoglycan 2 (perlecan) (HSPG2), mRNA

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SEQ ID NO:366

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45 LDLNLCVVPQAHAQVTHKRGSLPARHQTHGSLRLRHQVTPADSGEYVCHVVGTSGLPEASVLVTIEAS
VIPGPIPPVRIESSSSTVAEGQTLDLSCVAGQAHAQVTWYKRGGSLPARHQVGRSRLYIFQASPADAGQ
YVCRASNGMEASITVTVTGQGANLAYPAGSTQPIRIEPSSSQVAEGQTLDLNLCVVPQSHAQVTHKRG
GSLPVRHQTHGSLRLRYQASPADSGEYVCRVLGSSVPLEASVLVTIEPAGSVPALGVTPTVRIESSSQQV
AEGQTLDLNLCVAGQAHAQVTHKRGSLPARHQVHGSRLRLRHQVTPADSGEYVCRVVGSSGTQEASVLV
50 TIQQRLSGSHSQGVAYPVRIESSSASLANGHTLDLNLCLVASQAPHTITWYKRGGSLPSRHQIVGSRLRIP
QVTPADSGEYVCHVSNAGSRETSILVTIQSGSSHVPRVSPPIRIESSSPTVVEGQTLDLNLCVVARQPQ
AIITWYKRGGSLPSRHQTHGSHLRLHQMVSADSGEYVCRANNIDALEASIVISVSPSAGSPAPGSSMP
IRIESSSSHVAEGETLDLNCVVPQAHAQVTHKRGSLPSYHQTRGSRLRLHVS PADSGEYVCRVVGMS
SGPLEASVLVTIEASGSSAVHVPAPGGAPPRIEIPSSSRVAEGQTLDLKCVVPQAHAQVTHKRGGNLP
55 ARHQVHGPLRLNLNVSPADSGEYSCQVTGSSGTLEASVLVTIEPSSPGPIAPAGLAQPIYIEASSSHVTE
GQTLDLNLCVVPQAHAQVTHKRGSLPARHQTHGSLRLHVS PADSGEYVCRAGGPGPEQEASFTVT
VPPSEGSSYRLRSPVISIDPPSSTVQQGDASFKCLIHGDAAPISLEWKTRNQELEDNVHISPNGSIITI
VGTTRPSNHGTYRCVNASNYGVAQSVVNLSPVHGPPVTVSVLPEGPVWVKVGAVTLECVSAGEPRSSARWTR
ISSTPAKLEQRTYGLMDSHTVLQISSAKPSDAGTYVCLAQNALGTAQKQVEVIVDTGAMAPGAPQVQAE
60 ABLTVEAGHTATLRCSATGSPARTIHWKSLRSLPFWQHRLEGDTLIIPRVAQQDSGQYICNATSPAGHAE
ATIILHVESPPYATTVPEHASVQAGETVQLQCLAHGTFPLTFQWSRVGSSLPGRATARNELLHFERAAPE

5 DSGRYRCRVTNKVGSAEFAQLLVQGGPSLPATSIAGSTPTVQVTPQLETKISIGASVEFHCAVPSDRG
TQLRWFKEGGQLPPGHSVQDGLRIQNLQSCQGTIICQAHGPWGKAQASQALVIALPSVLINIRTSVQ
TVVVGHAVEFECLALGDPKPQVTSKVGHLRPGIVQSGGVVRIAHVELADAGQYRCTATNAAGTTQSHV
10 ILLVQALPQISMPQEVVRVPAGSAAVFPCIASGYPTPDISWSKLDGSLPPDSRLENNMLMLPSVQPQDAGT
YVCTATNRQGVKAFAPHLQVPERVVPYFTQTPYSFLPLPTIKDAYRKEFIKITFRPDSADGMLLYNGQKR
VPGSPTNLNARQPDFISFGLVGRPEFRFDAGSGMATIRHPTPLALGHFHTVTLRLSLTQGSILVGLDAP
VNGTSQKGFQGLDNEELYGGVPDYGAIPKAGLSGFIGCVRELRIQGEIIVFHDNLNLTAGHISHCPTC
RDRPCQNGGQCHDSESSSYVCPAGFTGSRCEHSQALHCHPEACGPDATCVNRPDRGRYTCRCHLRGSG
15 LRCEEGVTVTTPSLSGAGSYLALPALTNTHHELRLDVEFKPLAPDGVLLFSGGKSGPVEDFVSLAMVGGH
LEFRYELGSGLAVLRTAEPLALGRWHRVSAERLNKDGSLRVNGGRPVLRRSSPGKSQGLNLHTLLYLGGVE
PSVPLSPATNMSAHFRGCVGEVSVNGKRLDLYSFLGSQGIGQCYDSSPCERQPCQHGATCMPAGEYEFQ
CLCRDGIKGDLCHEENPCQLREPC LHGGTCQGT RCLCLPGFSGPRCQQGSGHGIAESDWHLEGSGGNDA
PGQYGAIFYHDDGFLAAPPGHVFSRSLPEVPETIELEVRTSTASGLLLWQGVVEGAGQGKDFISLGLQDGH
LVFRYQLGSGEGARLVSEPDINDGEWHRVTALREGRRSIQVDGEELVSGRSPGPNVAVNAKGSIIYGAP
20 DVATLTGGRFSSGITGCVKNLVLSARPGAPPPOLDLOHRAOAGANTRPCPS

SEO ID NO:367

PGR-1 (T-cell activation protein)

>GL3 8D 3 M13F Direction: N/A

20 ATATGCTCATCCAGATCAAACGCGAGGTGGAGGCCTCGGAGGAGAGCGCCCTCAACCACCTCCAGAACC CGGGCG
ACGCGGCCGAGGGCCGGGCGGCCAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCGANCGGAAGATTTGCTGAAAAC
TNGCATGTAGATGCTTGGTGGAGCTGTGTCCGGCTGGATTAGCAGTAAGAGCGAAGTTCAGTCGGTGAGCGCGGT
CGGGCGGTTTTCCAGGGTCCGATGGGATTCTCTTGGCCAACCTTGGTGGTAGATGTGGCTTGACTACCTTGGAA
25 GGAAAAGCCTGGATAAGCCTAGAAGAAGCCCCCTTTTGGTTGTATCTCTTCTNGTTCCTTCCTGTCTATTNCCTA
TCTTGCTCTTCAGCTTTTANANAGTTTAACAGGNTGTCTGCTTGGGCATAATTGGGCTCATGATGGGTATTCGAT
GACCCTTTCCGAATCATGGAANGTTTTTCGGAATTTTGTTAAACGGTGGTGAGTAGATTTTACGGGGGAAAAGG
TTAAATTGT

SEO ID NO:368

>GL3 26KV PCR G3F1 Direction: N/A

ATATGCTCATCCAGATCAAACGCAGGTGGAGG

ACGCGGCCGAGGGCCGGGCGGCCAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCAAGGGAGATTGCGAAGATGGCA
GAGATGCTGGTGGAGCTGGTCCGGCGGATAGAGAAGAGCGAGTCGTCTGTGAGCGCGGTTCGGCGTTTCCAGCCAA
TGGATTCTGGTCAACTGGTGGAGATTGGCTGACACCCTGGAGAAGCCGAAACCAGAGAGCCTTTTGTTCCTCTTT
TTTTTTCCTGTCTATGCTCTGTCTCACTTTAACAACACTACGTTTTCTGCTATGGGTCTCGGTGAGATTGATGACC

SEO ID NO:369

>GL3 27BP 3 M13F Direction: N/A

ATATGCTCATCCAGATCAAACGCAGGTGGAC

40 ACGCGGCCGAGGGCCGGGCGGCCAAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCAAGGAGATTGCGAAGATGGCA
GAGATGCTGGTGGAGCTGGTCCGGCGGATAGAGAAGAGCGAGTCGTCTGAGCGCGGTTCGGCGGTTTCCAGCCAA
TGGATTCTGGTCAACTGGTGGAGATTGGCTGACACCCTGGAGAAGCCGAAAACCAGAGAGCCTTTGTGTTTCCTC
TTTTTTTTCCCTGTCTATGCTCTGTCTCTCACTTAACACTACGTTTCCTGCTATGGTCATGTGGTTGATGACCCTC
AATATGAGTTTCGAATGGTAACGTGTATAGAGTAGTGGGAAGTAATTTGGTTTGAANAATGCTCTCACAAATACAG
45 GGAATTAGGGACCTAGGATTGTAAGCTCTTGCCAGGCAGGTCAACATTTTGTTCCTCGGGGCTTTGGGGGGTAATT
TCAAT

SEQ ID NO:370

>GL3 27BP 3 M13R Direction: anti-sense

50 CCCCGTTGAAGTCTGGTCCCTTTCTTCAGTAGTTGCTGCATGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCAG
CACCTCCAGAGCTGGAGAACTCCAACGTGAGTCTCATGTGTACACACAGACCCAAAGTTCCAGGGAGCTATCA
GGTCACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCCGGAACAAATGTGACTGCT
GCAAGAGCTTACAATCTAGGTCCTAATTCCTGTATGTGAGAGCATTTTCAAACAAAATTACTTCCCAAACAAAA
CACGTTAAACAATCGAAACTCATATTGAGGTCATCAACCACAGACCATAGCAGAAAAAGTAGTGTTAAGTGAGACA
55 GAGCATAGACGAGGAAAAAAGAGAAAAAAGGCTCTCTGGTTCTCGGCTTCTCCAGGGTGTGAGCCAATCTCC
ACCAGTTGACCAAGATCCATTGGCTGGAAACCGCGCAGCGCGCTCACGACGACTCGCTCTTCTCTATCCGCGGA
CCAGCTCCACCAGCATCTTCTGCCATCTTCGCAATCTCCTTGGCCTTCTCCTCGGCTTCTCGCACTCTT

SEQ ID NO:371

>GL3_8D_1_M13R Direction: anti-sense

CCCCGTTGAAGTCTGATCCTTTCTTCAGTAGTTGCTGCATGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCAG
CACCTCCAGAGCTGGAGAACTCCAACCTGTGAGTCTCATGTGTCACACACAGACCCAAAGTTCCAGGGAGCTATCA
GGTCACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCGGGAACAAATGTGACTGCT
GCAAGAGCTTACAATCTAGGCCCTAATTCCTGTATGTGAGAGCATTTTCAAACAAAATTACTTCCCAAACAAAA
CACGTTAACAATCGAACTCATATTGAGGTCATCAACCACAGACCATAGCAGAAAACGTAGTGTTAAGTGAGACA
GAGCATAGACAGGAAAAAAGAGAAAAACAAAAGGCTCTCTGGTTTCGGCTTCTCCAGGGTGTGAGCCAATCTCC
ACCAGTTGACCAGAATCCATTGGCTGGAAAC

SEQ ID NO:372

>GL3_8D_2_M13R Direction: anti-sense

CCCCGTTGAAGTCTGGTCCTTTCTTCAGTAGTTGCTGCATGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCAG
CACCTCCAGAGCTGGAGAACTCCAACCTGTGAGTCTCATGTGTCACACACAGACCCAAAGTTCCAGGGAGCTATCA
GGTCACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCGGGAACAAATGTGACTGCT
GCAAGAGCTTACAATCTAGGCCCTAATTCCTGTATGTGAGAGCATTTTCAAACAAAATTACTTCCCAAACAAAA
CACGTTAACAATCGAACTCATATTGAGGTCATCAACCACAGACCATAGCAGAAAACGTAGTGTTAAGTGAGACA
GAGCATAGACAGGAAAAAAGAGAAAAACAAAAGGCTCTCTGGTTTCGGCTTCTCCAGGGTGTGAGCCAATCTCC
ACCAGTTGACCAGAATCCATTG

SEQ ID NO:373

>GL3_8D_3_M13R Direction: anti-sense

CCCCGTTGAAGTCTGGTCCTTTCTTACAGTAGTTGCTGCATGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCA
GCACCTCCAGAGCTGGAGAACTCCAACCTGTGAGTCTCATGTGTCACACACAGACCCAAAGTTCCAGGGAGCTATC
AGGTACACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCGGGAACAAATGTGACTGC
TGCAAGAGCTTACAATCTAGGCCCTAATTCCTGTATGTGAGAGCATTTTCAAACAAAATTACTTCCCAAACAAAA
ACACGTTAACAATCGAACTCATATTGAGGTCATCAACCACAGACCATAGCAGAAAACGTAGTGTTAAGTGAGAC
AGAGCATAGACNGGAAAAAAGAGAAAAACAAAAGGCTCTCTGGTTTCGGCTTCTCCAGGGTGTGAGCCAATCTC
CACCAGTTGGCCAGAATCCATTGGCTGGAAACCGCCGACCGCTCACGACGACTCGCTCTTCTCTATCCGCCGG
ACCAGCTCCACCAGCATCTCTGCCATCTTC

SEQ ID NO:374

>GL3_8D_4_M13F Direction: N/A

AATATGCTCATCCAGATCAAAACGCAGGTGGAGGCCTCGGAGGAGAGCGCCCTCAACCACCTCCAGAACCCGGGGC
GACGCGGCCGAGGGCCGGGCGGCCAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCAAGGAGATTGCGAAGATGGCA
GAGATGCTGGTGGAGCTGGTCTGGCGGATAGAGAAGAGCGAGTCGTGAGCGCGGTTCGGCGGTTTCCAGCCAA
TGGATTCTGGTCAACTGGTGGAGATTGGCTGACACCTGGAGAAGCCGAAACCAGAGAGCCTTTTGTCTCTCTT
TTTTTCTCTGTCTATGCTCTGCTCACTTAACACTACGTTTTCTGCTATGGTCTGTGGTTGATGACCTCAATATG
AGTTTCGATGTGTTAACGT

SEQ ID NO:375

>GL3_8D_4_M13R Direction: anti-sense

CCCCGTTGAAGTCTGGTCCTTTCTTCAGTAGTTGCTGCATGGAGTCGTCTTCCAGAATTAATGCAGCTCCTTCA
GGCACCTCCAGAGCTGGAGAACTCCAACCTGTGAGTCTCATGTGTCACACACAGACCCAAAGTTCCAGGGAGCTAT
CAGGTACACAAGAAATAGCAAAGCACCTCAAAAATTTAGAAATAACCACCAAAGCCCGGGAACAAATGTGACTG
CTGCAAGAGCT

SEQ ID NO:376

>GL3_8D_PCR_G3F1 Direction: N/A

ATATGCTCATCCAGATCAAAACGCAGGTGAGGCCTCGGAGGAGAGCGCCCTCAACACCTCCAGAACCCGGGGCGA
CGCGGCGAGGCGGGCGGGCAAAAGTGCGAGAAGGCCGAGGAGAAGGCCAGGAGATTGCGAAGATTGCAGAGAT
GCTGGTGGAGCTGGTCCGGCGGATAGAGAAGAGCGAGTCGTGAGCGCGGTTCGGCGGTTTCCAGCCCATGGAT
TCTGGTCAACTGGTGGAGATTGGCTGACACCTGGAGAAGCCGAAACCAGAGAGCCTTTTGTCTCTCTTTTTT
TCCTGTCTATGCTCTGTCTCACTTAACACTACGTTTTCTGCTATGGTCTGTGGTTGATGACCTCAATATGAGTTT
CGATTGTTAACGTGTTTTTGTGGGAAGTAATTTGTTTGAATGCTCTCACATACAGGAATTA

SEQ ID NO:377

>gi|15193293|ref|NM_033296.1| Homo sapiens T-cell activation protein (PGR1), mRNA

TTGTCCGTGGCTTCTCTGAGAAGAAAAGTTGAAAAGGGTAAAAGTTTTCAGGAATATTCCGGGCTCTCTA

TTGCTAAGCATAGCGAGTGTCTCGGTTTTCTCTCTCCAACAGACATCGCTATTGCGGTTCCGAGGCGAGTGGG
AAGAGATGCGGCCCCCTGGACATCGTTCGAGCTGGCGGAACCGGAGGAAGTGGAGGTGCTGGAGCCCCGAGGA
GGATTTTCGAGCAGTTTTCTGCTCCCGGTCAACAAGAGATGCGCGAGGACATCGCGTCTGCTGACGCGCGAG
CACGGGCGGGCGTACCTGCGGAACCGGAGCAAGCTGTGGGAGATGGACAATATGCTCATCCAGATCAAAA
5 CGCAGGTGGAGGCCCTCGGAGGAGAGCGCCCTCAACCACCTCCAGAACCCGGGCGACGCGGCCGAGGGCCG
GGCGGCCAAGAGGTGCGAGAAGGCCGAGGAGAAGGCCAAGGAGATTGCGAAGATGGCAGAGATGCTGGTG
GAGCTGGTCCGGCGGATAGAGAAGAGCGAGTCGTCTGAGCGCGGTGCGCGGTTTCCAGCCAATGGATTTC
TGGTCAACTGGTGGAGATTGGCTGACACCCCTGGAGAAGCCGAAACCAGAGAGCCTTTTGTCTCTCTTTT
10 TTCCTGTCTATGCTCTGTCTCACTTAACACTACGTTTTCTGTCTATGGTCTGTGGTTGATGACCTCAATAT
GAGTTTCGATTGTAAACGTGTTTTTGTGGGAAGTAATTTGTTTGAAAATGCTCTCACATACAGGAAT
TAGGGCCTAGATTGTAAGCTCTTGACAGTCACATTTGTTCCCGGCTTTGGTGGTTATTTCTAAATTT
TTGAGGTGCTTTTGCTATTTCTTGTGTGACCTGATAGCTCCCTGGAACTTTGGGTCTGTGTGTGACACATG
AGACTCACAGTTGGAGTTCTCCAGCTCTGGAGGTGCTGAAGGAGCTGCATTAATTCTGGAAGACGACTCC
15 ATGCAGCAACTACTGAAGAAAGGACCAGACTTCAACGGGGAGTGTGGATGGGCGGACCTGGCTGGGACTC
GTGAATCTGGAGAAGAGCTGGAGAATGGATAGTATTGTCTGTATTGAGACTTTAATTTCTGTGTGAGA
CCAAAGGAGGAGAGATGTGTTTTGTTCAAAATTTAAATTTGTTGTGGTACACTATCTTATGTAACCTGTC
TGGTGAGTTTGTGGTGGACAACCTAACTCAGCTTTATTTGACATGGAACCTAAAATAGAAGATAAGATCTT
GATATTCTGTACAAGTTGATGTAATACCCTGATGCGTTTTAGAGGACTTGGCATAAAATGAAAGATTGGC
AAAGGCCCTTGAGGGGCTTGGGGATGACAGTATGGAACGTCTGCTGCATTGGACCCTAACTGGACTAGAAG
20 AGGCATCTTCAAGGTTCATACGTTGTCCAGCTGTAAGTTCAATTTGAGTAGCAGACCTAACAAATATTTGA
GGTCAGAACCCTACCATGTTAAACAAACAAAACCTTACCATGTTAATAAAAGTATTTCATTTGC

SEQ ID NO:378

>gi|15193294|ref|NP_150638.1| T-cell activation protein [Homo sapiens]
25 MRPLDIVELAEPEEVEVLEPEEDFEQFLLPVINEMREDIASLTREHGRAYLRNRSKLWEMDNMLIQIKTQ
VEASEESALNHLQNPGDAAEGRAAKRCEKAEKAKEIAKMAEMLVELVRRIEKSESS

SEQ ID NO:379

Phosphoribosyl pyrophosphate synthetase-associated protein 1

>GL3_38B_PCR_G3F1 Direction: N/A

CGCCCGCCCGGTTCCCCCGCCGGCCATGAACGCCGCTCGCACCCGGCTACCGAGTCTTCTCGGCCAACTCCACGGC
CGCTGTCACGGAGCTGGCCAAAGCGCATCACAGAGCGCCTTGGTGCTGAATTGGGGAAGTCTGTTGTATATGAAGA
GACCAATGGAGAAACAAGAGTTAAAATAAAAAGAAATCTGTTTCGTGGCCAAGATATTTTCATTATACAGACAATACC
35 CAGAGATGTGAATACAGCTGTGATGGAGTTGCTCATCATGGCTTACGCACTGAAGACTGCCTGTGCCAGGAACAT
TATTGGGGTTCATCCCTACTTCCCTTACAGCAAGCAGAGCAAGATGAGAAAGAGGGGTTCCATTGTGTGCAAGCT
GCTAGCATCCATGCTGGCGAAAGCAGGTTTAACTCACATTATCACTATGGATCTTCATCAAAAGGAAATACAAGG
CTTTTTTCAGCTTTTCTGTGGACAACCTTAGAGCCTCACCTTTCTGCTTCAGTATATCCGGAAGAAATCCAAAT
TACAGAAATGCAGTCATTGTAGCTAGTCTCCTGATGCTGCAAGAGGGGCCAGTCCTATGCGGAGAGACTGCGTC
40 TGGGTTTTGGCCGTCATTCACGGGGAAGCTCAGTGCACGGAACCTGG

SEQ ID NO:380

>GL3_8K_2_M13R Direction: sense

CTGCCCGCCCGGTTCCCCCTGCCNGGCCATGAACGCCGCTCTGCACCCGGCTACCGAGTCTTCTCGGCCAACTC
CACGGCCGCTGACGGAGCTGGCCAAGCGCATCACAGAGCGCCTTGGTGCTGAATTGGGGAAGTCTGTTGTATA
45 TGANAGAGACCAATGGAGGAAACCAAGAGTTACACANAGTACAAAGAANTCTGTTTCGTTGGCCAAGGATATTTTC
ATTATACAGACAATTAACCCAGAGATGTGAATACAGCTGTGATGGAGTTGCTCATCATGGCTTACGCACTGAAGA
CTGCCTGTGCCAGGAAC

SEQ ID NO:381

>GL3_8K_3_M13R Direction: sense

CGCCCGCCCGGTTCCCCCGCCGGCCATGAACGCCGCTCGCACCCGGTACCGAGTCTTCTCGGCCAACTCCACGGCGCC
TGACGGAGCTGGCCAAGCGCATACAGAGCGCCTTGGTGCTGAATTGGGGAAGTCTGTTGTATATTAAGAGACCAA
TGGGAAACAAGAGTTAAATAAAAAGATCTGTTTCGTGG

SEQ ID NO:382

>GL3_8K_4_M13F Direction: anti-sense

CGCCCGCCCGNGTTTCCCCCGCCGGCCATGAACGCCGCTCGCACCCGGTACCGAGTTCTTCTCGGCCAACTCCAC
GGCCGCTGACGGAGCCTTGGCCAAGCCGCATCACAGAGCGCCTTGGTGCTGAATGGGGAAGTCTGTGGTATA
TGAAGAGACCAATGGAGGAAACAAGAGTTAAAATAAAAAGAATTCGTTTCGTGGCCAAGATTATTTTTCATTATA
60 CAGACAATTACCCAGAGATGTTGAATTACAGCTTGTGATTGGAGTTTGCTCATTATGGCTTTACGCCACTGAA

GACTTGCCTTGTGTCAGGAACATTTATTGGGGTCATCCCCTTACTTCCCCTACAGCAAGCAGAGCAAAGATGAG
AAAGAGGGGTTCCATTGTGTGCAAGCTGCTTAGGCAATCCATGCTGGCCGAAAAGCNGGTTTAACTCACATTATC
ACTATGGATCTTCATCAAAGGAAATACAAGGGCTTTTACAAGCTTTCTTGTGGAACAAACCTTTTAGAAGCCT
TCAACCTTTTTCCTGCTTTCAGTATATCCCAGGAAGGAAATCCAAATTACCAGAAATGCAGGTCAATTTGGTAGCT
5 AAGTCTCCCTGATGCCTTGCCAAGGANGGGCCAGTCCTATTTCGGAGAANACATGCGTCTGGTTGGGCCGGAANTC
ACACGGGAAACCNCATGCACAGAACTCNGGACCTTGG

SEQ ID NO:383

>GL3_8K_PCR_G3F1 Direction: N/A

10 CGCCCGCCCCGGTTCCCCGCCGCCATGAACGCCGCTCGCACCGGCTACCGAGTCTTCTCGGCCAACTCCACGGC
CGCCTGCACGGAGCTGGCCAAGCGCATCACAGAGCGCCTTGGTGTGAATTGGGGAAGTCTGTTGTATATGAAGA
GACCAATGGAGAAACAAGAGTTAAATAAAAGAATCTGTTCTGGGCCAAGATATTTTCATTATACAGACAATACC
CAGAGATGTGAATACAGCTGTGATGGAGTTGCTCATCATGGCTTACGCACTGAAGACTGCCTGTGCCAGGAACAT
TATTGGGGTCATCCCCTACTTCCCCTACAGCAAGCAGAGCAAGATGAGAAAGAGGGGTTCCATTGTGTGCAAGCT
15 GCTAGCATCCATGCTGGCGAAAGCAGGTTTAACTCACATTATCACTATGATCTTCATCAAAAGGAAATACAAGGC
TTTTTTCAGCTTTCTGTGGACAACCTTAGAGCCTCACCTTTCCTGCTTCAGTATATCCGGAAGAAATCCAAATT
ACAGAAATGCAGTCATTGTAGCTAACGTCTCCTGATGCTGCAAGAGGGGCCAGTCCTATGCGGAGAGACTGCGT
CTGGGTTTGGCCGTCATTACGGGGAAGCTCAGTGCACGGAAGTGGACATTGGACGATGGTTCGTCAACTCCCCGC
20 TATGGTCAAAATGCTACTGTGCACCC

SEQ ID NO:384

>gi|4506130|ref|NM_002766.1| Homo sapiens phosphoribosyl pyrophosphate
synthetase-associated protein 1 (PRPSAP1), mRNA

25 GGTGCGCAAGGGCACGGACCTCGGAGCTCTCCCCGTCCCCCGCCGCCATGAACGCCGCTCGCACCGGC
TACCGAGTCTTCTCGCCAACTCCACGGCCGCTGCACGGAGCTGGCCAAGCGCATCACAGAGCGCCTTG
GTGCTGAATTGGGGAAGTCTGTTGTATATCAAGAGACCAATGGAGAAACAAGAGTTGAAATAAAAGAATT
TGTTCTGGCCAAGATATTTTCATTATACAGACAATACCCAGAGATGTGAATACAGCTGTGATGGAGATTG
CTCATCATGGCTTACGCACTGAAGACTGCCTGTGCCAGGAACATTATTGGGGTCATCCCCCTACTTCCCCT
ACAGCAAGCAGAGCAAGATGAGGAAGAGGGGTTCCATTGTGTGCAAGCTGCTAGCATCCATGCTGGCGAA
30 AGCAGGTTTAACTCACATTATCACTATGGATCTTCATCAAAAGGAAATACAAGGCTTTTTTCAGCTTTCT.
GTGGACAACCTTAGAGCCTCACCTTTCTGCTTCAGTATATCCAGGAAGAAATCCAAATTACAGAAATG
CAGTCATTGTAGCTAAGTCTCCTGATGCTGCAAGAGGGGCCAGTCCTATGCGGAGAGACTGCGTCTGGG
TTTGGCCGTCATTACGGGGAAGCTCAGTGCACGGAAGTGGACATGGACGATGGTTCGTCCTCCCCGCT
ATGGTCAAAAATGCTACTGTGCACCCAGGCTGCGAGTTGCCATTGATGATGGCCAAAGAGAAGCCACCGA
35 TAACTGTAGTTGGAGATGTTGGAGGCGCATCGCAATCATCGTGGATGACATTATTGACGATGTGGAGAG
TTTTGTTGCTGCCGCGGAGATCCTGAAAGAGAGAGGCGCCTATAAGATCTATGTTATGGCCACCCACGGC
ATCCTGTCTGCAGAGGCCCTCGCCTGATTGAGGAGTCTCCGTAGACGAGGTGGTGGTGACGAATACATG
TCCCTCATGAGGTTTCAAGAGCTGCAATGTCCCAAGATAAAGACTGTGGATATCAGTTTGATTCTTTCTGA
AGCCATTTCGGAGAATCCACAATGGAGAGTCCATGGCCTACCTTTTCCGAAACATCACTGTGGATGACTAG
40 CTTTTCAGAGGGTCTCGACCTGGACCTCCTGAGGGAACATGGAAAAGCAGTGCCATGAGTGATACAG
TGTTTCTTGAAGGGAGGACTCGAAACAGCCTGGAGTTAGATATCTTCTTTTGCCCGGATTGATGGGGA
GGAGGGATTAAAAGAGTCAGGAAGAAGACAGAGCTAATGGATAAATATCATAACATGGCCTTACATGTCT
GCTGTCTACAGCCCTGTTCTTAAAGTTCTAGCTGCTTTCTTAAATAATCTGAAAATCTTATTGATA
CTAAAGAGGAGTTAAAGGCACATAAAGTCTTAACTCTATAATGTTTCAATTTAGTTGTTTCAGCTCCAGGGA
45 AATGGAGGTATTGATGTTGAACCTGGTTAGGGAAGCTGAGCGCCTGTGGCCCTATTACTATCCAGTTGGC
CTCTCCCAAATCAACTTCAAGTCTTTTATAGAGAATCGTATTTTCTTTTTCAGAAATTGCTATGCCTACAG
CCATTGAAAATGAAGCATTCATGTTTACATCTTCCAAGGATGTCAGATTAGAAAATAGCATCCCACC
TCTGGGTATCTGAGTGGCTCTGAAGTTGCAAATAAAATAATTTGTTGT

SEQ ID NO:385

>gi|4506131|ref|NP_002757.1| phosphoribosyl pyrophosphate synthetase-
associated protein 1 [Homo sapiens]

55 MNAARTGYRVFLANSTAACTELAKRITERLGAEIGKSVVYQETNGETRVEIKEFVRGQDIFIQTIPRDV
NTAVMELLIMAYALKTACARNIIGVIPYFPYSKQSKMRKGSIVCKLLASMLAKAGLTHIITMDLHQKEI
QGFFSFPVDNLRASPFLLQYIQEIPNYRNAVIVAKSPDAAKRAQSYAERLRLGLAVIHGEAQCTELDMD
DGRHSPPMVKNAIVHPGLELPLMMAKEKPPITVVGDVGGRIAIIVDDIIDDVESFVAAAEILKERGAYKI
YVMATHGILSAEAPRLIESSVDEVVVTNTVPHEVQKLQCPKIKTVDISLILSEAIRRIHNGESMAYLFR
NITVDD

SEQ ID NO:386

Plakoglobin

>G3_1_90_PCR_G3F1 Direction: N/A

GTGCGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCACAACCTCTCCAC
5 CACCGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTTCTTGGTCCGCATGCTCAGCTCCCTTTT
GAGTCGGTCTCTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCCAAGATGGCCGTG
CGCCTGGCCGACGGGCTGCAAAAGATGGTGGCCCTGCTCAACAAGAACAACCCCAAGTTCTTGGCCATCACCACC
GACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGTGGGCCCCAGGGC
10 CCTCGGTGCACGATTATGCGTTACTTCTGTTTAAAAGC

SEQ ID NO:387

>G3_4_01_PCR_G3F1 Direction: N/A

CCAGTGCTGTGCTTGCCTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCAC
AACCTCTCCACACCGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTC
15 AGTCCCCCTTTTGGAGTCGGTCTCTGTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGC
CAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGGCCCTGCTCAACAAGAACAACCCCAAGTTCTTG
GCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGT
GGGCCCCAGGCCCTCGTGCAGATCATGCGTAACTACGTTATTAAAAGCTGCTC

SEQ ID NO:388

>G3_4_44_PCR_G3F1 Direction: N/A

TCCAGTGCTGTGCTGCGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCAC
AACCTCTCCACACCGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTC
25 AGTCCCCCTTTTGGAGTCTGTCTCTGTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGC
CAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGGCCCTGCTCAACAAGAACAACCCCAAGTTCTTG
GGCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGG
TGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACTACGTTATGAAAAGCTGCTCTGGACCACCAGTCTGTGCTC
AAGGTGCTATCCGTGTGTCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGATGCAGGCCCTGGGCAAGCAC
30 CTGACCAGCAACAGCCCCCGCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCTCTCAGATTTGGCCACCAGG
CAGGAGGGC

SEQ ID NO:389

>G3_4_90_PCR_G3F1 Direction: N/A

CCAGTGCTGTGCTGCGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCACA
35 ACCTCTCCACACCGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTCA
GCTCCCCCTGTGGAGTCTGTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCC
AAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGGCCCTGCTCAACAAGAACAACCCCAAGTTCTTG
GCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGT
GGGCCCCAGGCCCTCGTGCAGATCATGCGTAACTACGTTATGAAAAGCTGCTCTGGACCACCAGTCTGTGCTC
40 AAGGTGCTATCCGTGTGTCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGATGCAGGCCCTGGGCAAGCAC
CTGACCAGCAACAGCCCCCGCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCTCTCAGATTTGGCCACCAGG

SEQ ID NO:390

>G3_5_91_PCR_G3F1 Direction: N/A

TGCTGTGCTGCGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCACAACCT
45 CTCCACACACCGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTCAGCTC
CCCTTGGAGTCTGTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCCAAGATG
GCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGGCCCTGCTCAACAAGAACAACCCCAAGTTCTTGGCCATC
ACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGTGGGCCC
50 CAGGCCCTCGTGCAGATCATGCGTAACTACGTTATGAAAAGCTGCTCTGGACCACCAGTCTGTGCTCAAGGTG
CTATCCGTGTGTCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGATGCAGGCCCTGGGCAAGCACCTACCA
GCAACAGCCCCCGCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCTCTCAGATTTGGCCACCAGGAGGAGG
GCCTGGAGAGTGTGCTGAAAGATTCTGGTGA

SEQ ID NO:391

>G3_7_64_PCR_G3F1 Direction: N/A

AGCTTTTATAACTGTAGTTACGCATGATCTGCACGAGGGCCTGGGGCCACCATTTGGCCAGGATGATCAGCTTG
CTCTCCTGGTTGCCGTAGCCAGAGCTGCAGCAGTCGTGTATGCCAGAACTTGGGGTTGTTCTTGTGAGCAGGGG
60 CACCATCTTTTGCAGCCCGTCGCCAGGCGCACGGCCATCTTGGCGCCCTCCTGGTACAGGAGCAGGTTGTGCAGC
GTGGTGTATGATAGAACAGGACCGACTCCACANGGGAGCTGAGCATGCGGACCAGAGCAGGATGCCACCCACTTG

AAATGCAGCAGCCCCCTCCCGGTGTGGAGAGGTTGTGCAGGATGCTGTGGTGCAGCGGGCTGTGTCCAGTCGCTGT
ATTCTGCATGGTACGCACGACGCGCCACCACTGGGCGAGCCCATCAGGGCCCCGCGCGACCCCTCCTTTTCGACGC
TGTTCAACATCATGCCCCCTTGTCAC

5 SEQ ID NO:392

>GL1_34_HIGH_1_G3F1 Direction: N/A

10 GAGAGGCGCCATNGNCGGTGGCAGCGGTGGCTCCAGTGCTGTCTGTCGTACCATGCAGAATACCAGCGACCTGGA
CACAGCCCGCTGCACCACCAGCATCCTGCACAACCTCTCCACCACCGGGAGGGGCTGCTCGCCATCTTCAAGTC
GGGTGGCATCCCTGNTCTTGGTCCGCATGCTCAGCTCCCTGNTGGAGTCGGTCCTGTTCTATGCCATCACCACG
15 CTGCACAACCTGCTCCTGTACCAGGAGGGCGCCAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTG
CCCCTGCTCAACAAGAACAACCCCAAGTTCCCTGGCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAAC
CAGGAGAGCAAGCTGATCATCCTGGCCAATGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTAT
GAAAAGCTGCTCTGGACCACAGTCGTGTGCTCAAGGTGCTATCCGTGTGTCCCAGCAATAAGCCTGCCATTGTG
15 GAGGCTGGTGGGATGCAGGCCCTGGGCAAGCACCTGACCAGCAACAGCCCCCGCTGGTGCAGAACTGCCTGTGG
ACCTGCGCAACCTCTCAGATGTGGCCACCAGGCAGGAGGGCCTGGAG

SEQ ID NO:393

>GL1_34_HIGH_2_G3F1 Direction: N/A

20 GNCGGTGGCAGCGGTGGCTCCAGTGCTGTCTGTCGTACCATGCAGAATACCAGCGACCTGGACACAGCCCGCTGC
ACCACCAGCATCCTGCACAACCTCCCCACCACCGGGAGGGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCT
GCTCTGGTCCGCATGCTCAGCTCCCTGNTGGAGTCGGTCCTGTTCTATGCCATCACCACGCTGCACAACCTGCT
CCTGTACCAGGAGGGCGCCAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGGCCCTGCTCAACAA
GAACAACCCCAAGTTCTGGCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCT
25 GATCATCCTGGCCAATGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTATGAAAAGCTGCTCTG
GACCACCAGTCGTGTGCTCAAGGTGCTATCCGTGTGTCCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGAT
GCAGGCCCTGGGCAAGCACCTGACCAGCAACAGCCCCCGCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCT
CTCAGATGTGGCCACCAAGCAGGAGGGCCTGGAGAGTGTGCTGAAGATTCTGGTGAATCAGCTGAGTGTGGATGA
CGTCAACGTCTCTACCTGTGCCACGGGCACACTCTCCAACCTGACATGCAACAACAGCAAGAACAAGACGCTGGT
30 GACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCTGCGTGTGGTGAACAAGGACGACATCACGGAGCC
TGCCGTCTGCGCTCTGCGCCACCTCACTAGCCGNCACCCTGAGGNCGAGAACGGCCTGGCCCCAGTAACGGGCC
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SEQ ID NO:394

>GL1_34_HIGH_3_G3F1 Direction: N/A

35 GAGAGGCGCCATNGNCGGTGGCAGCGGTGGCTCCAGTGCTGTCTGTCGTACCATGCAGAATACCAGCGACCTGGA
CACAGCCCGCTGCACCACCAGCATCCTGCACAACCTCTCCACCACCGGGAGGGGCTGCTCGCCATCTTCAAGTC
GGGTGGCATCCCTGCTCTGGTCCGCATGCTCAGCTCCCTGATGGAGTCGGTCCTGTTCTATGCCATCACCACG
TGACAACCTGCTCCTGTACCAGGAGGGCGCCAAGATGGCCGTGCGCCTGGCCGACGGGCTGCAAAAGATGGTGC
40 CCCTGCTCAACAAGAACAACCCCAAGTTCCCTGGCCATCACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACC
AGGAGAGCAAGCTGATCATCCTGGCCAATGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTATG
AAAAGCTGCTCTGGACCACAGTCGTGTGCTCAAGGTGCTATCCGTGTGTCCCAGCAATAAGCCTGCCATTGTGG
AGGCTGGTGGGATGCAGGCCCTGGGCAAGCACCTGACCAGCAACAGCCCCCGCTGGTGCAGAACTGCCTGTGGA
CCCTGCGCAACCTCTCAGATGTGGCCACCAAGCAGGAGGGCCTGGAGAGTGTGCTGAAGATTCTGGTGAATCAGC
TGAGTGTGGATGACGTCAACGTCTCTACCTGTGCCACGGGCACACTCTCCAACCTGACATGCAACAACAGCAAGA
45 ACAAGACGCTGGTGACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGTGTGGTGACAAGGACG
ACATCACGGAGCCTGCCGTCTGCGCTCTGNGCCANCTCATTAGCCGCCACCCTGAGGGCGAGATGGNCCAGAACT
CTGTGCGTCNCAACTATGGCATCCCA

SEQ ID NO:395

>GL3_1.36_A3_M13F Direction: N/A

50 TGGTGGTCCAGAGCAGCTTTTTATAACTGTAGTTACGCATGATCTGCACGAGGGCCTGGGGCCCACCATTGGCCA
GGATGATCAGCTTGCTCTCCTGGTTGCCGTAGGCCAGGAGCTGNAGGCAGTCGGTGGTGTATGGCCANGAACTGG
GGTTGTNCTTGTGAGCAGGGGCACCATTTTTGTCAGCCCGTCGGCCAGGCGCACGGCCATCTTGGCGCCCTCCT
GGTACAGGAGCAGGTTGTGCAGCGTGGTGTATGGCATAGAACAGGACCGACTCCACAGGGGAGCTGATCATGCGGA
55 CCAGAGCAGGGATGCCACCCGACTTGAAGATGGCGAGCAGCCCCCTCCCGGTGGTGGGAGAGGTTGTGCAGGATGC
TGGTGGTGCAGCGGGCTGTGTCCAGGTCTGTTGATTCTGCATGGTACGCACGACAGCGGCCACCAGCTGGGGCG
AGCCCATCANGGCCCGNCGCGACGCCTCCTTGTTTCGACAGCTGGTCCACAATCATGGCCGNCTTGGTACCAACCA
CCGGGTCTCTCG

TGGTGGTCCAGAGCAGCTTTTATAACTGTAGTTACGCATGATCTGCACGAGGGCCTGGGGCCCACCATTTGGCCA
GGATGATCAGCTTGCTCTCTCGTTGCCGTAGGCCAGGAGCTGCAGGCAGTCGGTGGTGATGGCCAGGAACCTTGG

GGTTGTTCTTGTGAGCAGGGGCACCATCTTTTGCAGCCCGTCGGCCAGGCGCACGGCCATCTTGGCGCCCTCCT
GGTACAGGAGCAGGTTGTGTCAGCGTGGTGTATGATGGCATAGAACAGGACCGACTCCACAGGGGAGCTGAGCATGCGGA
CCAGAGCAGGGATGCCACCCGACTTGAAGATGGCGAGCAGCCCCCTCCCGGTGGTGGGAGAGGTTGTGTCAGGATGC
TGGTGGTGCAGCGGGCTGTGTCCAGGTCGCTGGTATTCTGTCATGGTACGCACGACAGCGGCCACCAGCTGGGGCG
5 AGCCCATCAGGGGCCGCGCGACGCCCTCCTTGTTCGACAGCTGGTTTCAATCATGGCCGCTTTGGTCACCAC
CACCGGGTCTCGTCGTTGAGCAGTTTGGTTAAGCTCGGGCAGGCGCGAGTGGCCAGCTCGGCATCGTCCTGGT
AGTTGATGAGATGCACAA

SEQ ID NO:401

>GL1_34_HIGHPLKS_1 Direction: N/A

CANGAGAGCAAGCTGATCATCTTGGCCAATGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACTACAGTTAT
GAAAAGCTGCTCTGGACCACCAGTCGTGTGCTCAAGGTGCTATCCGTGTGTCCAGCAATAAGCCTGCCATTGTG
GAGGCTGGTGGGATGCAGGCCCTGGGCAAGCACCTGACCAGCAACAGCCCCGACCTGGTGCAGAACTGCCTGTG
15 GACCCCTGCGCAACCTCTCAGATGTGGCCACCAGGCAGGAGGGCCTGGAGAGTGTGCTGAAGATTCTGGTGAATCA
GCTGAGTGTGGATGACGTCAACGTCTCACCTGTGCCACGGGCACACTCTCCAACCTGACATGCAACAACAGCAA
GAACAAGACGCTGGTGACACAGAACAGCGGTGTGGAGGCTCTCATGCCATCCTGCGTGTGGTGACAAGGA
CGACATCACGGAGCCTGCCGTCTGCGCTCTGCCACCTCACTAGCCGCCACCCTGAGGCCGAGATGGCCAGAA
CTCTGTGCGTCTCAACTATGGCATCCAGCCATCGTGAAGCTGCTCAACCAGCCCAACCAGTGGCCACTGGTCAA
20 GGCAACCATCGGCTTGATCAGGAATCTGGCCCTGTGCCCCAGCCCAACCATGCCCGCTGCAGGAGGCAGNGGTC
ATCCCCGCTCGTCCAACCTGCTGGTGAANGCCACCAGGATGCCCAGNGCCACGTANCTGCAGGCNCACCGCAGC

SEQ ID NO:402

>GL1_34_HIGHPLKS_2 Direction: N/A

CCCTGNATAATACNTTAGTGTGGATGACGTCAANGTCCTCINNCTGCTGCCACGGGGACACTCTCCAACCTGACAT
25 GCAACAACAGCAAGAACAAGACGCTGGTGACACAGAACAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGAT
GCTGGTGACAAGGACGACATCACGGAGCCTGCCGTCTGCGCTCTGCGCCACCTCACTAGCCGCCACCCTGAGGCC
GAGATGGCCAGAACTCTGTGCGTCTCAACTATGGCATCCAGCCATCGTGAAGCTGCTCAACCAGCCCAACCAG
TGGCCACTGGTCAAGGCAACCATCGGCTTGATCAGGAATCTGGCCCTGTGCCCAGCCAACCATGCCCGCTGCAG
30 GAGGCAGCGGTATCCCCGCTCGTCCAACCTGCTGGTGAAGGCCACCAGGATGCCAGCGCCACGTAGCTGCA
GGCACACAGCAGCCCTACACGGATGGTGTGAGGATGGAGGAGATTGTGGAGGGCTGCACCGGAGCACTGCACATC
CTCGCCCGGGACCCCATGAACCGCATGGAGATCTTCCGGCTCAACACCATTCCCCTGTTTGTGAGCTCCTGTAC
TCGTGCGTGGAGAACATCCAGCGGTGGCTGCCGGGGTGTGTGTGAGCTGGCCAGGACAAGGAGGCGGTGAC
GCCATTGATGCGAGGGGCCCTCGGCCCACTCATGGAGTTGCTGCACTCCCGCAACGAGGGCACTGCCACCTAC
35 GCTGCTGCCCGTCTGTTCCGCATCTCCGANGACAANAACCCAGACTACCGGAANCGCGTGTCCGTGGAGCTCAC
CAACTCCCTTCTTCANGCATGAACCCGGCTGCC

SEQ ID NO:403

>GL1_34_HIGHPLKS_3 Direction: N/A

GCACACTGNACTGATCNGGTATCTGGCCCNNTGCCAGCCAACCATGCCCGCTGCAGGAGGCAGCGGATCATCC
40 CCCGCTCGCTCCAACCTGCTGGTGAAGGCCACCAGGATGCCAGCGCCACGCTAGCTGCAGGCACACAGCAGCC
CTACACGGATGGTGTGAGGATGGAGGAGATTGTGGAGGGCTGCACCGGAGCACTGCACATCCTCGCCCGGGACCC
CATGAACCGCATGGAGATCTTCCGGCTCAACACCATTCCCCTGNTTTGTGAGCTCCTGTACTCGTCGGTGGAGA
ACATCCAGCGCTGGCTGCCGGGGTGTGTGTGAGCTGGCCAGGACAAGGAGGCGGCCGACGCCATTGATGCAG
45 AGGGGGCCTCGGCCCCACTCATGGAGTTGCTGCACTCCCGCAACGAGGGCACTGCCACCTACGCTGCTGCCGTCC
TGTTCCGCATCTCCGAGGACAAGAACCAGACTACCGGAAGCGCGTGTCCGTGGAGCTCACCAACTCCCTCTTCA
AGCATGACCCGGCTGCCCTGGGAGGCTGCCAGAGCATGATTCCCATCAATGAGCCCTATGGAGATGACTNGGATG
CCACCTACCGCCCCATGTACTCCAGCGATGTGCCCTTGAACCCGCTGGAGATGCACATGGACATGGATGGAGAC
TACCCCATCGACACCTACAGNGANGGCCCTCAGGCCCGGTACCCCACTGNAGACCACATGCTGNNCTACGCGGCC
TGGCCCCAGTACGNNCCCTCTTTGAGGCTTTTCTCTCTCTAGAAACCTCCTTCTGTTGGAGGCCCTCNCAA
50 AACCCANCAGNACAACCCACCACAGNGGTTACATAGATAAAGCGNCCGNTCGACTANTCTGAGGTCTGATACTCA
CTGACTGTCNTACACAGTGAACCTATAAANTAAAA

SEQ ID NO:404

>GL1_34_HIGHPLKS_4 Direction: sense

AACCTNTGAATGNCAGCCCTTTGTGTGAGCTGGCCCAAGGACAAGGCAGGCGGCCGACGCCATTGATGCANAGGG
55 GGCCTCGGCCCCACTCATGGAGTTGTGCACTCCCGCAACGAGGGCACTGCCACCTACGCTGCTGCCGTCTGTT
CCGCATCTCCGAGGACAAGAACCAGACTACCGGAAGCGCGTGTCCGTGGAGCTCACCAACTCCCTCTTCAAGCA
TGACCCGGCTGCCCTGGGAGGCTGCCAGAGCATGATTCCCATCAATGAGCCCTATGGAGATGACTTGGATGCCAC
CTACCGCCCCATGTACTCCAGCGATGTGCCCTTGACCCGCTGGAGATGCACATGGACATGGATGGAGACTACCC

CATCGACACCTACAGCGACGGCCTCAGGCCCCCGTACCCCACTGCAGACCACATGCTGGCCTAGGCGGCCTGGCC
CCAGTACGGCCCCCTCTTTGCAGGCTTTTCTCTCTCTAGAACCTCCTTCTGTTGGAGGCCCT

SEQ ID NO:405

>GL1_34_HIGH_1_G3R1 Direction: N/A

AGGGCCTCCAACAGAAGGAGGTTCTAGAGAGGAGGAAAAGCCTGCAAAGAGGGGGCCGTACTGGGGCCAGGCCGC
CTAGGCCANCATGTGCTCTGCAGTGGGGTACGGGGGCCCTGAGGCCGTGCTGTAGGTGTGATGGGGTAGTCTCC
ATCCATGTCCATGTGCATCTCCAGNNGGTCAAGGGGCACATCGCTGGAGTACATGGGGCGGTAGGTGGCATCCAA
GTCATCTCCATAGGGCTCATTGATGGGAATC

SEQ ID NO:406

>gi|4504810|ref|NM_002230.1| Homo sapiens junction plakoglobin (JUP),
transcript variant 1, mRNA

CGCCAGAGTCCGGAGCAGCCGCGCCGACCGAGCTCAGTTCGCTGTCCGCGCCGGTCCCCACCC
CGGCCCGACCCCGACCCGGCCCGGTACAGGCCCATACTCAGTAGCCACGATGGAGGTGATGAACCTGATG
GAGCAGCCTATCAAGGTGACTGAGTGGCAGCAGACATACCTACGACTCGGGTATCCACTCGGGCGCCA
ACACCTGCGTGCCTCCGTCCGTGAGCAGCAAGGGCATCATGGAGGAGGATGAGGCCTGCGGGCGCCAGTACAC
GCTCAAGAAAACCACCACTTACACCCAGGGGGTGCCTCCAGCCAAGGTGACCTGGAGTACCAGATGTCC
ACAACAGCCAGGGCCAAACGGGTGCGGGAGGCCATGTGCCCTGGTGTGTCAGGCGAGGACAGCTCGCTTC
TGCTGGCCACCCAGGTGGAGGGGAGGCCACCAACCTGCAGCGACTGGCCGAGCCGTCCCAGCTGCTCAA
GTCGGCCATTGTGCATCTCATCAACTACCAGGACGATGCCGAGCTGGCCACTCGCGCCCTGCCCCGAGCTC
ACCAAACCTGCTCAACGACGAGGACCCGGTGGTGGTGACCAAGGCGGCCATGATTGTGAACCAAGCTGTCTGA
AGAAGGAGGCGTTCGCGCGGGGCCCTGATGGGCTCGCCCCAGCTGGTGGCCGCTGTCGTGCGTACCATGCA
GAATACCAGCGACCTGGACACAGCCCGCTGCACCAACAGCATCCTGCACAACCTCTCCACCCAGGGAG
GGGTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTCAGCTCCCCGTGTGGAGT
CGGTCTGTCTTCTATGCCATCACACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCCAAGATGGCCGT
GCGCCTGGCCGACGGGCTGCAAAAGATGGTGGCCCTGCTCAACAAGAACAACCCCAAGTTCTTGCCATC
ACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACCAGGAGAGCAAGCTGATCATCCTGGCCAATGGTG
GGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTATGAAAAGCTGCTCTGGACCACCAAGTCTGT
GCTCAAGGTGCTATCCGTGTGTCCAGCAATAAGCCTGCCATTGTGGAGGCTGGTGGGATGCAGGCCCTG
GGCAAGCACCTGACCAGCAACAGCCCCCGCCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCTCTCAG
ATGTGGCCACCAAGCAGGAGGGCCTGGAGAGTGTGCTGAAGATTCTGGTGAATCAGCTGAGTGTGGATGA
CGTCAACGTCCTCACCTGTGCCACGGGCACACTCCCAACCTGACATGCAACAACAGCAAGAACAAGACG
CTGGTGACACAGAAGCAGCGGTGTGGAGGCTCTCATCCATGCCATCCTGCGTGTGGTGAACAAGGACGACA
TCACGGAGCCTGCCGTCTGCGCTCTGCGCCACCTCACTAGCCGCCACCCTGAGGCGGAGATGGCCAGAA
CTCTGTGCGTCTCAACTATGGCATCCAGCCATCGTGAAGCTGCTCAACCAGCCCAACCAAGTGGCCACTG
GTCAAGGCAACCATCGGCTTGATCAGGAATCTGGCCCTGTGCCAGCCAACCATGCCCCGCTGCAGGAGG
CAGCGGTCTATCCCCCGCCTCGTCCAACCTGCTGGTGAAGGCCACCAGGATGCCAGCGCCACGTAGCTGC
AGGCACACAGCAGCCCTACACGGATGGTGTGAGGATGGAGGAGATTGTGGAGGGCTGCACCGGAGCACTG
CACATCCTCGCCCGGGACCCCATGAACCGCATGGAGATCTTCCGGCTCAACACCATTCCCCTGTTTGTG
AGCTCCTGTACTCGTCCGTGGAGAATCCAGCGCGTGGCTGCCGGGGTGTGCTGTGTGAGCTGGCCAGGA
CAAGGAGGCGGCCGACGCCATTGATGCAGAGGGGGCTCGGCCCACTCATGGAGTTGCTGCACTCCCGC
AACGAGGGCACTGCCACCTACGCTGCTGCCCTCTGCTTCCGCTCTCCGAGGACAAGAACCAGACTACC
GGAAGCGCGTGTCCGTGGAGCTCACCAACTCCCTCTTCAAGCATGACCCGGCTGCCTGGGAGGCTGCCCA
GAGCATGATTCCCATCAATGAGCCCTATGGAGATGACATGGATGCCACCTACCGCCCCATGTACTCCAGC
GATGTGCCCTTGACCCGCTGGAGATGCACATGGACATGGATGGAGACTACCCCATCGACACCTACAGCG
ACGGCCTCAGGCCCCCGTACCCCACTGCAGACCACATGCTGGCCTAGGCGGCCTGGCCCCAGTGACGGCC
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ACCTGCGCTCCTTTTTTGGGGGGATCCTTTGCTGCTGAGCTTCCCCAAGCACGGTGTGCCCTGGCCTGCC
TTCTTCTTGTGCTTTTGGTGGGGATGGGGAGGCCATTCTCTGCTGGCCCTTCTGGGGGTGGTGGGCAGG
TGACACGGAGTGGCTTGAGCTTCTGGGGATGCAGGTCCACCGAGCCCTGACCCCTGTCTGTCCCCGCTC
CCCTAACAGGTGCGGTTCCCTCATCTGAGAGGCTCTCCGTGCAGGCGATGGGGCAAGACAGAAAAGTGCTT
GAGCTGGGGGAAGCCGGGGTGTAACTTCTGCTGCACCTGCGCCTCCAGAGGTCTCCGTAGGGTCTTTT
TTGGGATAGTGTCTGCTCCTGCTTTTCTGCTCTGGGCATGGGTCCAGGGCCTGACACCCCTCCCCGCC
CCTGTGGCCCTGGCCACTAAAGCTTCAGACTCAAGTACCCATTCTGTTTTCCCCCAGCAACGCCCCCTCCA
AACCTCCAGCCTCCCTGTCTCCAGCTGCCTGGGCCCCGAAGGGCTTTGGTTCTTCTCTGGGTCTGATTT
TCTACTGAACTCCACCGACCAACTGCCCTAAGCCCCAGGGCCTCCAGGGCCAGGTTGAGACCCAAA
CCCCAAAATCCAAAATTTCTTTGAAAAGTTACGGGACCGTCCAGGGGAGATGGGGAGGAGATAGGAG
TGAGTCACCTGCTCCAGAAGATGCCAGCTTCTCTCCAGGGTGTAGTTGGCTTTGCCCCACCCCTCAC
TCCCCAGGGAGCTCCGGGGACAGCTTCTCACACCCCTGTCCACCCACACAGCTGCCCTAGCTGACCCC
GAGAAGTGCTCTTGGCTGACCCCTCTGGTGTGTGGTGAAGGGCTTTCTCTTCCCTTCTCTGTTTCAGACC

CCCCATTTCCTCCGCACATGGTGTGGGGGGCTGGGGGAGGTCCAAGCAGAGTGTATTTATTATTATCGCTTT
ATGTTTTTGGTTATTGGTTTTTTTGTATAGACCAAAGCAAAGAAAATAAAAATAACACAG

SEQ ID NO:407

5 >gi|4504811|ref|NP_002221.1| junction plakoglobin, isoform 1; gamma-catenin
[Homo sapiens]
MEVMNLMEQPIKVTEWQOTYTYDSGIHSGANTCVPSVSSKGIMEEDEACGRQYTLKKTTTYTQGVPPSQG
DLEYQMSTTARAKRVREAMCPGVSGEDSSLLLATQVEGQATNLQRLAEPSSLKSAIVHLINYQDDAELA
10 TRALPELTCLLNDEDPVVVTKAAMIVNQLSKKEASRRALMGSPQLVAAVVRTMQNTSDLDRTARCTTSILH
NLSHREGLLAIFKSGGIPALVRMLSSPVESVLFYAITTLHNLLLYQEGAKMAVRLADGLQKMPVLLNKN
NPKFLAITTDCLQLLAYGNQESKLIILANGGPQALVQIMRNYSYEKLLWTTSRVLKVLVSVCPSPNKAIVE
AGGMQALGKHLTSNSPRLVQNCILWTLRNLSDVATKQEGLESVLKILVNQLSVDDVNVLTCTATGTLNLTCT
NNSKNKTLVTQNSGVEALIHAILRAGDKDDITEPAVCALRHLSRHPAEMAQNSVRLNYGIPAIVKLLN
QPNQWPLVKATIGLIRNLALCPANHAPLQEAAPVIRLVQLLVKAHQDAQRHVAAGTQQPYTDGVRMEIIV
15 EGCTGALHILARDPMNRMEIFRLNTIPLFVQLLYSSVENIQRVAAGVLCELAQDKEADAIDAEGASAPL
MELLHSRNEGATATYAAAVLFRISEDKNPDYRKRVSVELTNSLFKHDPAAWEAAQSMIPINEPYGDDMDAT
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SEQ ID NO:408

20 >gi|12056467|ref|NM_021991.1| Homo sapiens junction plakoglobin (JUP),
transcript variant 2, mRNA
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CGGCCCGACCCCGACCCGGCCCGGTGAGGCCCATACTCAGTAGCCACGATGGAGGTGATGAACCTGATG
GAGCAGCCTATCAAGGTGACTGAGTGGCAGCAGACATACCTACGACTCGGGTATCCACTCGGGCGCCA
25 ACACCTGCGTGCCCTCCGTGAGCAGCAAGGGCATCATGGAGGAGGATGAGGCCTGCGGGCGCCAGTACAC
GCTCAAGAAAACCACTTACACCCAGGGGGTCCCCCAGCCAAGGTGACCTGGAGTACCAGATGTCC
ACAACAGCCAGGGCCAACCGGGTGCAGGAGGCTGTCCTGGTGTGTCAGGCGAGGACAGCTCGCTTC
TGCTGGCCACCCAGGTGGAGGGGAGGCCACCAACCTGACGCGACTGGCCGAGCCGTCCAGCTGCTCAA
GTCGCCCATTTGTGCATCTCATCACTACCAGGACGATGCCGAGCTGGCCACTCGCGCCCTGCCCGAGCTC
30 ACCAACTGCTCAACGACGAGGACCCGGTGGTGGTGACCAAGGCGGCCATGATTGTGAACAGCTGTGCA
AGAAGGAGGCGTCCGCGCGGGCCCTGATGGGCTCGCCCCAGCTGGTGGCCGCTGTCGTGCGTACCATGCA
GAATACCAGCGACCTGGACACAGCCCGCTGCACCACCAGCATCCTGCACAACCTCTCCACCACCGGGAG
GGGCTGCTCGCCATCTTCAAGTCGGGTGGCATCCCTGCTCTGGTCCGCATGCTCAGCTCCCCCTGTGGAGT
CGGCTCCTGTTCTATGCCATCACCACGCTGCACAACCTGCTCCTGTACCAGGAGGGCGCCAAGATGGCCGT
35 CGCCTGGCCGACGGGTGCAAAAGATGGTGGCCCCCTGCTCAACAAGAACCAACCCCAAGTTCTGGCCATC
ACCACCGACTGCCTGCAGCTCCTGGCCTACGGCAACAGGAGAGCAAGCTGATCATCCTGGCCAATGGTG
GGCCCCAGGCCCTCGTGCAGATCATGCGTAACCTACAGTTATGAAAAGCTGCTCTGGACCAACGATGCTGT
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GGCAAGCACCTGACCAGCAACAGCCCCCGCCTGGTGCAGAACTGCCTGTGGACCCTGCGCAACCTCTCAG
40 ATGTGGCCACCAAGCAGGAGGGCCTGGAGAGTGTGCTGAAGATTCTGGTGAATCAGCTGAGTGTGGATGA
CGTCAACGTCTCACCTGTGCCACGGGCACACTCTCAACCTGACATGCAACAACAGCAAGAACAAGACG
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TCACGGAGCGTGCCTGCGCTCTGCGCCACCTCACTAGCCGCCACCCTGAGGCCGAGATGGCCCCAGAA
CTCTGTGCGTCTCAACTATGGCATCCAGCCATCGTGAAGCTGCTCAACCAGCCCAACCAAGTGGCCACTG
45 GTCAAGGCAACCATCGGCTTGATCAGGAATCTGGCCCTGTGCCAGCCAACCATGCCCCGCTGCAGGAGG
CAGCGGTCTATCCCCCGCCTCGTCCAACCTGCTGGTGAAGGCCACCAGGATGCCAGCGCCACGTAGCTGC
AGGCACACAGCAGCCCTACACGGATGGTGTGAGGATGGAGGAGATTGTGGAGGGCTGCACCGGAGCACTG
CACATCCTCGCCCGGGACCCCATGAACCGCATGGAGATCTCCGGCTCAACACCATTCCCCTGTTTGTGTC
AGCTCCTGTACTCGTCCGGTGGAGAACATCCAGCGCGTGGCTGCCGGGGTGTGCTGTGTGAGCTGGCCAGGA
50 CAAGGAGGCGGGCCGACGCCATTGATGCAGAGGGGGCCTCGGCCCACTCATGGAGTTGCTGCACTCCCGC
AACGAGGGCACTGCCACCTACGCTGCTGCCGTCTGTTCCGCATCTCCGAGGACAAGAACCAGACTACC
GGAAGCGCGTGTCCGTGGAGCTACCAACTCCCTCTTCAAGCATGACCCGGCTGCCTGGGAGGCTGCCCA
GAGCATGATTCCCATCAATGAGCCCTATGGAGATGATGGACCTACCGCCCCATGTAATCCAGC
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55 ACGGCCTCAGGCCCCCGTACCCCACTGCAGACCACATGCTGGCCTAGGCGGCTGGCCCCAGTGGCGGTT
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AAAGCTTCAGACTCAAGTACCCATTCTGTTTTCCCCCAGCAACGCCCTCCAAACCTCCAGCCTCCCTGT
60 CTCCAGCTGCCTGGGCCCCGGAAGGGCTTTGGTTCTTCTCTGGGTCTGATTTTCTCACTGAACTCCACCG
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TCTCTTGAAGTTTCAGGGACCGTCCAGGGGAGATGGGGAGGAGATATGGAGTGAGTCACCTGCTCCAGA
AGATGCCAGCTTCTCTCTCCAGGGTGCTTAGTTGGCTTTGCCACCCCTCACTCCCCAGGGAGCTCCGGG
GACAGCTTCTCACACCCCTGTCCACCCACACAGCTGCCCTAGCTGACCCCGAGAAGTGCTCTTGGCTG
ACCCCTCTGGTGTGTGGTGAGGGGCTTTCTCTCCCTTCTCTGTTTTCAGACCCCCCATTTCCCGCACAT
5 GGTGTGGGGGGCTGGGGGAGGTCCAAGCAGAGTGTTTTATTATTATCGCTTTATGTTTTTGGTTATTGGT
TTTTTTGTATAGACCAAAGCAAAGAAAATAAAAATAACACAG

SEQ ID NO:409

>gi|12056468|ref|NP_068831.1| junction plakoglobin, isoform 1; gamma-
catenin [Homo sapiens]
MEVMNLMEQPIKVTEWQQTYTYDSGIHSGANTCVPSVSSKGIMEEDEACGRQYTLKKTTTYTQGVPPSQG
DLEYQMSTTARAKRVREAMCPGVSGEDSSLLLATQVEGQATNLQRLAEPQLKSAIVHLINYQDDAELA
TRALPELTKLNDPVPVVTKAAMIVNQLSKKEASRRALMGSPQLVAAVVRTMQNTSDLD TARCTTSILH
NL SHHREGLLAIFKSGGIPALVRMLSSPVESVLFYAITTLHNLLLYQEGAKMAVRLADGLQKMPVLLNKN
15 NPKFLAITTDCLQLLAYGNQESKLIILANGGPQALVQIMRNYSYKLLWTTSRVLKVL SVCP SNKPAIVE
AGGMQALGKHLTSNSPRLVQNCLWTLRNLSDVATKQEGLESVLKILVNQLSVDDVNVLT CATGTLSNLTC
NNSKNKTLVTQNSGVEALIHAILRAGDKDDITEPAVCALRHLSRHPEAEMAQNSVRLNYGIPAIVKLLN
QPNQWPLVKATIGLIRNLALCPANHAPLQEA AVIPRLVQLLVKAHQDAQRHVAAGTQQPYTDGVRMEEIV
EGCTGALHILARDPMNRMEIFRLNTIPLFVQLLYSSVENIQRVAAGVLC ELAQDKEAADAIDAEGASAPL
20 MELLHSRNEGATYAAAVLFRISEDKNPDYRKRVSVELTNSL FKHPAAWEAAQSMIP INEPYGDDMDAT
YRPMYSSDVP LDPLEMHMDMDGDYPIDTYS DGLRPPYPTADHMLA

SEQ ID NO:410

Plasminogen activator inhibitor 1 (SERPINE1; PAI-1)

>GL3_6E_1_M13F Direction: N/A

AGGCANGNTACAAGTGTGATGGCAATGTGACTGGAACAGAAATAGTTTCTATCCAGGCACATCAATAAGCTCCCT
GTAATGCCCCGTAGATTCCATCCTGCAAAAGTGGCCCTCAGTTGGCGACACCCACGTGTCTGCATGATCCCCGCA
GTTGTGTGCTACGCACGTAGGACGAGCGTTGGAATGCAAGGTTGCCCANATCGGTCCCGCANGGCTTCACCGTC
TGTTTTGGATGACCTATCTAAGGGGAAGTTTCGTGCTTCTAAACGATTCTTCTTCTCCAAAGGGTCTCAAGGGT
30 CGGTAGACTATGGGAGCGATTTTGACCTTAAAAGGTTTNCCTTCCCAAGNGAGAGAAGGGCCCAACGGGAGTCCT
TGGGACGAAGCGAGGGAGTCCTGTGCTTTTACTCAACATCTGTCTTAATCAATAGAGTGNCAAGATGCTCTATCG
TGCTTTCCCTTCAGAGAAAGTGAGGTTCAATTGTAACAGCATAAC

SEQ ID NO:411

>GL3_37G_PCR_G3F1 Direction: N/A

TCGGAGTTTCTTCTTTCCCGATGCATCTCCAGTTTTGTCCCAGATGAAGGCGTCTTTCCCAAGGGTCAGGGGTTT
CATCACTTGGCCCATGAAAAGGACTGTTCCGTGTGGGGTGTGCCGGAACAACAAGAGGAAGGGTCTGTCCATGA
TGATCTCCTCGGGGGCCATGCGGGCTGAGACTATGACAGCTGTGGATGAGGAGGCCACCGTGCCACTCTCGTTCA
CCTCGATCTTCACTTTCTGCAGCGCCTGCGCGACGTGAGAGGCTCTTGGTCTGAAAGACTCGTGAAGTCAGCCTG
40 AAACGTGTCTGAACATGTCGGTCAATCCAGGTTCTCTAGGGGCTTCTGAGGTCGACTTCAGTCTCAGGGAGAA
CTTGGGCAGAACAGGAGGCGGGGCAGCCTGGTCATGTTGCCTTTCCAGTGGCTGATGAGCTGGGCACTCAGAAT
GTTGGTGAGGGCAGAGAGAGGCACCTCTTTTTCATAAGGGGCAGCAATGAACATGCTGAGGGTGTCCCGTGTA
GGCAGTTCCAGGATGTCGTATAATGGCCATCGGGCGTGGTGAAC

SEQ ID NO:412

>GL3_6E_1_M13R Direction: anti-sense

GACACACACAAAAGGTATGATCAGCAACTTGCTTGGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGCTGGT
GAATGCCCTCTACTTCAACGGCCAGTGAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCGCTCTTCCACAA
ATCAGACGGCAGCACTGTCTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAGTTACACAGCC
50 CGATGGCCATTACTACGACATCCTGGAAC TGCCCTACCACGGGGACACCCCTCAGCATGTTTATTGCTGCCCCCTTA
TGAAAAAGAGGTGCCCTCTCTTGCCCTACCAACATTCTGAGTGCCAGCTCCATCAAGCCACTGGAAAGGCAAC
ATGACCAGGGGC

SEQ ID NO:413

>GL3_6E_2_M13F Direction: anti-sense

GACACACACAAAAGGTATGATCAGCAACTTGCTTGGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGCTGGT
GAATGCCCTCTACTTCAACGGCCAGTGAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCGCTCTTCCACAA
ATCAGACGGCAGCACTGTCTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAGTTACACAGCC
CGATGGCCATTACTACGACATCCTGGAAC TGCCCTACCACGGGGACACCCCTCAGCATGTTTATTGCTGCCCCCTTA
60 TGAAAAAGAGGTGCCCTCTCTTGCCCTACCAACATTCTGAGTGCCAGCTCATCAGCCACTGGAAAGGCAACAT

GACCAGGCTGCCCCGCTCTGGTTCTGCCCAAGTTCTCCCTGGGAGACTGAAGTCGACCTCAGGAAGCCCCCTAGA
GAACCTGGGAATGACCGACATGTTTCAGACTCGTTTCAGGCTGACTTCACGAGTCTTTTCAGACCAAGAGCCTCTCC
ACGTGCGCGCAGGCCTGAG

5 SEQ ID NO:414

>GL3_6E_3_M13F Direction: anti-sense

10 GACACACACAAAAGGTATGATCAGCAACTTGCTTGGGAAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGCTGGT
GAATGCCCTCTACTTCAACGGCCAGTGAAGACTCCCTTCCCCGACTCCAGCACCCACCGCCGCTCTTCCACAA
ATCAGACGGCAGCACTGTCTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAGGTTACCACGCG
CCGATGGCCATTACTACGACATCCCTGGAAGTGCCTACCACGGGGACACCCTCAGCATGTTTCATTGCTGCCCCCT
T

SEQ ID NO:415

>GL3_36B_PCR_G3F1 Direction: N/A

15 AGGCAGTACAAGTGTGATGGCAATGTGACTGGAACAGAAATAGTTTCTACCAGGCACACAAAAGCTCCTGTAAGC
CCCGTAGTTCCATCCTGCAAAGGGCCTCAGTGGGAACCAAGTCTTGGCAACCCATGGGCAGAGAGACGGGTGGAAG
CAGGTGCCCCAGATGGTCCCGCAGGCGTCACCGTCTGGTTTGGAGACCTTAAGGGAGTTGTGCTTCAAACCTTCTC
TCCCAGGGGTCTCAGGTGGAGACTAGGGAGTTTGACCTAAAGGTCCCTCCAAGGAGAGGCCAAGGTCTTGGAGACA
20 GATCTGGTTTACCATCTTTTAACAAAAGGCAAATGTCTTCTCTTCCCTTCAGAAAAGAGTCATTAACACTAAAATTC
TTTCTTTCGGAGTTTCTTCTTCCCGATGCATCTCCAGTTTGTGCCAGATGAAGGCGTCTTTCCTCCAGGGGTCA
GGGTTCCATCACTTGGCCCATGAAAAGGACTGTTCTGTGGGGTTGTGCCGACCACAAAGAGG

SEQ ID NO:416

>GL3_6E_2_M13R Direction: sense

25 AGGCAGTACAAGTGTGATGGCAATGTGACTGGAACAGAAATAGTTTCTACCAGGCACACAAAAGCTCCTGTAAGC
CCCGTAGTTCCATCCTGCAAAGGGCCTCAGTGGGAACCAAGTCTGCAGACCCGAGTGGGCAGAGAGACGGGTGG
AAGCAGGTGCCCCAGATGGTCCCGCAGGCGTCACCGTCTGGTTTGGAGACCTTAAGGGAGTTGTGCTTCAAACCTT
CTCTCCCAGGGTCTCAGGTGGAGACTAGGGAGTTTGACCTAAAGGTCCCTCCAAGGAGAGGCCAAGGTCTTGGAGA
30 CAGATCTGGTTTACCATCTTTTAACAAAAGGCAAATGTCTTCTCTTCCCTTCAGAAAGAGTCATTAACACTAAAAT
TCTTTTCTTCGGAGTTTCTTCTTCCCGATGCATCTCCAGTTTGT

SEQ ID NO:417

>GL3_6E_3_M13R Direction: sense

35 CAGCTGGANCGAGCTCGGATCACTTANTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTCTCTCGGCATGGACGA
GCTGTACAAGGAGGAGGCGCCAAGGCCGTTGGCAGCGGTGGCTCCAGTGTGCTGGGTTCTTGCGGAGGCAGTACA
AGTGTGATGGCAATGTGACTGGAACAGAAATAGTTTCTACCAGGCACACAAAAGCTCCTGTAAGCCCCGTAGTTCT
CATCTGCAAAAGGGCCTCAGTGGGAACCAAGTCTGCAGACCCGAGTGGGCAGAGAGACGGGTGGAAGCAGGTGC
CCCAGATGGTCCCGCAGGCGTCACCGTCTGGTTTGGAGACCTTAAGGGAGTTGTGCTTCAAACCTTCTCTCCCAGG
40 GTCTCAGGTGGAGACTAGGGAGTTTGACCTAAAGGTCCCTCCAAGGAGAGGCCAAGGTCTTGGAGACAGATCTGGT
TTACCATCTTTTAACAAAAGGCAAATGTCTTCTCTTCCCTTCAGAAAGAGTCATTAACACTAAAATTCCTTTCT

SEQ ID NO:418

>GL3_6E_PCR_G3F1 Direction: N/A

45 AGGCAGTACAAGTGTGATGGCAATGTGACTGGAACAGAAATAGTTTCTACCAGGCACACAAAAGCTCCTGTAAGC
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GCAGGTGCCCCAGATGGTCCCGCAGGCGTCACCGTCTGGTTTGGAGACCTTAAGGGAGTTGTGCTTCAAACCTTCT
CTCCCAGGGTCTCAGGTGGAGACTAGGGAGTTTGACCTAAAGGTCCCTCCAAGGAGAGGCCAAGGTCTTGGAGACA
GATCTGGTTTACCATCTTTTAACAAAAGGCAAATGTCTTCTCTTCCCTTCAGAAAGAGTCATTAACACTAAAATTC
50 TTTTCTTCGGAGTTTCTTCTTCCCGATGCATCTCCCGTTTGTGCCAGATAAGGCGTCTTTCCTCCAGGGTCAAGG
GTTTCCATCACTTGGCCCATGAAAAGGACTGTTCTCT

SEQ ID NO:419

>gi|10835158|ref|NM_000602.1| Homo sapiens serine (or cysteine) proteinase
inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member
55 1 (SERPINE1), mRNA

GAATTCCTGCAGCTCAGCAGCCGCCGCGCCAGAGCAGGACGAACCGCCAATCGCAAGGCACCTCTGAGA
TCAGGATGCAGATGTCTCCAGCCCTCAGCTGCCTAGTCTGGGCTGGCCCTTGTCTTTGGTGAAGGGTCT
TGCTGTGCACCATCCCCATCCTACGTGGCCCCACCTGGCCTCAGACTTCGGGGTGAGGGTGTTCAGCAG
60 GTGGCGCAGGCCTCCAAGGACCGCAACGTGGTTTCTCACCTATGGGGTGGCCTCGGTGTTGGCCATGC
TCCAGCTGACAACAGGAGGAGAAACCCAGCAGCAGATTCAAGCAGCTATGGGATTCAAGATTGATGACAA

GGGCATGGCCCCCGCCCTCCGGCATCTGTACAAGGAGCTCATGGGGCCATGGAACAAGGATGAGATCAGC
 ACCACAGACGCGATCTTCGTCCAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCCCACTTCTTCAGGC
 TGTTCGGGAGCACGGTCAAGCAAGTGGACTTTTCAGAGGTGGAGAGAGCCAGATTTCATCATCAATGACTG
 5 GGTGAAGACACACACAAAAGGTATGATCAGCAACTTGCTTGGGAAAGGAGCCGTGGACCAGCTGACACGG
 CTGGTGTCTGGTGAATGCCCTCTACTTCAACGGCCAGTGGAAGACTCCCTTCCCCGACTCCAGCACCACCC
 GCCGCTCTTCCACAAATCAGACGGCAGCACTGTCTCTGTGCCCATGATGGCTCAGACCAACAAGTTCAA
 CTATACTGAGTTACACGCCCCGATGGCCATTACTACGACATCCTGGAACCTGCCCTACCACGGGGACACC
 CTCAGCATGTTTACTGTGCCCCCTTATGAAAAAGAGGTGCCTCTCTCTGCCCTCACCAACATTCTGAGTG
 10 CCCAGCTCATCAGCCACTGGAAGGCAACATGACCAGGCTGCCCCGCTCCTGGTTCTGCCCAAGTTCTC
 CCTGGAGACTGAAGTCGAGCTCAGGAAGCCCCCTAGAGAACCTGGGAATGACCGACATGTTTCAGACAGTTT
 CAGGCTGACTTACAGAGTCTTTTCAGACCAAGAGCCTCTCCACGTCGCGCAGGCGCTGCAGAAAGTGAAGA
 TCGAGGTGAACGAGAGTGGCAGGCTGGCCTCCTCATCCACAGCTGTCTAGTCTCAGCCCCGATGGCCCC
 CGAGGAGATCATCATGGACAGACCCCTTCTCTTTGTGGTCCGGCACAACCCACAGGAACAGTCTTTTC
 15 ATGGGCCAAGTGATGGAACCCCTGACCCTGGGGAAAGACGCCTTCATCTGGGACAAAACCTGGAGATGCATC
 GGGAAAGAAGAACTCCGAAGAAAAGAATTTTAGTGTTAATGACTCTTTCTGAAGGAAGAGAAGACATTT
 GCCTTTTGTAAAGATGGTAAACCAGATCTGTCTCCAAGACCTTGGCCTCTCCTTGGAGGACCTTTAGG
 TCAAACTCCCTAGTCTCCACCTGAGACCCCTGGGAGAGAAGTTTGAAGCACAACCTCCCTTAAGGTCTCCAA
 ACCAGACGGTGACGCCCTGCGGGACCATCTGGGGCACCTGCTTCCACCCGCTCTCTCTGCCCACTCGGGTCT
 20 GCAGACCTGGTTCCCACTGAGGCCCTTTCAGGATGGAACCTACGGGGCTTACAGGAGCTTTTGTGTGCCT
 GGTAGAAACTATTTCTGTTCCAGTCAACATTGCCATCACTCTGTACTGCCTGCCACCGCGGAGGAGCTG
 GTGACAGGCCAAAGGCCAGTGAAGAAACACCCTTTTCATCTCAGAGTCCACTGTGGCACTGGCCACCCCT
 CCCAGTACAGGGGTGCTGCAGGTGGCAGAGTGAATGTCCCCCATCATGTGGCCCAACTCTCCTGGCCTG
 GCCATCTCCCTCCCAGAAACAGTGTGCATGGGTTATTTTGGAGTGTAGGTGACTTGTTTACTCATTGAA
 25 GCAGATTTCTGCTTCTTTTATTTTATAGGAATAGAGGAAGAAATGTCAGATGCGTGCCCAGCTCTTCA
 CCCCCAATCTCTTGGTGGGGAGGGGTGTACCTAAATATTTATCATATCCTTGGCCTTGAGTGCTTGTTA
 GAGAGAAAGAGAACTACTAAGGAAAATAATATTTAAACTCGCTCCTAGTGTTCCTTTGTGGTCTGTG
 TCACCGTATCTCAGGAAGTCCAGCCACTTGACTGGCACACACCCCTCCGGACATCCAGCGTGACGGAGCC
 30 CACACTGCCACCTTGTGGCCGCTGAGACCTCGCGCCCCCGCGCCCCCGCGCCCCCTCTTTTCCCTT
 TGATGGAATTGACCATAACAATTTTCATCTCCTTCAGGGGATCAAAAGGACGGAGTGGGGGGACAGAGAC
 TCAGATGAGGACAGAGTGGTTTCCAATGTGTTCAATAGATTTAGGAGCAGAAATGCAAGGGGCTGCATGA
 CCTACCAGGACAGAACTTTCCCCAATTACAGGGTGAATCAGCCGATTTGGTGACTCACTTCAATGTGT
 CATTTCCGGCTGCTGTGTGTGAGCAGTGGACACGTGAGGGGGGGTGGGTGAGAGAGACAGGCAGCTCGG
 35 ATTCAACTACCTTAGATAATATTTCTGAAAACCTACCAGCCAGAGGGTAGGGCACAAGATGGATGTAAT
 GCACTTTGGGAGGCCAAGCGGGAGGATTGCTTGAAGCCAGGAGTTCAAGACCAGCCTGGGCAACATAACC
 AAGACCCCGTCTCTTTAAAAATATATATATTTTAAATATACTTAAATATATATTTCTAATATCTTTAA
 TATATATATATATTTAAAGACCAATTTATGGGAGAATTGCACACAGATGTGAAATGAATGTAATCTAAT
 AGAAGC

SEQ ID NO:420

40 >gi|10835159|ref|NP_000593.1| serine (or cysteine) proteinase inhibitor,
 clade E (nexin, plasminogen activator inhibitor type 1), member 1;
 plasminogen activator inhibitor, type I [Homo sapiens]
 MQMSPALTCLVLGLALVFEGLSAVHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPPYGVASVLAMLQ
 45 LTTGGETQQQIQAMGFKIDDKGMAPALRHLKELMGPWNKDEISTTDAIFVQORDLKLQGFMPHFRLF
 RSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNLALYFNGQWKTPFPDSSTHRR
 LFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYDILELPYHGDLSMFIAAPYEKEVPLSALTNILSAQ
 LISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKE
 VNESGTVASSSTAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP

50 SEQ ID NO:421

Proteosomal subunit Y>

ACACTGCCCTCCTTCTTGAGGGTCCCAGCCTGCGATGATGATTCCCGCCATCAGGTCTTCCCGGTATCGGTAACA
 CATCTCCTTAAAGAGACTGGCTGCTGTGTGGACCAGTGGAGGCTCATTCAAGTTCAATGCTGTGGAAACCGAGCTG
 GTAGGTGACAGCATCAGCTACTGCCTGGGTATCAGCAGCTGAGCCTGAGCGACAGCAGAAAATGCGGTGCTGAAT
 55 AGGTGTCAGCTTGTGAGTCACTCGATTGGCGATGTAGGACCCAGTGGTTGTTCTGGAGTCCGCCCCCAGAACCAC
 GCCCCCGTCAAACCTGCACGGCCATGATAGTGGTCCCAGTGGAACTTCTCGGCTTTCCAGTCTGGAGTGAACGC
 CTCCGGCCCCCAAGCCGGTGTGGCCCGGCTCCCCGAGCAGCTAGTAAGGTAG

SEQ ID NO:422

Rap2B

>GL3_37F_1_M13F Direction: N/A

5 CGAAGTCTTCGATGGTTCGGGTCGTAATCTCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTAATCTCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
CCACGCCGCCCGAGCCAGCACCACTTTGTACTCTCTCATGGCTCCGTCAGCGCTCTCGCCGCGCCTGCCGC
GGCCCCGTCGGGGCTGCGCGCGGGAAAGGCTGGGCTTGCGGGCTGGACTTCTCTTCCCTTCTCAGCTACGCA
GGAAAAACCCAGGAGAGAGCAACCCAGAGAACGCAGGGCGGAAACACCGAAACGGAAGGCGGGCGCCAGGCC
10 GGCCCCGCGCGCCGCGGGCAAGGCGNTAATCCCTGGGGGCTAGCACGGGGTCCCGGGGGCCACGGAAGGCAAGG
TCACCGGNAGGCAGGCAAGGACANGACAGCCCCNGNGGACGGGCAGAAAACCCGGGAANGAGGGGACAAATTGG
CCCACGGCAAGCCTTTGGCGNCACGNGAAGAAAAACACAAGGGCAACAAGGGGGNGTTAACGNCATTAAGGAA
TAACACAGCGCGGAGCCGAGAG

SEQ ID NO:423

15 >GL3_37F_4_M13F Direction: anti-sense

CGCAGCTGCGGGCATTGTCTCTCGGTTTCGCCGCCCGGGCTGCTGCTGCCGCCCGGACTGCTGCGGGGCCCGGA
CCCGCACCCAGGGATACGCTGCCGCCGTCGCCGCCCGGGCCCGGCTCCGTTTCGGTGGTTTCCGCCCTG
CGTTCTCTGGGTTGCTCTCTCTCGGTTTCTTCTGCGTAGCTGAGGAAGGGGAAGAGAAGTCCAGCCGCCAAGCC
20 CAGCCTTCCCGGCGCAGCCCCGACGGGGCGCCCGGACAGGCGCGGGCGGAGAAGCGCTGACGGAGCCATGAGGA
GAGTACACAAGTGGTGGTGCTAGGGCTCGAGGCAGGAGTGGGGCAAAGTCCGCGAGCTTCAACCGTGGCAAGATA
CGGTTGGAACACGGGGCATCTTCAATCGNAGAAAAGGTACGAACCCGAACNCATCGAAAGAACTTTTTTAACCGG
CCAAGGNAGNAATGGAGAGTGGGACCTCAGGNTACGNCCCCGTCGCCGGANGCTTGGAAGAATCC

SEQ ID NO:424

25 >GL3_37F_2_M13R Direction: sense

CGAAGTCTTCGATGGTTCGGGTCGTAATCTCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTAATCTCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
GCCCANAGACCGGACCGAGCCAGACACACCACTATATGTACTCATCTCAATGGCATCCGNCAGAGCTCATCG
30 NCCGACAGACCTGCCGNNGGACCCCGATACAGGGGGGCATTGCGAGCGCGNGGAAAAGGGCATNGGGGNCATAGG
ACAGGGACAATAGGGAACAGNTATCATCATTACACACATATCGCATCAAAGCNATACGCAAAGGGAACAAAN
AACGCCCAAGAGAAGAAAGAGGCAAAACCCCCAAGGAANNGAAAACAACAGGGCCAACAAGAGGGGACCGGGGAG
GAAAAAAA

SEQ ID NO:425

35 >GL3_37F_3_M13F Direction: N/A

CGAAGTCTTCGATGGTTCGGGTCGTAATCTCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTAATCTCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
CCACGCCGCCCGAGCCAGCACCACTTTGTACTCTCTCATGGCTCCGTCAGCGCTCTCGCCGCGCCTGCCGC
40 GGCCCCGTCGGGGCTGCGCGCGGGGAAGGCTGGGCTTGCGAGCTGGACTTCTCTTCCCTTCTCAGCTACGCA
GGAAAAACCCAGGAGAGAGCAACCCAGAGAACGCAGGGCGGAAACACCGAACGAGGCGGGCGCGGGCCGT
CCGGCCGACGANGGCAGTGCAGGGGCGAACCAGAGAGGAACAAATGCCCGAGAGGCCCTTGCGGCCGAAAAA

SEQ ID NO:426

45 >GL3_37F_4_M13R Direction: sense

CGAAGTCTTCGATGGTTCGGGTCGTAATCTCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTAATCTCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
CCACGCCGCCCGAGCCAGCACCACTTTGTACTCTCTCATGGCTCCGTCAGCGCTCTCGCCGCGCCTGCCGN
GGCCCCGTCGGGGCTGCGCGCGGGGAAGGCTGGGCTTGCGGGCTGGACTTCTCTTCCCTTCTCAGNTACGAG
50 GAAAAACCCAGGAGAGAGCAACCCAGGAGAACGCAGGGCGGAAAGCACGCGGAACGGAGTGCAGGGCGCGGGC
CGCCCCG

SEQ ID NO:427

55 >GL3_37F_PCR_G3F1 Direction: sense

CGAAGTCTTCGATGGTTCGGGTCGTAATCTCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
AAAAGTCTTCGATGGTTCGGGTCGTAATCTCCAGGATCTCCAGCACCGACGGCGACGAGTCCACCTCAATCTCCTTGCGGT
CCACGCCGCCCGAGCCAGCACCACTTTGTACTCTCTCATGGCTCCGTCAGCGCTCTCGCCGCGCCTGCCGC
GGCCCCGTCGGGGCTGCGCGCGGGGAAGGCTGGGCTTGCGGGCTGGACTTCTCTTCCCTTCTCAGCTACGAG
GAAAAACCCAGGAGAGAGCAACCCAGAGAACGCAGGGCGGAAACACCGAACGAGGCGGGCGCGGGCCGGCC
GGCGGCGGGCGGAGCGTATCCCTGGGGTGCGGGTCCGGGGCCCCGAGCAGTCCGCGGGCGGAGCAGCAGCCCGGG

SEO ID NO:428

GCACGTTCCGCGGGGACTCATGCCACGCGCGTCCCGGCCGACGCGCAATTAGCAGCCACCTCCGCGAGCC
CGCCGCCACCGCCTCCCTGCCCTCCCGGGCTGCCGAGCTAGGAGCTCCAGCCGTCGCCCTCGCGCAGGCT
GCGGGCATTGTCTCTCGGTTCCGCGCCCGGGCTGCTGCTGCCGCCGCGGACTGCTGCGGGGCCCGGACC
CGACCCCAGGGATACGCTGCCGCCGCCGCCGCGGCCCGGCCCTCCGTTCCGTTGGTTCCTCCGC
CCTGCGTTCTCTGGGTTCCTCTCTCTGGGTTTTTCTGCGTAGCTGAGGAAGGGGAAGAGAAGTCCAGC
CGCCAAGCCCAGCCTTCCCCGGCGCGCAGCCGCCGAGCGGGGCCGCGGAGGCGCGGCAGAGCGCTGACGG
AGCCATTGAGAGAGTACAAGATGGTGGTGCTGGGCTCGGGCGGCTGGGCAAGTCCCGCGCTACCGGTGCAG
TTCGTGACGGGCTCCTTCTCATCGAGAAGTACGACCCGACCATTGAAGACTTTTACCGCAAGGAGATTGAG
TGGACTCGTCGCCGTCGGTGCTGGAGATCCTGGATACGGCGGGCACCAGCAGTTCGCGTCCATGCGGGGA
CCTGTACATCAAGAACGGCCAGGGCTTCATCCTGGTCTACAGCCTCGTCAACCAGCAGAGCTTCCAGGAC
ATCAAGCCCATGCGGGACCAGATCATCCGCGTGAAGCGGTACGAGCGCGTGCCCATGATCCTGGTGGGCA
ACAAGGTGGACCTGGAGGGTGAGCGCGAGGTCTCGTACGGGGAGGGCAAGGCCCTGGCTGAGGAGTGGAG
CTGCCCCCTTCATGGAGACGTCGGCCAAAAACAAAGCCTCGGTAGACGAGCTATTTGCCGAGATCGTGCGG
CAGATGAACCTACGCGGGCGCAGCCCAACGGCGATGAGGGCTGCTGCTCGGCCTGCGTGATCCTCTGAGGCG
GCCACCGCGCGCCGGCGCGCTCTGCGCAACAAAGCCAAACGCATCCGACTCTCTAAATGTGATTTTATTT
CTTGCTTTGAGATTGGAGACCACCTTTGCAATTGGCCAGGGTGCTTTGGGAGCCCGGCTGCGCTCCGCGGCC
GGCGTCCCCGTGCC'TCCACCCTGTGCCGAGGGGGGTGTCCGGTCTGCCCATCCGATACCTCTGGTGGAAAT
GTGGCTCTTTGCAGCATGTACGTTTCTCCCTGATTTTGGTTGATGCATATTTCCCCGTTTAAAGTAGCCGT
TAGGGCGCAGTATCGGCAGCTTGACACCCACCAAGCAAAAGTTTCAGCCTGGAAAAAAAATGGGGGGGAA
GGGTGGATGAAAAGGAGGGAGAGAAGGTGGAAATGTTTTTTTTTTTTTTTTTCTATTTTCTTTCTTTTT
TTTTTTTTTTTTTTTTTGGTCAACAGCCGTTTTTTCTAGTTCCAAGTTTTAAATACATGGAAGGAAGTCCGG
GAGAACCATATGAAGGAGCAGGAGGAGAGGAAGAACTTTTTTTTCTTCTTTTCCAGGAGTAGCTGGAAA
TTAAGATCGGGTTCCTTTCTGCCAGCTTGGAAGGGCAACCCATGACATTTGCGATTCTGAGGATGTC
TATGCAAAAGTTGGATTCTTGTTACAGTGTATCCAATCTGAAGATTGCATATCGAATGCGACTGGGACTGTTAA
CACTGATGCGCAATACAGTGTGGGGGTGCCAGAAAGTGCTGCTGATATTTGTGG

SEO ID NO:429

MREYKVVVLGSGGVGKSALTVQFVTGSFIEKYDPTIEDFYRKEIEVDSSPSVLEILDTAGTEQFASMRDL
YIKNGQGFI¹LVYSLVNQQSFQDIKPMRDQII²RVKRYERVPMILVG³NKVDLEGEREVS⁴YGE⁵GKALAE⁶EWSC
PFMETS⁷AKNKASVDELFAEIVROMNYAAOPNGDEGCCSACVIL

40 SEQ ID NO:430

>GL3 10.20 A M13F Direction: anti-sense

CGGCAGAAAAACAGAGCCTGCCTAACCAGGCCCAGCCAGTTGGTGGGGCCAGGCCAGGACCACACAGTCCCCAGAC
45 TCAGCTGGAAGTCTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGG
ATGGGGCACGGACTGTCCACCTTTTCTGATGTGTGTTGTCTAGCCTGTGCTGTGGCATAGACATGGATGCGAGGAC
CACTTTGGGAGACTGGGGTGGCCTCAAGAGCACACAGAGAAGGGAAGAAGGGGCCATCACAGGATGCCAGCCCCCTG
CCTGGGTGGGGGCACTCAGCCACGACCAGCCCCCTTCCTGGGTATT'TATTTCTCTATTTATTGGGGATAGGAGAAG
AGGCATCCTGCTGGTGGGACAGGCCCTTCAGCCCCCTCTCCNCTCCCCGCCCTGGCCAGGGCAGGGCCACCCCA
50 CTCTACCTCCTTAGCTTTCCCTGTGCCACTTTGACTCAGAGGCTGGGAGCATAGCAGAGGGGCCAGGCCCAGGCA
GAGCTGACGGGAGGCCCCAGCTCTGAGGGGAGGGGGTCT

SEQ ID NO:431

CGGCAGCAAACAGANCTGCCTAACCCAGGACCCANCCAGTTGGTGGGGCCAGGCCAGGACCACACAGTCCCCAG
55 ACTCAGCTGGAAGTCTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGTCTTACTC
GGATGGGGCACGGACTGTCCACCTTTTCTGATGTGTGTTGTGTCAGCCTGTGCTGTGGCATAGACATGGATGCGAGG
ACCACTTTGGGAGACTGGGGTGGCCTCAAGAGCACACAGAGAAGGGAAGAAGGGGCCATCACAGGATGCCAGCCCC
TGCCCTGGGTGGGGGCACTCAGCCACGACCCAGCCCCCTTCCTGGGTATTTATTTCTCTATTTATTTGGGGATAGGAGA
AGAGGCATCTCGCTCGGTGGGACAGCCCCCTTCAGCCCCCTTCTCCNCTCCCCGACTGGCCAGGGCAGGGCCACCC
60 CACTCTACCTCCTNANATTCCCCGTGTC

SEQ ID NO:432

>GL3_9.67_B_M13F Direction: N/A

5 GCCAGTGTATTATTAGCAAGATGGAACCCAAAGGCGGCTGTGGCCTGGGCAGCAGAAGGCCACCAGGAGCCCCAC
CCATCTACCCAAGTGTCCCCCAGAGCTAATTACATCCACACCCATCCCCTGAAGTGGTGGACATAAGGGAGCCCT
GGGGAGCCTCTACCGGCCCCAGGCCTCTACCACGGACCCCTCCCCTCAGAGCTGGGGCCTCCCGTCAGCTCTGC
CTGGGCCTGGCCCCCTCTGCTATGCTCCAGCCTCTGAGTCAAAGTGGCACAGGGAAAGCTAAGGAGGTAGAGTGG
GGTGGCCCTGCCCTGGCCAGGCGGGAGGGGAGAAGGGGCTGAAGGGGCTGTCCCACCCAGGCAGGATGCCTCTT
10 CTCCTATCCCCAATAAATAGAGAATAAATACCCAGGAAGGGGCTGGTCGTGGCTGAGTGCCCCCAACCCAGGCAG
GGGCTGGCATCCTGTGATGGCCCCCTTCTTCCCTTCTCTGTGTGCTCTTGAGGCCACCCAGTCTCCAAAGTGGTC
CTCGCATCCATGTCTATGCCACAGCACAGGCTGACAACACACATCANAAAAGGTGGACAGTCCGTGCCCCATCCG
AGTAGGGCTTGCTCCCTCCCTTTGTCTGTAGATCTTGGCGGANGCTGTCCAGCAGGTANACTTCCAGCTGANTC
TGGGACTGTGTGGTCTGGCCTGGCCACCAACTGGNTGGCCTGGTTAGGCAGGTCTGTTTTCTTGC

15 SEQ ID NO:433

>GL3_9.67_B_M13R Direction: anti-sense

CGGCAGAAAACAGAGCCTGCCTAACCAGGCCAGCCAGTTGGTGGGGCCAGGCCAGGACCACACAGTCCCCAGAC
TCAGCTGGAAGTCTACCTGCTGGACAGCCTCCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGG
20 ATGGGGCACGGACTGTCCACCTTTTCTGATGTGTGTTGTGAGCCTGTGCTGTGGCATAGACATGGATGCGAGGAC
CACTTTGGAGACTGGGGTGGCCTCAAGAGCACACAGAGAAGGGAAGAAGGGGCCATCACAGGATGCCAGCCCCCTG
CCTGGGTTGGGGGCACCTCAGCCACGACCAGCCCCCTTCTGGGTATTTATTCTCTATTTATTGGGGATAGGAGAAG
AGGCATCCTGCCCTGGGTGGGACAGCCCCCTTACGCCCCCTTCTCCNCTCCCCGCTGGCCAGGGCAGGGCCACCCCA
CTCTACCTCCTTAGCTTTCCCTGTGCCACTTTGACTCAGAGGCTGGGAGCATAGCAGAGGGGGCAGGGCCAGGCA
GAGCTGACGGGAGGCCCCAGCTCTGAGGGGAGGGGTCCTGTGGTAGAGGCCCTGGGGCCGGTAGAGGCTCCCCAGG
25 GCTCCCTTATGTCCACCACTTCAGGGGATGGGTGTG

SEQ ID NO:434

>GL3_9.67_C_M13F Direction: N/A

30 GCCAGTGTATTATTAGCAAGATGGAACCCAAAGGCGGCTGTGGCCTGGGCAGCAGAAGGCCACCAGGAGCCCCAC
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GGGGAGCCTCTACCGGCCCCAGGCCTCTACCACGGACCCCTCCCCTCAGAGCTGGGGCCTCCCGTCAGCTCTGC
CTGGGCCTGGCCCCCTCTGCTATGCTCCAGCCTCTGAGTCAAAGTGGCACAGGGAAAGCTAAGGAGGTAGAGTGG
GGTGGCCCTGCCCTGGCCAGGCGGGAGGGGAGAAGGGGCTGAAGGGGCTGTCCCACCCAGGCAGGATGCCTCTT
CTCCTATCCCCAATAAATAGAGAATAAATACCCAGGAAGGGGCTGGTCGTGGCTGAGTGCCCCCAACCCAGGCAG
35 GGGCTGGCATCCTGTGATGGCCCCCTTCTTCCCTTCTCTGTGTGCTCTTGAGGNCACCCAGTCTCCAAAGTGGTC
CTCGCATCCATGTCTATGCCACAGCACAGGCTGACAACACACATCANAAAAGGTGGACAGTCCGTGCCCCATCCG
ANTAGGGCTTGCTCCCTCCCTTTGTCTGTAAATC

SEQ ID NO:435

>GL3_9.67_D_M13R Direction: sense

40 GCCAGTGTATTATTAGCAAGATGGAACCCAAAGGCGGCTGTGGCCTGGGCAGCAGAAGGCCACCAGGAGCCCCAC
CCATCTACCCAAGTGTCCCCCAGAGCTAATTACATCCACACCCATCCCCTGAAGTGGTGGACATAAGGGAGCCCT
GGGGAGCCTCTACCGGCCCCAGGCCTCTACCACGGACCCCTCCCCTCAGAGCTGGGGCCTCCCGTCAGCTCTGC
CTGGGCCTGGCCCCCTCTGCTATGCTCCAGCCTCTGAGTCAAAGTGGCACAGGGAAAGCTAANGAGGTAGAGTGG
45 GGTGGCCCTGCCCTGGCCAGGCGGGAGGGGAGAAGGGGCTGAAGGGGCTGTCCCACCCAGGCAGGATGCCTCTT
CTCCTATCCCCAATAAATAGAGAATAAATACCCAGGAAGGGGCTGGTCGTGGCTGAGTGCCCCCAACCCANGCAG
GGGCTGGCATCCTGTGATGGCCCCCTTCTTCCCTTCTCTGTGTGCTCTTGAGGCCACCCAGTCTCCAAAGTGGTC
CTCGCATCCATGTCTATGCCACAGCACAGGCTGACAACACACATCANAAAAGGTGGACAG

50 SEQ ID NO:436

>GL3_9.67_PCR_G3F1 Direction: N/A

55 GCCAGTGTATTATTAGCAAGATGGAACCCAAAGGCGGCTGTGGCCTGGGCAGCAGAAGGCCACCAGGAGCCCCAC
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GGGGAGCCTCTACCGGCCCCAGGCCTCTACCACGGACCCCTCCCCTCAGAGCTGGGGCCTCCCGTCAGCTCTGC
CTGGGCCTGGCCCCCTCTGCTATGCTCCAGCCTCTGAGTCAAAGTGGCACAGGGAAAGCTAAGGAGGTAGAGTGG
GGTGGCCCTGCCCTGGCCAGGCGGGAGGGGAGAAGGGGCTGAAGGGGCTGTCCCACCCAGGCAGGATGCCTCTT
CTCCTATCCCCAATAAATAGAGAATAAATACCCAGGAAGGGGCTGGTCGTGGCTGAGTGCCCCCAACCCAGGCAG
GGGCTGGCATCCTGTGATGGCCCCCTTCTTCCCTTCTCTGTGTGCTCTTGAGGCCACCCAGTCTCCAAAGTGGTC
CTCGCATCCATGTCTATGCCACAGCACAGGCTGACAACACACATCAGAAAAGGTGGACAGTCCGTGCCCCATCCG

AGTAGGGCTTGCTCCCTCCCTTTTGTCTGTAGATCTTGGCGGAGGCTGTCCAGCAGGTAGACTTCCAGCTGAGT
CTGGGGACTGTGTGGTCTGGCCTGGCCCCACCAACTGGCTGGGCCTGGTTAGGCAGGCTCTGTTTTCTGCCG

SEQ ID NO:437

5 >gi|1061350|gb|U38276.1|HSU38276 Human semaphorin III family homolog mRNA,
complete cds
CTGACTGGTGTCTCCCTCTCTTTTCATCTTGGGCTGTCTGCATGTGTCTCATTTCCCCACTCTCTCCTGTGC
CTCCCTCTACTCTAATAATCAGGTCCAGGTTTCTCTGTACTGGGAGAAAGACCTGTGGCTGGAGCAGGCA
10 GGGATGCACCCTATCTGTTCCCCATTCTCCAGGTGGGAGGGAGAAGGAGTAACCCACTTTATTGGCCAC
AGATGCAGGGGAGAAAGGAGAAAGCATGCTGGGAGCTGGAAAGAGCCCTAAGATCACCTGGTTTTCTAGAG
AGTGGAGCCTGCTTCTGCTAGGCCCTCCCACAATGCTTGTGCGCCGCTCTTCTTCTCTGGGCTTCCCT
ACTGACTGGGGCTGGCCATCCTTCCCTACCCAGGACCACCTCCCGGCCACGCCCCGGGTACGGCTCTCA
TTCAAAGAGCTGAAGGCCACAGGCACCGCCCACTTCTTCAACTTCTGTCTCAACACAACCGACTACCGAA
15 TCTTGCTCAAGGACGAGGACCAGCACCGCATGTACGTGGGCAGCAAGGACTACGTGCTGTCCCTGGACCT
GCACGACATCAACCGCGAGCCCTCATTATACACTGGGCAGCCTCCCCACAGCGCATCGAGGAATGCGTG
CTCTCAGGCAAGGATGTCAACGGCGAGTGTGGGAACCTTCGTCAAGGCTCATCCAGCCCTGGAACCGAACAC
ACCTGTATGTGTGCGGGACAGGTGCCTACAACCCCATGTGCACCTATGTGAACCGCGGACGCCGCGCCCA
GGATTACATCTTCTACCTGGAGCCTGAGCGACTCGAGTCAGGGAAGGGCAAGTGTCCGTACGATCCCAAG
20 CTGGACACAGCATCGGCCCTCATCAATGAGGAGCTCTATGCTGGTGTGTACATCGATTTTATGGGCACTG
ATGCAGCCATCTTCCGCACACTTGGAAAGCAGACAGCCATGCGCACGGATCAGTACAACCTCCCGGTGGCT
GAACGACCCGTCGTTTCATCCATGCTGAGCTCATTCCTGACAGTGCAGGAGAATGATGATAAGCTTTACTTC
TTCTTCCGTGAGCGGTGCGGCAGAGGCGCCGAGAGCCCGCGGTGTACGCCCGCATCGGGCGCATTTGCC
TGAACGATGACGGTGGTCACTGTTGCTGGTCAACAAGTGGAGCAATTCCTGAAGGCGCGGCTCGTCTG
25 CTCTGTCCCGGCGAGGATGGCATTGAGACTCACTTTGATGAGCTCCAGGACGTGTTTGTCCAGCAGACC
CAGGACGTGAGGAACCTGTCACTTACGCTGTCTTTACCTCCTCTGGCTCCGTGTTCCGAGGCTCTGCCG
TGTGTGTCTACTCCATGGCTGATATTGCGATGGTCTTCAACGGGCCCTTTGCCACAAAGAGGGGCCCAA
CTACAGTGGATGCCCTTCTCAGGGAAGATGCCCTACCCACGGCCGGGCACGTGCCCTGGTGGAACTTC
ACGCCATCTATGAAGTCCACCAAGGATATCTGTATGAGGTGATCAACTTCATGCGCAGCCACCCACTCA
30 TGTACCAGGCCGTGTACCTCTGCAGCGCGGCCCTGGTAGTCCGCACAGGTGCTCCCTACCGCCTTAC
CACTATTGCCGTGGACCAGGTGGATTACGCCGACGGGCGCTATGAGGTGCTTTTCTGGGCACAGACCGC
GGGACAGTGCAGAAGGTCAATTGTGCTGCCAAGGATGACCAAGAGATGGAGGAGCTCAGTGGAGGAGG
TGGAGGTCTTCAAGGATCAGCACCCGTCAAGACCATGACCATCTCTTCTAAGAGGCAACAACCTCTACGT
GGCGTCAGCCGTGGGTGTACACACACCTGAGCCTGCACCGCTGCCAGGCGTATGGGGCTGCCTGTGCTGAC
35 TGCTGCCTTGCCCGGACCCCTTACTGTGCTGGGATGGCCAGGCCTGCTCCCGCTATACAGCATCCTCCA
AGAGGCGGAGCCGCGGCAGGACGTCCGGCACGGAAACCCCATCAGGCAGTGCCGTGGGTTCAACTCCAA
TGCCAACAAGAATGCCGTGGAGTCTGTGCAATGAGCGTGGCCGGCAGCGCAGCCTTCCTTGAGTGCCAG
CCCCGCTCGCCCCAAGCCACTGTTAAGTGGCTGTTCCAGCGAGATCCTGGTGACCGGCGCGGAGAGATT
GTGCAGAGGACCGCTTCCTGCGCACAGAGCAGGCTTGTGCTCCGTGCACTGCAGCTCAGCGATCGTGG
CCTCTACTCCTGCACAGCCACTGAGAACAACTTTAAGCACGTCGTCACACGAGTGCAGCTGCATGTA
40 GGCCGGGACGCGCTCCATGCTGCCCTCTTCCACCACTGTCCATGAGCGCCCCGCCACCCCGAGCGCAG
GCCCCCAACGCTCCTTACCAGGAGTTAGCCAGCTGTGTCGCCAGCCAGAAGTGGGCCTCATCCACCA
GTACTGCCAGGGTTACTTGGCGCCATGTGCCCCCAGCCCCAGGGAGGCTCCAGGGGACCCCGGTCTCCT
GAGCCCCAGGACCAGAAAAAGCCCCGGAACCGCGGCACCACCTCCGGACACATGAGGCCAGCTGCCTG
TTCTGCCATGGGCAGCCTAGCCCTTGTCCCTTTTAAATATAAAAGACATATATATATATATATATATAT
45 ATATAAAATATCTATATCTATACACACCTGCCCTGCAAAGACAGTATTTATTGGTGGGTGGAATAT
AGCCTGCCTCAGTGGCAGCATCCTCCAAAACCTTAGACCCATGCTGGTTCAGAGACGGCAGAAAAACAGAGCC
TGCCCTAACAGGCCAGCCAGTTAGTGGGGCCAGGCCAGGACCACACAGTCCCCAGACTCAGCTGGAGTCT
ACCTGCTGGACAGGCCTTGCGCCAAGATCTACAGGACAAAGGGAGGGAGCAAGCCCTACTCGGATGGGGC
ACGGACCGTCCACCTTTCTGATGTGTGTGTGTCAGCCTGTGCTGTGGCATAGACATGGATGCGAGGACCAC
50 TTTGGAGACTGGGGTGGCCTCAAGAGCACACAGAGAAGGGGAAGAAGGGGCCATCACAGGATGCCACCCCT
GCCTTGGGTGGGGGCACTCTGCCACGACCAGCCCCCTTCTGGGTATTTATTCTCTATTTATTGGGGATA
GGAGAAGAGGCATCCTGCCTGGGTGGGACAGCCCCCTTGGGGCCCCCTTCTCCCTCCCCGCTGGCCAGGGA
GGGCCACCCCACTCTACCTCCTTAGCTTTCCCTGTGCCACTTTGACTCAGAGGCTGGGAGCATAGCAGAG
GCCAGGCCAGGACAGCTGACGGGAGGCCCCAGCTCTGAGGGGAGGGGTCCGTGGTAGAGCCTGGGGC
55 AGGTAGAGGCTCCCCAGGGCTCCCTTATGTCCACCACCTCAGGGGATGGGTGTGGATGTAATTAGCTCTG
GGGGGCAAGTTGGGTAGATGGGTGGGGCTCCTGGTGGCCTTCTGCTGCCCAGGCCACAGCCGCTTTGGG
TTCCATCTTGCTAATAAACACTGGCTTTGGAATAAAAAAAAAAAAAAAAAA

SEQ ID NO:438

60 >gi|1061351|gb|AAB18276.1| semaphorin III family homolog
MLVAGLLWASLLTGAWPSFPTQDHLPATPRVRLSFKELKATGTAHFFNFLNTTDYRILLKDEHDHDMY

VGSKDYVLSLDLHDINREPLIIHWAASPORIEECVLSGKDVNGECGNFVRLIQPNRTHLYVCGTGAYNP
MCTYVNRGRRAQDYIFYLEPERLESGKGKCPYDPKLDTASALINEELYAGVYIDFMGTDAAI FRTLGLKQT
AMRTDQYNSRWLNDPSFIHAELIPDSAENDDKLYFFFRERSAEAPQSPAVYARIGRICLNDDGGHCCLVN
KWSTFLKARLVCSVPGEDGIETHFDELQDVFVQQTQDVNRNPIYAVFTSSGVSFRGSAVCVYSMADIRMV
5 FNGPFAHKEGPNYQWMPFSGKMPYPRPGTCTPGGTFTPSMKSTKDYPDEVINFMRSHPLMYQAVYPLQRRP
LVVRTGAPYRLTTIAVDQVDSADGRYEVLFGLTDRGTQVKVIVLPKDDQEMEELMLEEVEVFKDPAPVKT
MTISSKRQQLYVASAVGVTHLSLHRCQAYGAACADCCCLARDPYCAWDGQACSRYTASSKRRSRRQDVHVG
NPIRQCRGFNSNANKNAVESVQYGVAGSAAFLECPQPRSPQATVKWLFQRDPGDRRREIRAEDRFLRTEQG
10 LLLRALQLSDRGLYSCTATENNFKHVTVRQLHVLGRDAVHAALFPPLSMSAPPPGAGPPTPPYQELAQ
LLAQPEVGLIHQYCGQYWRHVPPSPREAPGAPRSPEPQDQKKPRNRHHPDPT

SEQ ID NO:439

SPARC

>gi|4507170|ref|NM_003118.1| Homo sapiens secreted protein, acidic,
15 cysteine-rich (osteonectin) (SPARC), mRNA

CGGGAGAGCGCGCTCTGCCTGCCGCTGCCTGCCCTGAGGGTTCACAGCACCATGAGGGCCTGGA
TCTTCTTTCTCTTTGCTGCGCGGAGGGCCTTGGCAGCCCCCTCAGCAAGAAGCCCTGCTGATGAGAC
AGAGGTGGTGAAGAACTGTGGCAGAGGTGACTGAGGTATCTGTGGGAGCTAATCCTGTCCAGGTGGAA
20 GTAGGAGAATTTGATGATGGTGCAGAGGAAACCGAAGAGGAGGTGGTGGCGGAAAATCCCTGCCAGAACC
ACCACTGCAAACACGGCAAGGTGTGCGAGCTGGATGAGAACAACACCCCCATGTGCGTGTGCCAGGACCC
CACCAGCTGCCAGCCCCCATTTGGCGAGTTTGAGAAGGTGTGCGAGCAATGACAACAAGACCTTCGACTCT
TCCTGCCACTTCTTTGCCACAAAGTGCACCCTGGAGGGGCACCAAGAAGGGCCACAAGCTCCACCTGGACT
ACATCGGGCCTTGCAAATACATCCCCCTTGCTGGACTCTGAGCTGACCGAATTCCTCCCTGCGCATGCG
GGACTGGCTCAAGAAGCTCCTGGTCACCTGTATGAGAGGGATGAGGACAACAACCTTCTGACTGAGAAG
25 CAGAAGCTGCGGGTGAAGAAGATCCATGAGAATGAGAAGCGCCTGGAGGCAGGAGACCACCCGTTGGAGC
TGCTGGCCCGGACTTCGAGAAGAACTATAACATGTACATCTTCCCTGTACACTGGCAGTTTCGGCCAGCT
GGACCAGCACCCCATTTGACGGGTACCTCTCCACACCGAGCTGGCTCCACTGCGTGCTCCCTCATCCCC
ATGGAGCATTGCAACACCCGCTTTTTCGAGACCTGTGACCTGGACAATGACAAGTACATCGCCCTGGATG
AGTGGGCCGGCTGCTTCGGCATCAAGCAGAAGGATATCGACAAGGATCTTGTGATCTAAATCCACTCCTT
30 CCACAGTACCGGATCTCTCTTTAACCCTCCCCCTTCGTGTTTTCCCCCAATGTTTAAAATGTTTGGATGGT
TTGTTGTTCTGCTTGGAGACAAGGTGCTAACATAGATTTAAGTGAATACATTAACGGTGTCTAAAAATGAA
AATTCTAACCCAAAGACATGACATTCTTAGCTGTAACCTAATTAAGGCCTTTTCCACACGCATTAATA
GTCCCATTCTTCTTGGCATTGTAGCTTTGCCATTGCTTCTTATTGGCACATGGGTGGACACGGATCTG
CTGGGCTCTGCCTTAAACACACATTGCAGCTTCAACTTTTCTCTTTAGTGTTCTGTTTGAACCTAATACT
35 TACCGAGTCAGACTTTGTGTTTCAATTTCAATTTAGGGTCTTGGCTGCCTGTGGGCTTCCCGAGTGGCCTG
GAGGTGGGCAAAGGGAAGTAACAGACACACGATGTTGTCAAGGATGGTTTTGGGACTAGAGGCTCAGTGG
TGGGAGAGATCCCTGCAGAATCCACCAACCAGAACGTGGTTTTGCCTGAGGCTGTAAGTGAAGAGAAAGATT
CTGGGGCTGTCTTATGAAAATATAGACATTCTACATAAGCCAGTTTCATCACCATTCTCTCTTTTACCT
TTCACTGACGTTTCTTTTACATTAGGCTGTTGGTTCAAACTTTTGGGAGCACGGACTGTCAGTTCTCTG
40 GGAAGTGGTCAGCGCATCTTCAGGGCTTCTCCTCCTCTGTCTTTTGGAGAACCAGGGCTCTTCTCAGGG
GCTCTAGGGACTGCCAGGCTGTTTCAGCCAGGAAGGCCAAAATCAAGAGTGAGATGTAGAAAGTTGTAAA
ATAGAAAAAGTGGAGTTGGTGAATCGGTTGTTCTTTCTCACATTTGGATGATTGTCTAAGGTTTATAGG
CATGTTCTCTCTTTTCTTCAACCTCCCCCTTTGTTCTTCTATTAATCAAGAGAACTTCAAAGTTAATGGG
ATGGTTCGGATCTCACAGGCTGAGAACTCGTTACCTCCAAGCATTTTCATGAAAAAGCTGCTTCTTATTA
45 TCATACAAACTCTCACCATGATGTGAAGAGTTTCAAAATCTTTCAAATAAAAAGTAATGACTTAGAAA
CTGAAAAA

SEQ ID NO:440

>gi|4507171|ref|NP_003109.1| secreted protein, acidic, cysteine-rich
50 (osteonectin); Osteonectin (secreted protein, acidic, cysteine-rich) [Homo
sapiens]

MRWIFFLLCLAGRALAAPQOEALPDETEVVEETVAEVTESVSGANPVQVEVGEFDDGAEETEEVVAEN
PCQNHCKKHGKVCLENDNTPMCVCQDPTSCPAPIGEFEKVCSDNKTDFDSSCHFFATKCTLEGTKKHGK
LHLDYIGPCKYIPCLDSELTEFLMRDWLKNVLVTLYERDEDNNLLTEKQKLRVKKIHENEKRLEAGD
55 HPVELLARDFEKNYNMYIFPVHWQFGQLDQHPIDGYLSHTELAPLRAPLIPMEHCTTRFFETCDLNDKY
IALDEWAGCFGIKQDKIDKDLVI

SEQ ID NO:441

ssDNA binding protein-1

>GL1_4_1_G3F1 Direction: sense

CTGGCAGACCCTGGCCCAATCCTAACAGTGCTAACTCAATTCCATACTCCTCCTCATCACCTGGCTACCTATGTG
GGACCCCTGGNTGGTGGCGGTCTCTCAGGAACACCCATTATGCCAGTCCCGCAGATTCAACAAATTCCAGTGA
CAACATCTACACAATGATTAATCCAGTGCCGCCTGGAGGCAGCCGGTCCAACCTCCCGATGGGTCCCGGCTCGAA
CGGTCCGATGGGCGGCATGGGTGGCATGGAGCCACACCACATGAATGGATCATTAGGGTCAGGCGACATAGACGG
NCTTCCAAAAAATTCTCTAACAACATAAGTGGCATTAGCAATCCTCCAGGCACCCCTCGAGATGACGGCGAG

SEQ ID NO:442

>GL1_4_1_G3R1 Direction: anti-sense

CTCGCCGTCATCTCGAGGGGTGCCTGGAGGATTGCTAATGCCACTTATGTTGTTAGGAGAATTTTTTGGAAAGTCC
GTCTATGTGCGCTGACCCTAATGATCCATTTCATGTGGTGTGGCTCCATGCCACCCATGCCGCCCATCGGACCGTT
CGAGCCGGGACCCATCGGGAAGTTGGACCGGTGCCTCCAGGCGGCACTGGATTAATCATTTGTGTAGATGTTGTC
ACTGGAATTTGTTGAATCTGCGGGACTGGGCATAATGGGTGTTCTTGGAGGACCGCCACCACCAGGGGGTCCCAC
ATAGGTACCAGGTGATGAGGAGGAGTATGGAATTGAGTTAGCACTGTTAGGATTGGGCCAGGGTCTGCCAG

SEQ ID NO:443

>GL1_4_2_G3F1 Direction: sense

CTGGCAGACCCTGGCCCAATCCTAACAGTGCTAACTCAATTCCATACTCCTCCTCATCACCTGGTACCTATGTGG
GACCCCTGGCTGGTGGCGGTCTCTCAGGAACACCCATTATGCCAGTCCCGCAGATTCAACAAATTCCAGTGAC
AACATCTACACAATGATTAATCCAGTGCCGCCTGGAGGCAGCCGGTCCAACCTCCCGATGGGTCCCGGCTCGAAC
GGTCCGATGGGCGGCATGGGTGGCATGGAGCCACACCACATGAATGGATCATTAGGGTCAGGCGACATAGACGGA
CTTCCAAAAAATTCTCCTAACAACATAAGTGGCATTAGCAATCCTCCAGGCACCCCTCGAGATGACGGCGAG

SEQ ID NO:444

>GL1_4_2_G3R1 Direction: anti-sense

CTCGNCGATCATCTCNAGGGGTGCCTGTAAGGATNGCATAAGTGCCACTTATGTTGTTNAGGAGAATTTTTTGGAA
GTCCGTCTATGTGCGCTGACCCTAATGATCCATTTCATGTGGTGTGGCTCCATGCCACCCATGCCGCCCATCGGAC
CGTTTCGAGCCGGGACCCATCGGGAAGTTGGACCGGTGCCTCCAGGCGGCACTGGATTAATCATTTGTGTAGATGT
TGTCAGTGAATTTGTTGAATCTGCGGGACTGGGCATAATGGGTGTTCTTGGAGGACCGCCACCACCAGGGGGTTC
CCACATAGGTACCAGGTGATGAGGAGGAGTATGGAATTGAGTTAGCACTGTTAGGATTGGGCCAGGGTCTGCCAG

SEQ ID NO:445

>gi|21314683|ref|NM_018070.2| Homo sapiens single stranded DNA binding
protein 3 (SSBP3), mRNA

CCGCGCCCGGGGCTGACGCTTTGACAGCTGGAAAGAGCGCGGAGCCAGCGCCTGGGGGGGAGGGAGGGGA
GCGCGGCGAGGAGAGCGCCAGCGAGCGAGAGCGAGCGAGCGCGGGGAGGGGGCCGGGAGCGAGGGGC
AGCTCGGGAGAGCCGGAGCGGTAGCGGCGGCGGCGGCGGCGGCGGCGAGGCTCGGCGCCCTCTTCCCTGC
AAACCATGTTTGGCAAAGGCAAAGGCTCGGCGGTGCCCTCGGATGGGCAGGCTCGGGAAAAGTTAGCTTT
ATACGTCTACGAATATTTACTGCACGTAGGAGCACAGAAATCTGCACAGACCTTCTTATCGGAGATTCTGA
TGGGAAAAAACATCACGTTGGGAGAACCGCCTGGGTTTTTGCACCTCGTGGTGGTGTGTATTTTGGGACC
TTTACTGTGCAGCTCCTGAAAGGAGAGACACTTGTGAACATTCAAGTGAAGCAAAAGCCTTTCATGATTA
TAGTGCAGCAGCTGCCCCGAGCCCCGTGCTTGGCAACATTCCCCCAACGATGGGATGCCGGGAGGCCCC
ATCCCGCCAGGTTTCTTTTCAAGGTCTCCGGGGTACAGCCCTCGCCGCACGCACAGCCTCCACCTCACA
ATCCTAGCAGCATGATGGGACCCACAGTCAGCCTCCGGGAGGAGTTCTTGGGACACAGCCATTGCTGCC
CAATTTCTATGGATCCACACGACAACAAGGCCACCCCAACATGGGAGGATCAATGCAGAGAATGAACCCCT
CCCCGAGGCATGGGGCCCATGGGTCCCGGCCACAGAATTACGGCAGCGGCATGAGACCACCACCCAACT
CCCTCGGCCCCCGCATGCCCGGGATTAACATGGGCCCCGGGAGCTGGCAGACCCTGGCCCAATCCTAACAG
TGCTAACTCAATTCCATACTCCTCCTCATCACCTGGTACCTATGTGGGACCCCTGGTGGTGGCGGTCTCT
CCAGGAACACCCATTATGCCAGTCCCGCAGATTCAACAAATTCCAGTGACAACATCTACACAATGATTA
ATCCAGTGCCGCCTGGAGGCAGCCGGTCCAACCTCCCGATGGGTCCCGGCTCGGACGGTCCGATGGGCGG
CATGGGTGGCATGGAGCCACACCACATGAATGGATCATTAGGGTCAGGCGACATAGACGGACTTCCAAAA
AATTCTCTAACAACATAAGTGGCATTAGCAATCCTCCAGGCACCCCTCGAGATGACGGCGAGCTAGGAG
GGAATCTTCTCCACTCCTTTTCAAGACGAATTATTTCTCAAGCATGACGATGAGTGTGTGATCCCCCTT
TCTCCGAGACGCTGAGAGAGCAGGCATTGTCAGGCGGGAAGATGCCAGAAATTATGCAAGAAGTGAGGTGT
CATTATCCAGGAGCTGGTGGGGAGGGCATCTCCCTGCTCCCCCTCAACCCCTCCACCCCATCCAGGCC
CCTACCTTTTCCCAATTTTAGTTTCATGCAATAAAAAGGCCAAACTTTTTATTCCATAAAACAAAAA
AAAAAAAAAAAAAAAAAAAAA

SEQ ID NO:446

>gi|21314684|ref|NP_060540.2| single stranded DNA binding protein 3;
sequence-specific single-stranded-DNA-binding protein [Homo sapiens]
MFAKGKGSAPVSDGQAREKLALYVVEYLLHVGAQKSAQTFLSEIRWEKNITLGEPPGFLHSWVCVFDLY
CAAPERDRTCEHSSEAKAFHDYSAAAAPSPVLGNIPPNDGMPGGPIPPGFFQGGPPGSQPSPHAQPPPHNP
SSMMGPHSQPPGGVPGTQPLLPNSMDPTRQQGHPNMGGSMQRMNPPRGMGPMGPGPQNYGSGMRPPPNLS
GPAMPGINMGPAGRPWPNPNSANSIPYSSSSPGTYVGPGGGGPPGTPIMPSPADSTNSSDNIYTMINP
VPPGGSRSNFPMPGPGSDGPMGGMGMEPHHMGSLGSGDIDGLPKNSPNNISGLSNPPGTPRDDGELGGN
FLHSFQNDNYSPTSMTMSV

SEQ ID NO:447

SUMO-specific protease-1 (SUSP-1)

>G3_1_41_PCR_G3F1 Direction: sense

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GTATAGCCCCGTCTGAACGTGGGAGCGCAGCCCGCTGACGGCTGAGCCCGAGGCCCGCAACCCTGCGGCGTCTA
CCCTCCTCCGGCGCGGCCCTCATCCCGCGAGCACGGCGCGGTGTGGGCCATGGATTAAGAAGGAGGCGGCGT
GGGAGGAGGAAGATGGCGGCCGGAAGAGCGCGGTAGCGCAGGGGAGATTACTTTTCTGGAAGCTTTGGCTAGA
TCAGAGTCTAAGAGAGATGGAGCCGCGAGAACCAGCACAGTGGTTAGATGATAAGCGGCCGCTCGACTAGTTCT

SEQ ID NO:448

>GL3_1.41_A_M13F Direction: sense

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TGGCCTGCCTTTGTATAGGCCGTCTGAACGTGGGAGCGCAGCCCGCTGACGGCTGAGCCCGAGGCCCGCAACC
CTGCGGCGTCTACCTCCTCCGGCGCGGCCCTCATCCCGCGAGCACGGCGGCGGTGTGGGCCATGGATTAAGA
AGGAGGCGGCTGGGAGGAGGAAGATGGCGGCCGGAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAA
GCTTTGGCTAGATCAGAGTCTAAGAGAGATGGAGCCGCGCANAACCAGCACAGTGGTTAGATAGATAAAGCGGCCGC
TCGACTAGTCTGAGGTCTGATACTCACTGACTGTGTCGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTG
GATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTTGTGAAATTGTTATCCGCTCAC
AATCCACACAACA

SEQ ID NO:449

>GL3_1.41_A_M13R Direction: anti-sense

ATCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTACGACAGTCAGTGAGTATCAGACCTCAGACTAGTC
GAGCGGCCGCTTTATCTATCTAACCAC'TGTGCTGGTTCTGCGGCTCCATCTCTCTTAGACTCTGATCTAGCCAAA
GCTTCCAGAAAAGTAATCTCCCTGCGCTACCGCCGCTCTTGCCGGCCGCCATCTTCTCCTCCCACGCCGCCCTC
CTTCTTAATCCATGGCCACACCGCCGCCGTGCTCGCCGGGATGAGGGGCCGCGCCGAGGAGGGTAGACGCCGC
AGGGTTGCGGGCCTCGGGCTCAGCCGTCAGGCGGGCTGCGCCGAGTCCACGTTTCAGACGGGCCATACAAAGGCAGGC
CAGGCGCGCCCGGCCCTGTCCGCGGGCTGGCGGGCAGCGAGGCCCGCGGCCCGAGCTTCTCAGGCCTCTCCGGGG
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CC

SEQ ID NO:450

>GL3_1.41_B_M13F Direction: sense

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TGGCCTGCCTTTGTATAGGCCCGTCTGAACGTGGGAGCGCAGCCCGCTGACGGCTGAGCCCGAGGCCCGCAACC
CTGCGGCGTCTACCTCCTCCGGCGCGGCCCTCATCCCGCGAGCACGGCGGCGGTGTGGGCCATGGATTAAGA
AGGAGGCGGCGTGGGAGGAGGAAGATGGCGGCCGGAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAA
GCTTTGGCTAGATCAGAGTCTAAGAGAGATGGAGCCGCGAGAACCAGCACAGTGGTTAGATAGATAAAGCGGCCGC
TCGACTAGTCTGAGGTCTGATACTCACTGACTGTGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTGG
ATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTTGTGAAATTGTNATCCGCTCACAA
TTCCACACAACATACGAGCCGGAAGCAT

SEQ ID NO:451

>GL3_1.41_B_M13R Direction: anti-sense

CGGATCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTTCGACAGTCAGTGAGTATCAGACCTCAGACTAG
TCGAGCGGCCGCTTTATCTATCTAACCAC'TGTGCTGGTTCTGCGGCTCCATCTCTCTTAGACTCTGATCTAGCCA
AAGCTTCCAGAAAAGTAATCTCCCTGCGCTACCGCCGCTCTTGCCGGCCGCCATCTTCTCCTCCCACGCCGCC

TCCTTCTTAATCCATGGCCACACCGCCGCGTGCCTCGCCGGGATGAGGGGCCGCGCCGGAGGAGGGTAGACGCC
GCAGGGTTGCGGGCTCGGGCTCAGCCGTCAGGCGGGCTGCGCTCCACGTTTACAGACGGGCCTATACAAAGGCAG
GCCAGGCGCGCCCGGGCTGTCCGCGGGCTGGCGGGCAGCGAGGCCCGCGGCCGAGCTTCTCAGGCCTCTCCGG
GGGAACGCGACCGGCGACGACGACGACGCGCTTCCCGGGCCCGGTTCTCTCGGCCACGACTCCCCATCCACC
GCCC

SEQ ID NO:452

>GL3_1.41_C_M13F Direction: sense

GGGCGGTGGATGGGGAGTCTGTGGGCCGAGAGGAACCGGGCCCGGAAGCGCCGTCGTCGTCGTCGCGGTGCGGT
TCCCCCGGAGAGGCCTGAGAAGCTCGGGCCGCGGGCCTCGCTGCCCGCCAGCCCGCGGACAGGCCCGGGCGCGCC
TGGCCTGCCTTTGTATAGGCCCGTCTGAACGTGGGAGCGCAGCCCGCCTGACGGCTGAGCCCGAGGCCCGCAACC
CTGCGGCGTCTACCTCTCTCCGGCGCGGCCCTCATCCCGCGAGCACGGCGGCGGTGTGGGCCATGGATTAAGA
AGGAGGCGGCGTGGGAGGAGGAAGATGGCGGCCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAA
GCTTTGGCTAGATCAGAGTCTAAGAGAGATGGAGCCGCAAGACGACAGTGGTTAGATAGATAAAGCGGCCGC
TCGACTAGTCTGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTG
GATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCC

SEQ ID NO:453

>GL3_1.41_C_M13R Direction: anti-sense

GCTCGGATCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTACGACAGTCAGTGAGTATCAGACCTCAGA
CTAGTCGAGCGGCCGCTTTATCTATCTAACCCTGTGCTGGTTCTGCGGCTCCATCTCTCTTAGACTCTGATCTA
GCCAAAGCTTCCAGAAAAGTAATCTCCCTGCGCTACCGCCGCTCTTGCCGGCCGCCATCTTCTCTCTCCACGC
CGCTCTCTTCTAATCCATGGCCACACCGCCCGGTGCTCGCCGGGATGAGGGGCCGCGCCGGAGGAGGGTAGA
CGCCGAGGGTTGCGGGCCTCGGGCTCAGCCGTCAGGCGGGCTGCGCTCCACGTTTACAGCGGCCCTATACAAAG
GCAGGCCAGGCGCGCCCGGGCCTGTCCGCGGGCTGGCGGGCAGCGAGGCCCGCGGCCGAGCTTCTCAGGCCTCT
CCGGGGGAACGCGACCGGCGACGACGACGACGCGCTTCCCGGGCCCGGTTCTCTCGGCCACGACTCCCCATC
CACCGCCC

SEQ ID NO:454

>GL3_1.41_D_M13F Direction: sense

GGGCGGTGGATGGGGAGTCTGTGGGCCGAGAGGAACCGGGCCCGGAAGCGCCGTCGTCGTCGTCGCGGTGCGGT
TCCCCCGGAGAGGCCTGAGAAGCTCGGGCCGCGGGCCTCGCTGCCCGCCAGCCCGCGGACAGGCCCGGGCGCGCC
TGGCCTGCCTTTGTATAGGCCCGTCTGAACGTGGGAGCGCAGCCCGCCTGACGGCTGAGCCCGAGGCCCGCAACC
CTGCGCGCTCTACCTCTCTCCGGCGCGGCCCTCATCCCGCGAGCACGGCGGCGGTGTGGGCCATGGATTAAGA
AGGAGGCGGCGTGGGAGGAGGAAGATGGCGGCCGCGCCGCGGTAGCGCAGGGGAGATTACTTTTCTGGAA
GCTTTGGCTAGATCAGAGTCTAAGAGAGATGGAGCCGCAAGACGACAGTGGTTAGATAGATAAAGCGGCCGC
TCGACTAGTCTGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGTG
GATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCG

SEQ ID NO:455

>GL3_1.41_D_M13R Direction: anti-sense

GATCACTAGTAACGGCCGCCAGTGTGCTGGAATTCGCCCTTACGACAGTCAGTGAGTATCAGACCTCAGACTAGT
CGAGCGGCCGCTTTATCTATCTAACCCTGTGCTGGTTCTGCGGCTCCATCTCTCTTAGACTCTGATCTAGCCAA
AGCTTCCAGAAAAGTAATCTCCCTGCGCTACCGCCGCTCTTGCCGGCCGCCATCTTCTCTCTCCACGCCGCT
CCTTCTTAATCCATGGGCCACACCGCCCGTGTCTCGCCGGATGAGGGGCCGCGCCGGAGGAGGTTTCTGGA
CAGGGTTGCGGGCCTCGGGCTCAGCCGTCAGGCGGGCTGCGCTCCACGTTTACAGCGGGCCTATACAAAGGCAGG
CCAGGCGCGCCCGGGCCTGTCCGCGGGCTGGCGGGCAGCGAGGCCCGCGGCCGAGCTTCTCAGGCCTCTCCGGG
GGAACGCGACCGGCGACGACGACGACGCGCTTCCCGGGCCCGGTTCTCTCGGCCACGACTCCCCATCCACCG
CCC

SEQ ID NO:456

>gi|7662311|ref|NM_015571.1| Homo sapiens SUMO-1-specific protease (SUSP1), mRNA

ATGGCGGCCCGCAAGAGCGGCGGTAGCGCAGGGGAGATTACTTTTCTGGAAGCTTTGGCTAGATCAGAGT
CTAAGAGAGATGGAGGTTTTTAAATAATTGGAGCTTTGATCATGAAGAAGAAAGTGAAGGAGATACAGA
TAAAGATGGGACAAATCTGCTCAGTGTGGATGAAGATGAGGATTCTGAAACCTCAAAAGGAAAAAGTTA
AATCGTCGATCTGAAATTGTTGCTAATAGCTCTGGTGAATTCATCTTGAAGACATATGTAAGACGAAACA
AGTCTGAAAGTTTTTAAACTTTGAAAGGCAACCAATTGGACTTAACATGTTGAGCAACAATAAGAAATT
GAGTGAATAATGCAAAATACGTCATTATGTTCTGGAAGTGTAGTTCATGGTAGACGTTTTTCATCATGCT
CATGCACAGATACCAGTAGTAAAAACAGCAGCCCAAAGCAGTCTGGACCGAAAAGAAAGGAAAGAATACC

5 CACCTCATGTCCAAAAAGTTGAAATTAATCCTGTAAGGTTAAGTCGGCTCCAAGGTGTTGAACGTATAAT
GAAGAAAACAGAAGAGTCCGAATCACAAGTGGAGCCTGAAATTAAGAGGAAAGTACAACAGAAACGGCAC
TG TAGTACCTATCAGCCTACTCCTCTCTATCCTGCTTCAAAAAATGTTTAACCCATTTAGAGGATT
10 TGCAAAGAAATTGCAGACAAGCTATTACTTTGAATGAGTCTACTGGACCATTATTAAGAACGTCAATTCA
TCAGAATTCTGGAGGACAGAAGTCAAAAAACAGGATTAACAACCAAGAAGTTTTATGGCAACAATGGT
GAAAAGGTTCCAATTGATATTATTGTGAATTGTGATGACAGTAAACACACTTATTTACAGACTAATGGAA
AAGTCATTTTACCTGGGGCAAAAAATACCCAAAAATCACAACCTTGAAAGAAAGGAAAACAAGTTTGTGAGA
CCTAAATGATCCAATCATTGTTGTCCAGTGATGATGATGATGACAACGACAGAACTAACAGAAGAGAAAGC
15 ATATCTCCTCAGCCTGCTGATTGAGCATGTTCTTCCCTGCACCATCCACTGGAAAAGTAGAAGCAGCAC
TAAATGAAAATACTTGAGAGCAGAGCGTGAACTACGAAGCATTCAGAAAGACTCAGAGTTAAATACAGT
TACATTGCCAAGAAAAGCAAGAATGAAAGACCAGTTTGGCAATTCTATTATCAACACACCTCTGAAACGT
CGTAAAGTGTCTTCTCAAGAACCTCCAGATGCTTTAGCTTTAAGCTGCCAAAGTTCTTTGACAGTGTCA
TTTTAACTGTGCAAGTATACGAGTAGGAACACTCTCCGGCTGTTAATAGAGCCTGTAATTTTTTGT
20 AGATTTTATCAAGATACAGCTAGACGAACCAGACCATGATCCTGTAGAGATTATATTAACCTCTGAT
CTAACTAAATGTGAATGGTGTAAATGTCCGAAAATTACCTGTAGTGTCTTCAAGCAATTCAGCAGTTT
ATCAAAAGCTGAGCATCCAATGCAATGAATAAGGAGGATAAAGTTTGAATGATTGTAAAGGAGTAAA
TAAATTAACAAATTTAGAAGAACAATATATAATTTTAAATTTTCAAAATGGCCTTGATCCTCCGGCAAT
ATGGTATTTGAAAGTATCATTAAATGAAATTGGTATAAAGAATAACATCTCCAATTTTTTTGCGAAAATTC
25 CTTTGAAGAAGCTAATGGCAGACTTGTTGCCTGTACAAGAACCCTATGAAGAGAGCATCAAAGGAAGTTG
TGGGCAAAAGGAAAACAAAATTAAGTGTATCATTTGAATCTAAAATACAACTTAGAAGCAAACAAGAA
TTTCAGTTTTTGTGATGAAGAAGAAGAACTGGAGAAAACACACCATCTTCATTGGCCCAGTAGAAAAGT
TGATAGTATATCCACCACCTCCAGCTAAGGAGGCATCTCTGTTACCAATGAGGACCTGCACGTGTCTAAA
TGAAGGAGAATTTTAAATGATGTTATTATAGACTTTTATTGAAATACTTGGTGCTTGAAAACTGAAG
AAGGAAGACGCTGACCGAATTCATATATTCAGTTCTTTTTTCTATAAACGCCCTTAATCAGAGAGAGGGA
30 GAAATCATGAAACAATACTGTCTAATACAGCAAAACGGCATGGGAGAGTAAAAACATGGACCCGGCA
CGTAGATATTTTGAAGAAGGATTTTATTTTTGTACCCCTTAATGAAGCTGCACACTGGTTTTTGGCTGTT
GTTTGTTCCTCCGGTTTGGAAAAACCAAGTATGAACCTAATCCTCATTACCATGAAAATGCTGTCATAC
AGAAATGTTCAACTGTAGAGGACAGTTGTATTTCTTCTTCAGCCAGTGAAATGGAGAGTTGTTCAAAAA
CTCTTCGCAAGCCTGTAATTAAGAAGATGCTAAACAAAAAACATTGCATAGCTGTAATTGATTCCAAT
35 CCTGGGCAGGAAGAAAGTGACCTCGTTATAAGAGAAACATATGCAGTGTAATAACAGTGTGAAAAAA
TAAATCATACTGCGAGTGAAAATGAAGAATAAGAGAGAATCTACATCCCAGAAAGTTGCTGATAG
GACTAAAAGTGAGAATGGCCTACAGAATGAAAGTTTAAAGTTCCACACATCATAAGATGGCTTAAGCAA
ATCAGACTAACTATAGCGATGAATCACCTGAAGCTGGTAAAATGCTTGAAGATGAACCTCGTCGACTTCT
CAGAAGATCAGGATAACCAGGATGATAGCAGTGACGATGGATTCTCGCTGATGACAACCTGCAGTTCCAGA
40 AATAGGACAGTGGCATTAAAGCCTACTATCTGTAAACAACCTTGATCCTACTTATGGACTCACTCCGA
GGCCCTTCTCGGTCAAATGTTGTCAAAATTTTAAAGAGAGTATTTAGAAGTGGAATGGGAAGTTAAAAAAG
GAAGCAAAAGAAGTTTTTCCAAAGATGTTATGAAGGGCTCTAATCCAAAAGTACCACAGCAAAACAACCTT
CAGTGACTGTGGTGATATGATTTGAGTATGTAGAGAGCTTTTTTGAAGATCCAATTCTCAGTTTTGAA
CTACCTATGAATTTGGCAAACTGGTTTCTCCACCAAGAATGAGAACAAAAAGAGAAGAAATCCGAAACA
45 TAATTTCTGAAGCTACAGGAAGATCAGAGCAAAAGAGAAAAGAAAGCATAAGGACACTTACTCAACAGAAGC
ACCTTTAGGCGAAGGAACAGAAACAATGTGTCAATAGTATCTCAGATTGACCATTCTGTGTTGTCATT
TCTACTTTTCAAGAACTAAATGACTTTCAAATTTGGGTATAGACAATAAAGAACTGAAGTGCTCACTACTC
AGTGATTTGGAATTTTGTATGCTGTATAAATGTGAGATAATTAATTTCCAAAGGCGTATGTATTAAGTA
AAAGTCTGTAAATATGTTAATGAGGCCAATTTTCCAGCATTTATAATTATTTTTTTCACTTGTTAGGAA
50 GCTTTTGTATGATTTTTCTGTAAATAGTACCTAAAATTGCAACTTCTAAACCCAAATAAAAAAGAAAATA
TTTATAGGAGGAAATGATTAATTTGATATTCTTTAGTGAACCTGTTTAAATTCCTCAGTGGGTGTGACATA
TTTCATGGGAATATTTCAAATATCTATGGTAATATTTTGACCCTTTATATTTGTTCTAAAATAAGTCAAAA
TGTGAAAATAATATTAATCTAAGATATTTTGAACCTAAGCATCTTTATATGCTTGTGTAAACAGGAACAAA
GTAACAGCCTTTCAATTCATATACTGCCTTGTGTTAGTGAACCCAAAGAAATGTAATAAATATTTGTAAT
55 TTTACACAAATATTTAAGAGGAAAGAGTATTAAGAGCAATTCAAAAAAGTAACCTTATACTACTAAAAA
AAAAATTTCTGCATATATTATCATCAAATGCATTTTGAAGACATCAAAGACTCAGGTTAAAACATTTTT
GGTAAGTGCAGCTTGAATTTCAAATATCCCGTGTACCTTTCTCTATTACAGCTTAAAGTATGCTACAAT
CTGTGTCATATAGTTAATTGATAAGCATTTTTAATCTGTGTAAACACAGGAATTTAAATAGGAATTTACT
ATTTTTTTAT

SEQ ID NO:457

>gi|7662312|ref|NP_056386.1| SUMO-1-specific protease [Homo sapiens]
MAAGKSGGSAGEITFLEALARSESKRDGGFKNNWSFDHEEESGDDTKDGTNLLSVDEDEDESETSKGKKL
NRRSEIVANSSGEFILKTYVRRNKSESFKTLKGNPIGLNMLSNKKLSENMQNTSLCSGTVVHGRFRFHA
60 HAQIPVVKTAQSSSLDRKERKEYPPHVQKVEINPVRLSRLQGVVERIMKKTEESQVEPEIKRKVQQRH
CSTYQPTPPLSPASKKCLTHLEDLQRNCRQAITLNESTGPLLRTSIHQNSGGQKSQNTGLTTKKFYGNV

EKVPIDIIIVNCDDSKHTYLQTNQKVLPGAKIPKITNLKERKTSLSLDNDPIILSSDDDDNDRTNRRES
 ISPPADSSACSSPAPSTGKVEAALNENTCRAERELRSIPEDSELNTVTLPRKARMKDQFGNSIINTPLKR
 RKVFSQEPDALALSCQSSFDSVILNCRSIRVGTFLRLLIEPVIFCLDFIKIQLDEPDHDPVEIILNTSD
 LTKCEWCNVRKLPVVFLQAIIPAVYQKLSIQLQMNKEDKVNNDCKGVNKLTNLEEYIILIFQNGLDPPAN
 5 MVFESIINEIGIKNNISNFFAKIPFEEANGRLVACTRYEESIKGSCGQKENKIKTVSFESKIQLRSKQE
 FQFFDEEEETGENHTIFIGPVEKLIVYPPPPAKGGISVTNEDLHCLNEGEFLNDVIDFYLYLVLEKLEK
 KEDADRIHIFSSFFYKRLNQRRERNHETTNLSIQQKRHGRVKTWTRHVDIFEKDFIFVPLNEAAHWFLAV
 VCFPGLEKPKYEPNPHYHENAVIQKCSTVEDSCISSASEMESCSQNSSAKPVIKMLNKKHCIAVIDSN
 PGQESDPRYKRNICSVKYSVKKINHASENEEFNKGESTSQKVADRTKSENGLQNESLSSTHTDGLSK
 10 IRLNYSDESPEAGKMLEDELVDFSEDQDNQDDSSDDGFLADDNCSSSEIGQWHLKPTICKQPCILLMDSLR
 GPSRSNVVKILREYLEVEWEVKKGSKRSFSKDVMMKGSNPKVPQNNFSDCGVYVLQYVESFFENPILSFE
 LPMNLANWFPFPRMRTKREEIRNIIILKLQEDQSKEKRKHKDTYSTEAPLGEGTEQCVNSISD

SEQ ID NO:458

15 Synaptophysin homologue (pantophysin)

>GL2_71_G03_G3F1 Direction: sense

ACAGGAACACAAAGACTGCAAAGGTAACATAGAATTGTGCAGAAGAAGAGTAATCGCCTATGAGGACGTAATCTT
 TCCAATTTACATCACATATGTTTACACCTGGAGGTGGCTGAAATGATGCCTCATTCAACCTGAATGGATAACCAA
 AAGTAGCTGTAACAGTTTTATTCTCAGTAAGTGCAGGAGGACAATTCAGTTGAATTTCTGTTTGGCCCTTAAAC
 20 CTCCACAGGTGGCAAAGCAAAGATAGAAGCAATCCACTCGAGGACCTTGATGAAGCCGAGTGGCTCCTTGAGCG
 GGTGAGGTTGATCTGGAAGCCGCCGAGGACCCAGCGCAGTGGTTAGATAGATAAAGCGACCGCTCGACTAGTC
 TGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTCGTTTAAACCTGCAGGACTAGTCCCTTTAGTGAGGGT
 TAATCTGAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAATTCACACA
 ACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTTGCGTTG
 25 CGCTCACTGGCCGCTTTCCAGTCGGGAAAACCTTGTCTGTCAGTGATTAATGAATCGGCCAACGCCGCGGGG
 NAGAGGNCGGGTAGCGTNAATAGGGGGCGCCCTTACCCGGTTTCTCCCGCTCANTTGAATCCGCTTGCCCC
 CGGGCG

SEQ ID NO:459

30 >GL2_71_G04_G3F1 Direction: sense

ACAGGAACACAAAGACTGCAAAGGTAACATAGAATTGTGCAGAAGAAGAGTAATCGCCTATGAGGACGTAATCTT
 TCCAATTTACATCACATATGTTTACACCTGGAGGTGGCTGAAATGATGCCTCATTCAACCTGAATGGATAACCAA
 AAGTAGCTGTAACAGTTTTATTCTCAGTAAGTGCAGGAGGACAATTCAGTTGAATTTCTGTTTGGCCCTTAAAC
 CTCCACAGGTGGCAAAGCAAAGATAGAAGCAATCCACTCGAGGACCTTGATGAAGCCGAGTGGCTCCTTGAGCG
 35 GGTGAGGTTGATCTGGAAGCCGCCGAGGACCCAGCGCAGTGGTTAGATAGATAAAGCGACCGCTCGACTAGTC
 TGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTCGTTTAAACCTGCAGGACTAGTCCCTTTANTGAGGGT
 TAATCTGAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAATTCACACA
 ACATACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCCTTAAATGAGTTGAGCTAACTCACATTAATTTGCG
 TTTGCGCTCACTTGGGCCGCTTTCCAGGTTCCGGGGAAAACTGTCTGTCAGTTGCTTAATGAATCGGGCAACG
 40 CGCGGGGAGAGGCGGTGGGTATNG

SEQ ID NO:460

>GL2_71_G05_G3F1 Direction: sense

ACAGGAACACAAAGACTGCAAAGGTAACATAGAATTGTGCAGAAGAAGAGTAATCGCCTATGAGGACGTAATCTT
 45 TCCAATTTACATCACATATGTTTACACCTGGAGGTGGCTGAAATGATGCCTCATTCAACCTGAATGGATAACCAA
 AAGTAGCTGTAACAGTTTTATTCTCAGTAAGTGCAGGAGGACAATTCAGTTGAATTTCTGTTTGGCCCTTAAAC
 CTCCACAGGTGGCAAAGCAAAGATAGAAGCAATCCACTCGAGGACCTTGATGAAGCCGAGTGGCTCCTTGAGCG
 GGTGAGGTTGATCTGGAAGCCGCCGAGGACCCAGCACAGTGGTTAGATAGATAAAGCGGCCGCTCGACTAGTC
 TGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTCGCGGCCGCTAAATTCAGCTTATAGTG

SEQ ID NO:461

>GL2_71_G06_G3F1 Direction: sense

ACAGGAACACAAAGACTGCAAAGGTAACATAGAATTGTGCAGAAGAAGAGTAATCGCCTATGAGGACGTAATCTT
 TCCAATTTACATCACATATGTTTACACCTGGAGGTGGCTGAAATGATGCCTCATTCAACCTGAATGGATAACCAA
 55 AAGTAGCTGTAACAGTTTTATTCTCAGTAAGTGCAGGAGGACAATTCAGTTGAATTTCTGTTTGGCCCTTAAAC
 CTCCACAGGTGGCAAAGCAAAGATAGAAGCAATCCACTCGAGGACCTTGATGAAGCCGAGTGGCTCCTTGAGCG
 GGTGAGGTTGATCTGGAAGCCGCCGAGGACCCAGCACAGTGGTTAGATAGATAAAGCGGCCGCTCGACTAGTC
 TGAGGTCTGATACTCACTGACTGTCTGTAAGGGCGAATTCGCGGCCGCTAAATTCAGCTTATAGTGAGTCG
 TATTACAATTCAGTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCTTGGCGTTACCCAACCTTAATCGCCTT
 60 GCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGACCGATCGCCCTTCCCAACAGTTGCGCA

GCCTATACGTACGGCAGTTTAAAGGTTTTACNACCTATTAAAAGAGAGAGCCCGGTATCGTCTGTTGTGGATGTNC
AGAGTGATATTTATTTGGAACCCCGGGGAAAGAAT

SEQ ID NO:462

5 >gi|5803184|ref|NM_006754.1| Homo sapiens synaptophysin-like protein
(SYPL), mRNA
TGAACCGAGGCAAGGGGGCGCGGCGCAGCAGTATGGCGCCCAACATCTACTTGGTTCGCCAGCGGATCA
GTGCGACTCGGCCAGAGGATGTCCGGCTTCCAGATCAACCTCAACCCGCTCAAGGAGCCACTCGGCTTCAT
10 CAAGGTCCTCGAGTGGATTGCTTCTATCTTTGCTTTTGCCACCTGTGGAGGTTTAAAGGGCCAAACAGAA
ATTCAAGTGAATTGTCTCCTGCAGTTACTGAGAATAAACTGTTACAGCTACTTTTGGTTATCCATTCA
GGTTGAATGAGGCATCATTTTCAGCCACCTCCAGGTGTAAACATATGTGATGTAAATTGGAAAGATTACGT
CCTCATAGGCGATTACTCTTCTCTGCACAATTCTATGTTACCTTTGCAGTCTTTGTGTTCCCTGTACTGC
ATTGCTGCCCTTCTGCTTTATGTTGGCTACACGAGTCTGTATCTGGATAGTCGTAAACTTCCTATGATAG
15 ACTTTGTTGTTACACTTGTGGCACTTTTTTGTGGTTGGTGAGCACTTCAGCCTGGGCTAAAGCTCTGAC
AGATATTAATAAGCTACTGGTCACAATATTATTGATGAACCTCCGCTTGTAAAGAAGAAAGCAGTACTG
TGTTACTTTGGCTCTGTGACCAGTATGGGATCCCTAAATGTATCTGTGATATTTGGCTTTCTAAATATGA
TACTCTGGGGAGGAAATGCTTGGTTTGTGTACAAGGAGACCAGCCTACACAGTCCATCAAATACATCTGC
CCCTCATAGCCAAGGAGGTATTCCACCTCCTACCGGAATATAATTAAAGGGAGAAATACACTGTATGAAG
TATATGTTGATACTATGACATGTTGCCAACACCTTGAGAAGCATTATTTGTTTCTAATAAAAGTAATGGC
20 TTTGTCAATATATTGGTGGGTTTAAACTTTGCTGCTTTTTTACATAAAGCCTGTGCCTTTCTAGAAAG
TTAAGATGTAAATGTATTCTCACATGTAAATTTGAAAGTTCAGGGGTCTATTATGAAATGGATTACACAT
TTTAAATGAACCCATAATTTTTTTCTACTAAAGCTGTTTGCCCTCCAAAGTGTTTACACCTAAGCCTAACA
TGATATCGCTCATTCAGAAAACCTGTTATATTGTATACCATAGTAGGAAGAAAAACCTTTATTTGGAATAT
ACACTACTGTAAAGTTTGTACAGATCATATACCTACCACCTGCTTTGCTTAAAGAGCCTTGATTACATAA
25 ATATGTAGGAAAAAACATATTGAGTTCAAAATTTATATCTAACATTGTTTATGTTATGATTTTTTTTAAAT
TGCAAAAGACTAGGTGTATATTTTTTTCTGTTTTTCTAAATGACCCGTGGTACTTAATAGGTGTACTAAAA
TTGTGTTGGGAGCAGGGATTGGAATTTCTGAGAGATGTGTAGTTAATTAGTAATCTGTTTCATGAGA
TATGATCTGTTATGCTAGTGGTTTAAATAGGCTTGCTATGTAAGTAGAACGTGGCTCAACTAGATATCTTA
TATGATGGGCATTACCTCTTAGTGATATTTGTTTCTGCTCCTTTGTTGCTCATGCTGTTTAAAGTGCAGG
30 CTGAGACCCAGCCTCTTTGTAAGTACAGTAAAATAATCCACCGTTTTTTACAGACCCTAGTCAAAGGGTT
AAAAAAATTAAGATTGCTTTCCATGTTTGAAATTTACCATTGAGAGTCAATGAAGTTGCTATTTTGAGTT
TAGCATTGATATTGTGAAAATAAGTGCAATTTGGATTTTCATGTTTCTTAATATTCACTCTTGTTTCACAA
ATGAATGATTAAGGAATTATGCATCATAAAGGAACCTAAGTGAGGTATATGATGAGTGTATTGCTTTTGC
ACACACATATAGGTATATTCTGAATACAAGCTTATTCATTTTGCTTCTTAATCTTTTTTGTGTACAGGGA
35 TTCAGGTTTCTTATTCTTACAACATGATTGTTTATATGTGAAGCACATCTTGCTGTTGCCTTATTTTTGA
TGCTTTTATTTCATGACAAGAATTGTCAATATAAGAATGTATATCTTGCCGCAACCAATTTAATAAAGGA
GTTGAAAGAAAAA

SEQ ID NO:463

40 >gi|5803185|ref|NP_006745.1| synaptophysin-like protein; pantophysin [Homo
sapiens]
MAPNIYLVRQRISRLGQRMSSGFQINLNPLKEPLGFIKVLEWIASIFAFATCGGFKGQTEIQVNCPPAVTE
NKTVTATFGYPFRLNEASFQPPPGVNICDVNWKDYVLIGDYSSSAQFYVTFVAVFVFLYCIAALLLVGYT
SLYLDNRKLPIMIDFVVTFLVATFLWLVTSAWAKALTDIKIATGHNIIDELPPCKKKAVLCYFGSVTSMGS
45 LNVSVIFGFLNMILWGGNAWFVYKETSLSHPSNTSAPHSQGGIPPTGI

SEQ ID NO:464

Thrombospondin-1

>GL2_199_2_M13R Direction: anti-sense
50 CCAATGTAGTTAGTGC GGATGGCAGGGCTGGAACCATTCACCACGTTGTTGTCAAGGGTGAGGAGGACACTGGTA
GAGCTGGAGCAGCCTTTGTTCTGAGGATGTCTTCTGGTGTGGTTCCAAAGACAAACCTCACATTCTGCAGCACC
CCCTGGAAAATGTCA

SEQ ID NO:465

55 >GL2_199_1_M13R Direction: sense
TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACA
AAGGCTGCTCCAGCTCTACCAGTGTNCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGGCATCC
GNACTAACTACATTGG

SEQ ID NO:466

>GL2_199_3_M13F Direction: sense

TGACATTTTCCAGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAA
AGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:467

>GL2_66_F01_G3F1 Direction: sense

TGACATTTTCCAGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCTGGCATCCGACTA
ACTACATTGG

SEQ ID NO:468

>GL2_66_F02_G3F1 Direction: sense

TGACATTTTCCAGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
ACTAACTACATTGG

SEQ ID NO:469

>GL2_66_F03_G3F1 Direction: sense

TGACATTTTCCAGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:470

>GL2_66_F04_G3F1 Direction: sense

TGACATTTTCCAGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAA
AGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:471

>GL2_86_2A01_G3F1 Direction: sense

TGACATTTTCCAGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:472

>GL2_86_2A02_G3F1 Direction: sense

TGACATTTTCCAGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:473

>GL2_86_2A03_G3F1 Direction: sense

TGACATTTTCCAGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:474

>GL2_86_2A04_G3F1 Direction: N/A

TGACATTTTCCAGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACAGCGTCTCCTCA

SEQ ID NO:475

>GL2_86_2A06_G3F1 Direction: sense

TGACATTTTCCAGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAATCACACCAGAAGACATCCTCAGGAACAAAGG
CTGCTCCAGCTCTACCAGTGTCTCCTCACCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCGCAC
TAACTACATTGG

SEQ ID NO:476

>GL2_86_2A07_G3F1 Direction: sense

CGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAA
AGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
CACTAACTACATTGG

SEQ ID NO:477

>GL2_86_2A08_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
ACTAACTACATTGG

SEQ ID NO:478

>GL2_86_2A09_G3F1 Direction: sense

GTGACATTATCCAGTGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACNCAGAAGACATCCTCAGGAAC
AAAGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGNCAT
CCGCACTAACTACATTGG

SEQ ID NO:479

>GL2_199_3_M13R Direction: anti-sense

CCAATGTAGTTAGTGCGGATGGCAGGGCTGGAACCATTCACCACGTTGTGTCAAGGGTGAGGAGGACACTGGTA
GAGCTGGAGCAGCCTTTGTTCTGAGGATGTCTTCTGGTGTGGTTCCAAAGACAAACCTCACATTCTGCAGCACC
CCCTGGAAAATGTCA

SEQ ID NO:480

>GL2_86_2A05_G3F1 Direction: sense

TGACATTTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGGAACCACACCAGAAGACATCCTCAGGAACAAA
GGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGACAACAACGTGGTGAATGGTTCCAGCCCTGCCATCCG
ACTAACTACATTGG

SEQ ID NO:481

>gi|4507484|ref|NM_003246.1| Homo sapiens thrombospondin 1 (THBS1), mRNA

GGACGCACAGGCATTCCCCGCGCCCCCTCCAGCCCTCGCCCGCCCTCGCCACCGCTCCCGGCCGCGCGCTC
CGGTACACACAGGATCCCTGCTGGGCACCAACAGCTCCACCATGGGGCTGGCCTGGGGACTAGGCGTCTCT
GTTCTGTATGCATGTGTGTGGCACCAACCGCATTCCAGAGTCTGGCGGAGACAACAGCGTGTGTTGACATC
TTTGAACCTCACCGGGGCGCGCCGCAAGGGGTCTGGGCGCCGACTGGTGAAGGGCCCCGACCCTTCCAGCC
CAGCTTTCCGCATCGAGGATGCCAACCTGATCCCCCTGTGCCTGATGACAAGTTCCAAGACCTGGTGGGA
TGCTGTGCGGGCAGAAAAGGGTTTCTCTCTTCTGGCATCCCTGAGGCAGATGAAGAAGACCCGGGGCAGC
CTGCTGGCCCTTGGAGCGGAAAGACCACTCTGGCCAGGTCTTCAGCGTGGTGTCCAATGGCAAGGCGGGCA
CCCTGGACCTCAGCCTGACCGTCCAAGGAAAGCAGCAGTGGTGTCTGTGGAAGAAGCTCTCCTGGCAAC
CGGCCAGTGGGAAGAGCATCACCCCTGTTTGTGTCAGGAAGACAGGGCCAGCTGTACATCGACTGTGAAAAG
ATGGAGAATGCTGAGTTGGACGTCCCCATCCAAAGCGTCTTCACCAGAGACCTGGCCAGCATCGCCAGAC
TCCGCATCGCAAAGGGGGGCGTCAATGACAATTTCCAGGGGGTGCTGCAGAATGTGAGGTTTGTCTTTGG
AACCACACCAGAAGACATCCTCAGGAACAAAGGCTGCTCCAGCTCTACCAGTGTCTCCTCACCCCTTGAC
AACAACGTGGTGAATGGTTCCAGCCCTGCCATCCGCACTAACTACATTGGCCACAAGACAAGGACTTGC
AAGCCATCTGCGGCATCTCCTGTGATGAGCTGTCCAGCATGGTCTTGGAACCTCAGGGGCCTGCGCACCAT
TGTGACCACGCTGCAGGACAGCATCCGCAAGTGACTGAAGAGAAACAAAGAGTTGGCCAATGAGCTGAGG
CGGCCTCCCCTATGCTATCACAACGGAGTTTCAGTACAGAAATAACGAGGAATGGACTGTTGATAGCTGCA
CTGAGTGTCACTGTGAGAACTCAGTTACCATCTGCAAAAAGGTGTCTGCCCCATCATGCCCTGCTCCAA
TGCCACAGTTCTCTGATGGAGAATGCTGTCTCGCTGTGTCGCGCCAGCGACTCTGCGGACGATGGCTGGTCT
CCATGGTCCGAGTGGACCTCCTGTTCTACGAGCTGTGGCAATGGAATTCAGCAGCGCGGCGCTCCTGCG
ATAGCCTCAACAACCGATGTGAGGGCTCCTCGGTCCAGACACGGACCTGCCACATTACAGGAGTGTGACAA
AAGATTTAAACAGGATGGTGGCTGGAGCCACTGGTCCCCGTGGTTCATCTTGTCTGTGACATGTGGTGTAT
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AAGCGCGGGAGACCAAAGCCTGCAAGAAAGACGCTGCCCCATCAATGGAGGCTGGGGTCTTGGTCAAC
ATGGGACATCTGTTCTGTACCTGTGGAGGAGGGGTACAGAAACGTAGTCGTCTCTGCAACAACCCCGCA
CCCCAGTTTGGAGGCAAGGACTGCGTTGGTGTATGTAACAGAAAACAGATCTGCAACAAGCAGGACTGTG
CAATTGATGGATGCCTGTCCAATCCCTGCTTTGCCGGCGTGAAGTGTACTAGCTACCCTGATGGCAGCTG
GAAATGTGGTGTGTTGTCCTGCTTACAGTGGAAATGGCATCCAGTGCACAGATGTTGATGAGTGCAAA
GAAGTGCCTGATGCCTGCTTCAACCACAATGGAGAGCACCGGTGTGAGAACACGGACCCCGCTACAAC

GCCTGCCCTGCCCCCCACGCTTCACCGGCTCACAGCCCTTCGGCCAGGGTGTGCAACATGCCACGGCCAA
CAAACAGGTGTGCAAGCCCCGTAAACCCCTGCACGGATGGGACCCACGACTGCAACAAGAACGCCAAGTGC
AACTACCTGGGCCACTATAGCGACCCCATGTACCGCTGCGAGTGCAAGCCTGGCTACGCTGGCAATGGCA
TCATCTGCGGGGAGGACACAGACCTGGATGGCTGGCCCAATGAGAACCTGGTGTGCGTGGCCAATGCGAC
5 TTACCACTGCAAAAAGGATAATTGCCCAACCTTCCCAACTCAGGGCAGGAAGACTATGACAAGGATGGA
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ATTACAACCCAGCTCAGTATGACTATGACAGAGATGATGTGGGAGACCGCTGTGACAACCTGTCCCTACAA
CCACAACCCAGATCAGGCAGACACAGACAACAATGGGGAAGGAGACGCCTGTGCTGCAGACATTGATGGA
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10 ATGGGGTTGGAGATCAGTGTGACAATTGCCCTTGGAACACAATCCGGATCAGCTGGACTCTGACTCAGA
CCGATTTGGAGATACCTGTGACAACAATCAGGATATTGATGAAGATGGCCACCAGAACAATCTGGACAAC
TGTCCCTATGTGCCCCAATGCCAACCAGGCTGACCATGACAAAGATGGCAAGGGAGATGCCTGTGACCACG
ATGATGACAACGATGGCATTCTGTATGACAAGGACAAC'TGCAGACTCGTGCCCAATCCCGACCAAGGA
CTCTGACGGCGATGGTCGAGGTGATGCCTGCAAAGATGATTTTGACCATGACAGTGTGCCAGACATCGAT
15 GACATCTGTCTGTAGAATGTTGACATCAGTGAGACCGATTTCCGCCGATTCCAGATGATTCTCTGGACC
CCAAAGGGACATCCCAAATGACCCTAACTGGGTGTACGCCATCAGGGTAAAGAACTCGTCCAGACTGT
CAACTGTGATCCTGGACTCGCTGTAGGTTATGATGAGTTTAATGCTGTGGACTTCAGTGGCACCTTCTTC
ATCAACACCGAAAGGGACGATGACTATGCTGGATTTGTCTTTGGCTACCAGTCCAGCAGCCGCTTTTATG
TTGTGATGTGGAAGCAAGTCACCCAGTCTTACTGGGACACCAACCCACGAGGGCTCAGGGATACTCGGG
20 CCTTTCTGTGAAAGTTGTAACCTCCACACAGGGCCTGGCGAGCACCTGCGGAACGCCCTGTGGCACACA
GGAAACACCCCTGGCCAGGTGCGCACCCCTGTGGCATGACCCCTCGTCACATAGGCTGGAAAGATTTCACCG
CCTACAGATGGCGTCTCAGCCACAGGCCAAAGACGGGTTTTATTAGAGTGGTGTATGTAAGGGAAGAA
AATCATGGCTGACTCAGGACCCATCTATGATAAAACCTATGCTGGTGGTAGACTAGGGTTGTTTGTCTTC
TCTCAAGAAATGGTGTCTTCTCTGACCTGAAATACGAATGTAGAGATCCCTAATCATCAAATTGTTGAT
25 TGAAAGACTGATCATAAACCAATGCTGGTATTGCACCTTCTGGAACATATGGGCTTGAGAAAACCCCAAG
ATCACTTCTCCTTGGCTTCTTCTTTCTGTGCTTGCAATCAGTGTGGACTCCTAGAACGTGCGACCTGCC
TCAAGAAAATGCAGTTTTCAAAAACAGACTCATCAGCATTAGCCTCCAATGAATAAGACATCTTCCAAG
CATATAACAATTTGCTTTGGTTTCTTTTGA AAAAGCATCTACTTGGCTTCAGTTGGGAAGGTGCCCATTC
CACTCTGCCTTTGTACAGAGCAGGGTCTATTGTGAGGCCATCTCTGAGCAGTGGACTCAAAGCATTT
30 TCAGGCATGTGAGCAAGGGAGGACTCTAGTAATTAGCAAAACAAACCACCTGACATCTCTCCTTCAGG
AACACGGGGAGCAGAGGCCAAAGCACTAAGGGGAGGCGCATACCCGAGACGATTGTATGAAGGGAATAT
GGAGGAATGTTACATGTTTCGGTACTAAGTCATTTTCAGGGGATTGAAAGACTATTGCTGGATTTTATGA
TGCTGACTGGCGTTAGCTGATTAACCCATGTAAATAGGCACCTTAAATAGAAGCAGGAAGGGAGACAAAG
ACTGGCTTCTGGACTTCTCCTGATCCCCACCTTACTCATCACCTTGCAGTGGCCAGAATTAGGGAAT
35 CAGAATCAAACAGTGTAAAGCAGTGTGGCTGCCATTGCCCTGGTCACATTGAAATTGGTGGCTTCATTC
TAGATGTAGCTTGTGAGATGTAGCAGGAAAATAGGAAAACCTACCATCTCAGTGAGCACCAGCTGCCTC
CCAAAGGAGGGGAGCCGTGCTTATATTTTTATGGTTACAATGGCACAAAATTATTATCAACCTAACTAA
AACATTCTCTTTCTCTTTTCCGTAATTACTAGGTAGTTTTCTAATTCTCTCTTTTGGAAAGTATGATTT
TTTTAAAGTCTTTACGATGTAAATATTTATTTTACTTATTCTGGAAGATCTGGCTGAAGGATTATTCT
40 ATGGAACAGGAAGAAGCGTAAAGACTATCCATGTCTATTTGTTGAGAGTCTTCGTGACTGTGAAGATTGT
AAATACAGATTATTTATTAACCTCTGTTCTGCCTGGAAATTTAGGCTTCATACGGAAAGTGTGAGAGCA
AGTAGTTGACATTTATCAGCAAATCTCTTGCAAGAACAGCACAAAGGAAATCAGTCTAATAAGCTGCTCT
GCCCCTTGTGCTCAGAGTGGATGTTATGGGATTCCTTTTCTCTGTTTTATCTTTTCAAGTGAATTAG
TTGGTTATCCATTTGCAAATGTTTTAAATTGCAAAGAAAGCCATGAGGTCTTCAATACTGTTTTACCCCA
45 TCCCTTGTGCATATTTCCAGGGAGAAGGAAAGCATATACACTTTTTCTTTTCATTTTTCCAAAAGAGAAA
AAAATGACAAAAGGTGAACTTACATACAAATATTACCTCATTTGTTGTGTGACTGAGTAAAGAATTTTT
GGATCAAGCGGAAAGATTTAAGTGTCTAACAAACTTAAAGCTACTGTAGTACCTAAAAAGTCAGTGTG
TACATAGCATAAAAACTCTGCAGAGAAGTATTTCCCAATAAGGAAATAGCATTGAAATGTTAAATACAATT
TCTGAAAGTTATGTTTTTTTTCTATCATCTGGTATACCATTTGCTTTATTTTTATAAATTATTTTCTCATT
50 GCCATTGGAATAGAATATTAGATTGTGTAGATATGCTATTTAAATAATTTATCAGGAAATACTGCCTGT
AGAGTTAGTATTTCTATTTTTATATAATGTTTGCACACTGAATTGAAGAATTGTTGGTTTTTTTTCTTTTT
TTGTTTTTTTTTTTTTTTTTTTTTTTTTTTGTCTTTGACCTCCCATTTTACTATTTGCCAATACCTTTTT
CTAGGAATGTGCTTTTTTTTTGTACACATTTTATCCATTTTACATTTCTAAAGCAGTGTAAAGTTGTATATT
ACTGTTTCTTATGTACAAGGAACAACAATAAATCATATGGAAATTTATATTT

SEQ ID NO:482

>gi|4507485|ref|NP_003237.1| thrombospondin 1 [Homo sapiens]
MGLAWGLGVFLMHVCGTNRIPESGGDNSVFDIFELTGAARKGSGRRLVKGPDPSSPAFRIEDANLIPPV
PDDKFQDLVDVAHEKGFLLLASLRQMKKTRGTLALLERKDHSGQVFSVVSNGKAGTLDLSLTQVGKQHV
60 VSVEEALLATGQWKSITLFVQEDRAQLYIDCEKMENAEILDVPIQSVFTRDLASIALRLRIAKGGVNDNFQ
VLQNVRFVFGTTPEDILRNKGCSSSTSVLLTLDNNVNGSSPAIRNTYIGHKTKDLQAICGISDELSSM

VLELRGLRTIVTTLQDSIRKVTENKELANELRRPPLCYHNGVQYRNNEEWTVDSCTECHCQNSVTICKK
VSCPIMPSCSNATVPDGECCPRCWPSDSDADDGWSWPSEWTSCSTSCGNGIQQRGRSCDSLNNRCEGSSVQT
RTCHIQECDKRFKQDGGWSHWPSSCSVTGCGDVITRIRLCNSPSPQMNGKPCGEARETKACKKDACP
INGGWGPWSPWDICSVTCGGGVQKRSRLCNNPAPQFGGKDCVGDVTENQICNKQDCPIDGCLSNPCFAGV
5 KCTSYPDGSGWKCGACPPGYSGNGIQCTDVDECKEVPDACFNHNGEHRCENTDPGYNCLPCPPRFTGSQPF
GQGVEHATANKQVCKPRNPCTDGTDCNKNACNYLGHYSDFMYRCECKPGYAGNGIICGEDTDLDGWPN
ENLVCVANATYHCKKDNCNPLNSGQEDYDKDGI GDACDDDDNDKI PDDRDNCPFHYNPAQYDYDRDDV
GDRCDNCPYNHNPDAQADTDNNGEGDACAADIDGDGILNERDNCQYVYNVDQRDTMDGVGDQCDNCPLEH
10 NPDQLDSDSDRIGDTCNNQDIDEDGHQNNLDNCPYVNPANQADHDKDGKGDACDHDNDGIPDDKDNC
RLVPNPDPQKSDSDGGRGDACKDDFDHDSVPDIDDICPENVDISETDFRRFQMIPLDPKGTSONDPNWVVR
HQQKELVQTVNCDPGLAVGYDEFNAVDFSGTFFINTERDDYAGFVFGYQSSSRFYVVMWKQVTSYWDT
NPTRAQGYGLSVKVVNSTTGPGEHLRNALWHTGNTPGQVRTLWHDPRHIGWKDFTAYRWRLSHRPKTGF
IRVVMYEGKKIMADSGPIYDKTYAGGRLGLFVFSQEMVFFSDDLKYECDP

SEQ ID NO:483

Transgelin 2

>GL3_30H_PCR_G3F1 Direction: sense

CACTGTACCCGAGGGGCGAGGCCCCAGTAAAGAAGATCAGGCCTCCACCATGGCCTTCAAGCAGATGGAGCAGATC
TCTCAGTTCTCTG

SEQ ID NO:484

>gi|4507356|ref|NM_003564.1| Homo sapiens transgelin 2 (TAGLN2), mRNA
GCCCTTGCTTGTAGTCAGTGCCTGCTCTCCAGCCCGCTTGAACGCTCCCCGAGCCACCGCCACCCATT
GGAATGGCCAAACAGGGGACCTGCATATGGCCTGAGCCGGGAGGTGCAGCAGAAGATTGAGAAACAATATG
25 ATGCAGATCTGGAGCAGATCCTGATCCAGTGGATCACCACCCAGTGCAGAAAGGATGTGGGCCGGCCCCA
GCCTGGACGCGAGAACTTCCAGAACTGGCTCAAGGATGGCACGGTGCTATGTGAGCTCATTAATGCACTG
TACCCCGAGGGGCGAGGCCCCAGTAAAGAAGATCCAGGCCTCCACCATGGCCTTCAAGCAGATGGAGCAGA
TCTCTCAGTTCTCTGCAAGCAGCTGAGCGCTATGGCATTAAACCACTGACATCTTCCAAACTGTGGACCT
CTGGGAAGGAAAGAACATGGCCTGTGTGACGCGACGCTGATGAATCTGGGTGGGCTGGCAGTAGCCCGA
30 GATGATGGGCTCTTCTCTGGGGATCCCAACTGGTTCCCTAAGAAATCCAAGGAGAATCCTCGGAACCTCT
CAGATAACCAGCTGCAAGAGGGCAAGAACGTGATCGGGTTACAGATGGGCACCAACCGCGGGGCGTCTCA
GGCAGGCATGACTGGCTACGGGATGCCACGCCAGATCCTCTGATCCACCCCGAGCCTTGCCCTGCCCT
CCCACGAATGGTTAATATATATAGTATATATATTTTAGCAGTGACATTCCCAGAGAGCCCCAGAGCTCT
CAAGCTCCTTTCTGTGACGGGTGGGGGTTTCAAGCCTGTCTGTACCTCTGAGGTGCCTGTCTGGCATCCTC
35 TCCCCCATGCTTACTAATACATTCCCTTCCCCATGACATCAAACTGGACCAACTGGCCTCTTCTCTTTC
CCCTGGGACCAAAATTTAGGGGCTCAGTCCCTACCGCCATGCCCTGGCCTATTCTGTCTCTCTCTCTT
CCCCCTGGCCTGTTCTGTCTCTGAGCTCTGTGTCTCCTCGTTTATTCCATGGCTGGGAGTCACTGATGCTG
CCTCTGCCTTCTGATGCTGGACTGGCCTTGTCTTCTACAAGTATGCTTCTCCACAGCTGTGGCTGCAGGA
ACTTAATTTATAGGGAGGAGCCTGTGGCAGCTGCTGCCCCAGCCACAGCTGCACTGACTGTGCTCACCAC
40 ACATCTGGGGCAGCCTTCCCTGGCAGGGGCCCCCTCGTGGCTTCTCATTTTCCATTCCCTTCACTGTGGCTA
AGGGGTGGGGTGAGGGGATGGAGAGGGAGGGCTGCCTACCATGGTCTGGGGCTTGAGGAAGATGAGTTTG
TTGATTTAAATAAAGAATTTGTCAATTTTG

SEQ ID NO:485

>gi|4507357|ref|NP_003555.1| transgelin 2; SM22-alpha homolog [Homo sapiens]

MANRGPAYGLSREVQOKIEKQYDADLEQILIQWITTQCRKDVGRPQPGRENFQNLKDGTVLCELINALY
PEGQAPVKKIQASTMAFKQMEQISQFLQAAERYGINTTDIFQTVDLWEGKNMACVQRTLMNLGGLAVARD
DGLFSGDPNWFPKSKENPRNFSNQLQEGKNVIGLQMGTNRGASQAGMTGYGMPROIL

SEQ ID NO:486

Vigilin

>GL3_43A1_1_M13F Direction: anti-sense

CCGGGCAGCTTCGCAGTTGGCTCGCTTGCCTGTGATGATAATGGTCTCTGAATTGCTATTCTCTGCTGGAAGGGT
CGATTTTGGTGTGTGCTTTCTTACGAATCTTTTAAATGTTTGCCTCTCTTCCCAATGATATTCTTGTGAAACT
GTTTGAAGATCGGAACAGAAATTGAATAGCTATTTTCCACCAGATCTGCCACCATCTTCTGCATGTATTTTGTGC
ATTTTTCACCTCATTTCTAGGTCTCTGAGCTGGACAATGTCACTTTTTTGTGCTGGG

SEQ ID NO:487

>GL3_43A1_1_M13R Direction: sense

CCCAGCACAAAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGCACAAAATACATGCA
GAAGATGGTGGCAGATCTGGTGGAAAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAGTTTCACAAGAATAT
5 CATTGGGAAAAGGAGGCGCAAACATTAAAAAGATTTCGTGAAGAAAGCAACACCAAATCGACCTTCCAGCAGAGAA
TAGCAATTCAGAGACCATTATCATCACAGGCAAGCGAGCCAACCTGCGAAGCTGCCCGG

SEQ ID NO:488

>GL3_43A1_2_M13F Direction: sense

CCCAGGACAAAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGCACAAAATACATGCA
GAAGATGGTGGCAGATCTGGTGGAAAATAGCTATTCAATTTGCTGTTCCGATTCTTCAAACAGTTTCACAAGAA
TATCATTGGGAAAAGGAGGCGCAAACGATTCAAGAAAGATTTCGTGAAGAAAGCAACACCAAATCGACCTTCCAGC
AGAGAATAGCAATTTTCAGAGACCATTATCAGTCACAGGCAAGCGAGCCAACCTGCGAAGGGTTGCCCTGGTCCGCT
15 AGAAACCCAGCACAGGTGGTTAGATGGATACAAGCGGCCGCTCGACTAGTCTGAGGTCTGATACTTCACTGACTA
GTCGTTAAGGGCGAATTCCAGCACACTGGCGGCCGCTCGACTAGTGGATCCGAGCTC

SEQ ID NO:489

>GL3_43A1_2_M13R Direction: anti-sense

CCGGGCAGCTTCGCAGTTGGCTCGCTTGCCCTGTGATGATAATGGTCTCTGAATTGCTATTCTCTGCTGGAAGGTC
20 GATTTTGGTGTGCTTTCTTCACGAATCTTTTAAATGTTTGCCTCCTTTCCCAATGATATTCTTGTGAAACTG
TTTGAAGATCGGAACAGAAATTGAATAGCTATTTTCCACCAGATCTGCCACCATCTTCTGCATGTATTTGTGCA
TTTTTCCACCTCATTTCTTAGGTCCTCTGAGCTGGACAATGTCACTTTTTTGTGCTGGG

SEQ ID NO:490

>GL3_43A1_4_M13F Direction: sense

CCCAGCACAAAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGCACAAAATACATGCA
GAAGATGGTGGCAGATCTGGTGGAAAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAGTTTCACAAGAATAT
CATTGGGAAAAGGAGGCGCAAACATTAAAAAGATTTCGTGAAGAAAGCAACACCAAATCGACCTTCCAGCAGAGAA
TAGCAATTCAGAGACCATTATCATCACAGGCAAGCGAGCCAACCTGCGAAGTTGCCCGGCCGAGAAACCCAGCAC
30 AGTGGTTAGATAGATAAAGCGGCCGCTCGACTAGTCTGAGGTCTGATACTCACTGACTGTGTAAGGGCGAATTC
CAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTACCAAGCTTGGCGTAATCATGGT

SEQ ID NO:491

>GL3_43A1_4_M13R Direction: anti-sense

CCGGGCAGCTTCGCAGTTGGCTCGCTTGCCCTGTGATGATAATGGTCTCTGAATTGCTATTCTCTGCTGGAAGGTC
35 GATTTTGGTGTGCTTTCTTCACGAATCTTTTAAATGTTTGCCTCCTTTCCCAATGATATTCTTGTGAAACTG
TTTGAAGATCGGAACAGAAATTGAATAGCTATTTTCCACCAGATCTGCCACCATCTTCTGCATGTATTTGTGCA
TTTTTCCACCTCATTTCTTAGGTCCTCTGAGCTGGACAATGTCACTTTTTTGTGCTGGG

SEQ ID NO:492

>GL3_43A_PCR_G3F1 Direction: sense

CCCAGCACAAAAAAGTGACATTGTCCAGCTCAGAGGACCTAAGAATGAGGTGGAAAAATGCACAAAATACATGCA
GAAGATGGTGGCAGATCTGGTGGAAAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAGTTTCACAAGAATAT
CATTGGGAAAAGGAGGCGCAAACATTAAAAAGATTTCGTGAAGAAAGCAACACCAAATCGACCTTCCAGCAGAGAA
45 TAGCAAGTTCAGAGACCATTATCATCACAGGCAAGCGAGCCAACCTGCGAAGCTGCCCGG

SEQ ID NO:493

>gi|4885408|ref|NM_005336.1| Homo sapiens high density lipoprotein binding
protein (vigilin) (HDLBP), mRNA

50 GAATTCGGGGGGCGAGTAAGCCAGCGGCAGGACCGCGGGCGGGGCCACAACAAAGCTGGCAGGCTGA
CAGAGGCGGCCTCAGGACGGACCTTCTGGCTACTGACCGTTTTGCTGTGGTTTTCCCGGATTGTGTGTAG
GTGTGAGATCAACCATGAGTTCCGTTGCAGTTTTGACCCAAGAGAGTTTTGCTGAACACCGAAGTGGGCT
GGTTCGCGAACAAATCAAAGTTGCCACTCTAAATTCAGAAGAGGAGAGCGACCCTCCAACCTACAAGGAT
GCCTTCCCTCCACTTCTTGAGAAAGCTGCTTGCCCTGGAAAGTGCCAGGAACCCGCTGGAGCCTGGGGGA
55 ACAAGATCCGACCCATCAAGGCTTCTGTATCACTCAGGTGTTCCATGTACCCCTGGAGGAGAGAAAATA
CAAGGATATGAACAGTTTGGAGAAGGTGAACAAGCAAAAATCTGCCTTGAGATCATGCAGAGAAGTGGT
GCTCACTTGGAGCTGTCTTTGGCCAAAGACCAAGGCCCTCTCCATCATGGTGTGAGGAAAGCTGGATGCTG
TCATGAAGAGCTCGGAAGGACATTGTTGCTAGACTGCAGACTCAGGCCTCAGCAACTGTTGCCATTCCCAA
AGAACACCATCGCTTTGTTATTGGCAAAAATGGAGAGAAACTGCAAGACTTGGAGCTAAAAACTGCAACC
60 AAAATCCAGATCCCACGCCAGATGACCCAGCAATCAGATCAAGATCACTGGCACCAAGAGGGCATCG

AGAAAGCTCGCCATGAAGTCTTACTCATCTCTGCCGAGCAGGACAAACGTGCTGTGGAGAGGCTAGAAGT
AGAAAAGGCATTCCACCCCTTCATCGCTGGGCCGTATAATAGACTGGTTGGCGAGATCATGCAGGAGACA
GGCACGCGCATCAACATCCCCCACCAGCGTGAACCGGACAGAGATTGTCTTCACTGGAGAGAAGGAAC
AGTTGGCTCAGGCTGTGGCTCGCATCAAGAAGATTTATGAGGAGAAGAAAAAGAAGACTACAACCATTGC
5 AGTGGAAAGTGAAGAAATCCCAACACAAGTATGTTCATTGGGCCCCAAGGGCAATTCATTGCAGGAGATCCTT
GAGAGAACTGGAGTTTCCGTTGAGATCCACCCCTCAGACAGCATCTCTGAGACTGTAATACTTCGAGGCG
AACCTGAAAAGTTAGGTGAGGCGTTGACTGAAGTCTATGCCAAGGCCAATAGCTTCACCGTCTCCTCTGT
CGCCGCCCTTCTGGCTTCACCGTTTCATCATTGGCAAGAAAGGGCAGAACCTGGCCAAAATCACTCAG
10 CAGATGCCAAAGGTTACATCGAGTTCACAGAGGGCGAAGACAAGATCACCTTGGAGGGCCCTACAGAGG
ATGTCAATGTGGCCAGGAACAGATAGAAGGCATGGTCAAAGATTTGATTAACCGGATGGACTATGTGGA
GATCAACATCGACCACAAGTTCCACAGGCACCTCATTGGGAAGAGCGGTGCCAACATAAACAGAATCAAA
GACCAGTACAAGGTGTCCGTGCGCATCCCTCCTGACAGTGAGAAGAGCAATTTGATCCGCATCGAGGGGG
ACCCACAGGGCGTGACAGGCGCAAGCAGAGCTGCTGGAGCTTGATCTCGCATGGAAAATGAGCGTAC
15 CAAGGATCTAATCATTTGAGCAAAGATTTTCATCGCACAATCATTTGGGCAGAAGGGTGAACGGATCCGTGAA
ATTCTGTGACAAATTTCCAGAGGTTCATCTTAACCTTTCCAGACCCAGCACAAAAAGTGACATTGTCCAGC
TCAGAGGACCTAAGAATGAGGTGGA AAAATGCACAAAATACATGCAGAAGATGGTGGCAGATCTGGTGG
AAATAGCTATTCAATTTCTGTTCCGATCTTCAAACAGTTTCAAGAATATCATTGGGAAAGGAGGCGCA
AACATTA AAAAGATTCTGTGAAGAAAGCAACACCAAAATCGACCTTCCAGCAGAGAATAGCAATTCAGAGA
20 CCATTATCATCACAGGCAAGCGAGCCAACTGCGAAGCTGCCCCGAGCAGGATTCTGTCTATTTCAGAAAGA
CCTGGCCAAACATAGCCGAGGTAGAGGTCTCCATCCCTGCCAAGCTGCACAACTCCCTCATTGGCACCAAG
GGCCGTCTGATCCGCTCCATCATGGAGGAGTGCGGCGGGGTCCACATTCACCTTTCCCGTGGAAAGGTTTCAG
GAAGCGACACCGTTGTTATCAGGGGCCCTTCTCGGATGTGGAGAAGGCCAAGAAGCAGCTCCTGCATCT
25 GGCGGAGGAGAAGCAAAACCAAGAGTTTCACTGTTGACATCCGCGCCAAGCCAGAATACCACAAATTCCTC
ATCGGCAAGGGGGGCGGCAAAATTCGCAAGGTGCGCGACAGCACTGGAGCACGTGTCTCTTCCCTGCGG
CTGAGGACAAGGACCAGGACCTGATCACCATCATTGGAAAGGAGGACGCCGTCCGAGAGGCACAGAAGGA
GCTGGAGGCCTTGATCCAAAACCTGGATAATGTGGTGGAAAGACTCCATGCTGGTGGACCCCAAGCACCAC
CGCCACTTCGTCATCCGCAGAGGCCAGGTCTTGCGGGAGATTGCTGAAGAGTATGGCGGGGTGATGGTCA
30 GCTTCCACGCTCTGGCACACAGAGCGCAAAAGTCACCTCAAGGGCGCCAAGGACTGTGTGGAGGCAGC
CAAGAAACGCATTTCAGGAGATCATTGAGGACCTGGAAGCTCAGGTGACATTAGAATGTGCTATACCCAG
AAATTCATCGATCTGTATGGGCCCCAAAGGTTCCAGAATCCAGCAGATTACTCGGGATTTTCAGTGTTC
AAATTAATTTCCAGACAGAGAGGAGAAACGCAGTTTCACAGTACAGAGCCAGTTGTCCAGGAGAATGGGA
35 CAGGCTGGGGAGGGGAGAGAGGCTAAAGATTGTGACATCCGCGCTCTCCAAGGAGGTGTGACATCATC
ATCTCTGGCCGGAAGAAAAGTGTGAGGCTGCCAAGGAAGCTCTGGAGGCATTGGTTCTGTACCATTTG
AAGTAGAGGTGCCCTTTGACCTTACCGTTACGTTATTGGGCAGAAAGGAAGTGGGATCCGCAAGATGAT
GGATGAGTTTGAGGTGAACATACATGTCCGGGCACCTGAGCTGCAGTCTGACATCATCGCCATCACGGGC
40 CTCGCTGCAAATTTGGACCGGGCCAAGGCTGGACTGCTGGAGCGTGTGAAGGAGCTACAGGCCGAGCAGG
AGGACCGGGCTTTAAGGAGTTTTAAGCTGAGTGTCACTGTAGACCCCAAATACCATCCCAAGATTATCGG
GAGAAAGGGGGCAGTAATTACCCAAATCCGTTGGAGCATGACGTGAACATCCAGTTTCTGTATAAGGAC
GATGGGAACCAAGCCAGGACCAAAATTACCATCACAGGGTACGAAAAGAACACAGAAGCTGCCAGGGATG
45 CTATCTGAGAATTGTGGGTGAACCTTGAGCAGATGGTTCTGAGGACGTCCTGAGGACCGCGTTCA
CGCCGCTCATTTGGTGGCCGCGGCAAGGCCATTGCGCAAAATCATGGACGAATTCAGGTGGACATTCGC
TTCCACAGAGCGGAGCCCAAGCCCAACTGCGTCACTGTGACGGGGCTCCAGAGAATGTGGAGGAAG
CCATCGACCACATCCTCAATCTGGAGGAGGAATACCTAGCTGACGTGGTGGACAGTGAGGCGCTGCAGGT
50 ATACATGAAACCCCAAGCACACGAAGAGGCCAAGGCACCTTCCAGAGGCTTTGTGGTGGCGGACGCACCC
TGGACCGCCAGCAGCATGAGAAGGCTCCTGACATGAGCAGCTCTGAGGAATTTCCAGCTTTGGGGCTC
AGGTGGCTCCCAAGACCCTCCCTTGGGGCCCCAAACGATAATGATCAAAAAGAACAGAACCCTCTCCAGC
CTGCTGACCCGAACCAACACACAATGGTTTGTCTCAATCTGACCCAGCGGCTGGACCTCCGTAAATT
GTTGAGCGCTCTTCCCTTCCCGAGGTCCGAGGGAGCCTAGCGCTGGCTGTGTGTGCGGCCGCTCCTC
55 CAGGCTGGCCGTGCCCGCTCAGGACCTGCTCCACTGTTTAAACAATAAACCAAGGTCATGAGCATTTCGAG
CTAAGATAACAGACTCCAGCTCCTGGTCCACCCGCATGTGAGTCAGCACTCTGGCCTTCATCACGAGAG
CTCCGACGCGTGGCTAGGATTCCACTTCTGTGTGATGACCTCAGGAAATAAACGTCCTTGACTTTATA
AAAGCCCCGAATTC

SEQ ID NO:494

>gi|4885409|ref|NP_005327.1| high density lipoprotein binding protein;
vigilin [Homo sapiens]
MSSVAVLTQESFAEHRSLVPQQIKVATLNSSEESDPPTYKDAFPPLPEKAACLES AQEPAGAWGNKIRP
IKASVITQVFHVPLEERKYKDMNQFGEGEQAKICLEIMQRTGAHLELSLAKDQGLSIMVSGKLDVAMKAR
KDIVARLQTQASATVAIPKEHHRFVIGKNGEKLQDLELKTATKIQIPRDDPSNQIKITGTKEGIEKARH
60 EVLLISAEQDKRAVERLEKAFHPFIAGPYNRLVGEIMQETGTRINIPPPSVNRTEIVFTGEKEQLAQ
VARIKKIYEEKKKTTTIAVEVKKSQHKYVIGPKNSLQEI LERTGVSV EIPPSDSIS ETVILRGEPEKL

5 GQALTEVYAKANSFTVSSVAAPSWLHRFIIIGKKGQNLAKITQQMPKVHIEFTEGEDKITLEGPTEDVNVA
QEQIEGMVKDLINRMDYVEINIDHKFHRHLIGKSGANINRIKDQYKVSVRIPPDSEKSNLIRIEGDPQGV
QQAKRELLELASRMENERTKDLIIIEQRFHRTIIIGQKGERIREIRDKFPEVIINFPDPAQKSDIVQLRGPK
NEVEKCTKYMQMADVLDVENSYSISVPIFKQFHKNIIGKGGANIKKIREESNTKIDLPAENSNSETIIIT
10 GKRANCEAARSRLSIQKDLANIAEVEVSIPAKLHNSLIGTKGRLIRSIMEECGGVHIHFPVEGSGSDTV
VIRGPSSDVEKAKKQLLHLAEKQTKSFTVDIRAKPEYHKFLIGKGGKIRKVRDSTGARVIFPAAEDKD
QDLITTIIGKEDAVREAQKELEALIQLNDNVVEDSMLVDPKHHRHFVIRRGQVLREIAEEYGGVMVSFPRS
GTQSDKVTLLGAKDCVEAAKKRIQEIIEDLEAQVTLECAIPQKFHRSVMGPKGSRIQQITRDFSQIKFP
DREENAVHSTEPVQENGDEAGEGREAKDCDPGSPRRCDIIISGRKEKCEAAKEALEALVPVTIEVEVP
15 FDLHRYVIGQKSGIRKMMDEFEVNIHVPAPELQSDIIATGLAANLDRAKAGLLERVKELQAEQEDRAL
RSFKLSVTVPKYHPKIIIGRKGAIVITQIRLEHDVNIQFPDKDDGNQPDQITITGYEKNTEAARDAILRI
VGELEQMVSEDPVLDHRVHARIIGARGKAIRKIMDEFKVDIRFPQSGAPDPNCVTVTGLPENVEBAIDHI
LNLEEEYLADVVDSEALQVYMKPPAHEEAKAPSRGFVVRDAPWTASSEKAPDMSSEEFPSFGAQVAPK
TLPWGPKR

SEQ ID NO:495

Vimentin

>G3_8_04_PCR_G3F1 Direction: N/A

20 GCCGTCCAGGCCATCGCCACCCTCCGCAGCCATGTCCACCAGGTCCGTGTCTCTCGTCTCTACCCGAGATGTTT
GGCGGCCCGGGCACC CGCAGCCGGGCGAGCTCCAGCCGGAGCTACGTGACTACGTCCACCCGCACCTACAGCCT
GGCAGCGCGCTGCGCCCGCAGCAGCCAGCAGCCTCTACGCCTCGTCCCCGGGCGGCGTGTATGCCACGCGCTCC
TCTGCCGTGCGCTGCGGAGCAGCGTGCCTGCGGGTGCCTGCTGCGAGACTCGGTGGAGTTCTCGCTGGCCGAC
GCCATCAACACCGAGTTCAAGAACACCCGCACCAACAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCA
25 CTATATCGACAGGTGCGCTTCTGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCAGCTCAAGGGCCAA
GGCAAGTCGCGCTGGGGACCTCTACGAGGAGGAGATGCGGGAGCTGCGCCGGC

SEQ ID NO:496

>gi|4507894|ref|NM_003380.1| Homo sapiens vimentin (VIM), mRNA

30 GGGCGCGCCAGAGACGCGAGCCGCGCTCCCAACACCCACACCCACCGCGCCCTCGTTGCGCTCTTCTCCGG
GAGCCAGTCCGCGCCACCGCCGCGCCAGGCCATCGCCACCCTCCGCAGCCATGTCCACCAGGTCCGTG
TCCTCGTCTCTACCGCAGGATGTTTCGGCGGCGCGGCGCCGCGAGCCGCGGAGCTCCAGCCGGAGCT
ACGTGACTACGCTCACCCGCACCTACAGCCTGGCAGCGCGCTGCGCCCCAGCACCAGCCGAGCCTCTA
CGCCTCGTCCCCGGGCGGCGTGTATGCCACGCGCTCCTCTGCGCTGCGCCTGCGGAGCAGCGTCCCGGG
35 GTGCGGCTCCTGCAGGACTCGGTGGACTTCTCGCTGGCCGACGCCATCAACACCGAGTTCAAGAACACCC
GCACCAACGAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCAACTACATCGACAAGGTGCGCTT
CCTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCAGCTCAAGGGCCAAGGCAAGTCGCGCCTA
GGGGACCTCTACGAGGAGGAGATGCGGGAGCTGCGCCGGCAGGTGGACCAGCTAACCAACGACAAAGCCC
GCGTCGAGGTGGAGCGCGACAACCTGGCCGAGGACATCATGCGCCTCCGGGAGAAATGCGAGGAGGAGAT
GCTTCAGAGAGAGGAAGCCGAAAACACCTGCAATCTTTCAGACAGGATGTTGACAATGCGTCTCTGGCA
40 CGTCTTGACCTTGAACGCAAGTGGAATCTTTGCAAGAAGAGATTGCGCTTTTGAAGAACTCCACGAAG
AGGAAATCCAGGAGCTGCGGCTCAGATTAGGAACAGCATGTCCAAATCGATGTGGATGTTTCAAGCC
TGACCTCACGGCTGCCCTGCGTGACGTACGTGACCAATGAAAGTGTGGCTGCCAAGAACCTGACGCGCTGC
GCAGAAGAATGGTACAAATCCAAGTTTGCTGACCTCTCTGAGGCTGCCAACCGGAACAATGACGCGCTGC
45 GCCAGGCAAAGCAGGAGTCCACTGAGTACCGGAGACAGGTGCAGTCCCTCACCTGTGAAGTGGATGCCCT
TAAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATGGAAGAGAACTTTGCCGTTGAAGCTGCT
AACTACCAAGACACTATTGGCCGCCTGCAGGATGAGATTGAGAATATGAAGGAGGAAATGGCTCGTCACC
TTCTGTAATACCAAGACCTGCTCAATGTTAAGATGGCCCTTGACATTGAGATTGCCACCTACAGGAAGCT
GCTGGAAGGCGAGGAGAGCAGGATTTCTCTGCCTCTTCCAACTTTTCTCCTGAACTGAGGGAACT
AATCTGGATTCACTCCCTCTGGTTGATACCACTCAAAAAGGACATTCTGATTAAGACGGTTGAACTA
50 GAGATGGACAGGTTATCAACGAAACTTCTCAGCATCAGCATGACCTTGAATAAAAATGACACACTCAG
TGGCAGGCGATATATTACCCAGGCAAGAATAAAAAAGAAATCCCATATCTTAAAGAAACAGCTTTCAAGT
GCCTTTCTGCAGTTTTTTCAGGAGCGCAAGATAGATTTGGAATAGGAATAAGCTCTAGTTCTTAACAACCG
ACACTCCTACAAGATTTAGAAAAAAGTTTACAACATAATCTAGTTTACAGAAAAATCTTGTGCTAGAATA
CTTTTTTAAAGGTATTTTGAATACCATTAAACTGCTTTTTTTTTTTCAGCAAGTATCCAACCAACTGG
55 TTCTGCTTCAATAAATCTTTGAAAACCTCCA

SEQ ID NO:497

>gi|4507895|ref|NP_003371.1| vimentin [Homo sapiens]

60 MSTRSVSSSSSYRRMFGPGTASRPSSSSRSYVTTSTRYSLGSLRPSSTRSLYASSPGGVYATRSSAVRL
RSSVPGVRLQLQDSVDFSLADAINTEFKNTRTNEKVELQELNDRFANYIDKVRFLQONKILLAELEQLKG

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGTG
ACGATGGCTGGTTTGTGGGTGTCTCCCGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCGG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
ACCCCCGCCCACATCCTCCTTCCCCAGGACCTGAGCTCCAGCATCTGCAGACGACCCCCGCAGCCTTTCCCTCG
5 GACCCCCCTCGAAGCCCCCTGGACTGATTCCCACCACGATC

SEQ ID NO:508

>GL3_15J_2_M13F Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGT
10 GACGATGGCTGGTTTGTGGGTGTCTCCCGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCG
GTGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAG
GACCCCCGCCCACATCCTCCTTCCCCAGGACCTGAGCTCCAGCATCTGCAGACGACCCCCGCAGCCTTTCCCTC
GGACCCCTCGAA

15 SEQ ID NO:509

>GL3_15J_2_M13R Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGAGATGCTGGGAGCTCAGGTCTGGGGAAGGAGGATGTGGGCG
20 GGGGTCTCTCCCTCCCACGAGTGCCACCGCTCCCCACCCCATCCTGGCTGGCTCCAAGTTGCCATGGAGACCAC
TCACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCC
ATCGTCACTGCTGCATGACATCCACCTGTCCCCCTCGCGCAGCTCCAGCTCGTCTTCGTTCTGGGGCCTGTA
CTGGT

25 SEQ ID NO:510

>GL3_15J_3_M13F Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGAGATGCTGGGAGCTCAGGTCTGGGGAAGGAGGATGTGGGCG
30 GGGTCTCTCCCTCCCACGAGTGC

SEQ ID NO:511

>GL3_15J_4_M13F Direction: N/A

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
35 GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGAGATGCTGGGAGCTCAGGTCTGGGGAAGGAGGATGTGGGCG
GGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCCATCCTGGCTGGCTCCAAGTTGCCATGGAGACCACT
CACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCCA
TCGTACAC

40 SEQ ID NO:512

>GL3_15J_PCR_G3F1 Direction: N/A

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
45 GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGAGATGCTGGGAGCTCAGTCTGGGGAAGGAGGATGTGGGCGG
GGGTCTCTCCCTCCCACAGTGCCACGTCCCCCACCCATCCTGGGCGTGGCTCCAAGTTGCCATGGAGAAC
ACTCACCACCGGGGCAACCGGTAATTTCCAAGGGAACCGGTTCCCGAAATTTCTGGGGTCCCTCCGGGAAAA
AACCAACAAAACAAGCCCTACGGCA

50 SEQ ID NO:513

>GL3_37B_PCR_G3F1 Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTGAGATGCTGGGAGCTCAGTCTGGGGAAGGAGGATGTGGGCGG
55 GGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCCATCCTGGCTGGCTCCAAGTTGCCATGGAGACCACT
CACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCCA
TCGTCACTGCTGCATGACATCCACCTGTCCCCCTCGCGCAGCTCCGCTCGTCTTCGTTCTGGGGCCTGTACT
GGT

SEQ ID NO:514

>GL3_37D_1_M13R Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
5 GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTCTGCAGATGCTGGGAGCTCAGGTCTGGGGAAGGAGGATGTGGGCG
GGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCATCCTGGCTGGCTCCAAGTTGCCATGGAGACCACTC
ACACCGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCCAT
CGTCACACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGCTCCAGCTCGTCTTCGTTCTGGGGCCTGTACT
10 GGTCCGAGAAAACCCAGCACAGTGGTTAGATACGATAAAGCGGACCGCTCGACTAGTCTGAGGTCTGATACTCA
ACTGGACTGTCTAATGGGGCGAATTCTTGGCAAGATTTTCATCACACTTGCGGGGCGTCGAAGCATGCAT

SEQ ID NO:515

>GL3_37D_2_M13R Direction: anti-sense

ACCAGTACAGGCCCCAGAACGAAGACGAGCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCATGCAGCAGTGTG
15 ACAGTGGCTGGTTTGTGGGTGTCTCCCGAGGAGCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCCGG
TGTGAGTGGTCTCCATGGCAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGG
ACCCCCGCCACATTCTCCTTTCCCAGGACCTGAGCTCCAGCATCTGCAGACGAACCCCGGAAGCTTTCCCTCG
GA

SEQ ID NO:516

>GL3_37D_3_M13R Direction: N/A

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTTCAAAGCAGACCTCTGTATTTGGGGAGTGGG
GTGGAGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGATCGGTGGGTGGGAATCAGTCCAGGGGGCTT
CGAGGGGGTCCGAGGGAAAGGCTGCGGGGGTCTGTCTGCAGATCCTGGGAGCCTCAGGTCTGGGGAAGGAGGAT
25 GTGGGCGGGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCATCCTGGCTGGCTCCAAGTTGCCATGG
AGACCACTCACACCGGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGAACACCCACA
AACCAGCCATCGTCACACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGCTCCCAGCTCGTCTCCGTNCTG
GGCCTGTACTGGTC

SEQ ID NO:517

>GL3_37D_4_M13R Direction: sense

CTTGGGGTCTGGTCTCAATAAGGCCTGGAAATGGTCTCCGCTTCAAAGCAGACCTCTGTATTTGGGGAGTGGGGT
GGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGGG
GGGTCCGAGGGAAAGGCTGCGGGGGTCTGTCTGCAGATGCTTGGGAGCTCAGGTCTGGGGAAGGGGGATGTGGGC
35 GGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCAACCCATCCTGGCTGGCTCCAAGTTGCCATGGAGACCAC
TCACACCGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCC
ATCGTCGCACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGTTCAGCTCGTCTTACGTTCTGGGGCCTGT
AACTGGGT

SEQ ID NO:518

>GL3_37D_PCR_G3F1 Direction: sense

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TGGGGAGGAAATGAAAGGGCTGTGGGAGGAATGCCTGTGAGTCGTGGGTGGGAATCAGTCCAGGGGGCTTCGAGG
45 GGGGTCCGAGGGAAAGGCTGCGGGGGTCTGTCTGCAGATGCTGGGAGCTCAGTCTGGGGAAGGAGGATGTGGGCG
GGGGTCTCTCCCTCCCACGAGTGCCACCGTCCCCACCCATCCTGGCTGGCTCCAGTTGCCATGAACCACTCA
CACCAGGGCAACGTAATTTCCAGGGAACGTTCCGAATTTCTGGGTCTCCGGGAGACACCCACAAACCAGCCATC
GTCACACTGCTGCATGACATCCACCCTGTCCCCCTCGCGCAGTTCAGCTCGTCTTCTGTTCTGGGGCCTGTACTGG
TCCGCAACCCAGCACAGTGGTTAGATGATTAAGCGGCCGCTCGACTAGTCTGAGGTCTGATACTCACTGACTTT
50 TTAA

SEQ ID NO:519

>gi|19923334|ref|NM_005775.2| Homo sapiens vinexin beta (SH3-containing adaptor molecule-1) (SCAM-1), mRNA

CGGACGCGTGGGCAGGCAGCAGCCGGGCAGGGATGCTCCTGCGCTCCCGGGCGGCCTCGGGCCAGCCAC
55 CTGCTCGCCGGGGAAGAGGACACGCAGAGGAGCAGCTGGCTTGCCCGAGTCTCTCCACCTTGACCCAAG
CATGCAGGGCCACCCCGCAGCCTCCGCGCTGGGCTCAGCCTGGACGACTTCATCCCTGGCCACCTCCAG
TCCCACATAGGCTCTTCCTCCCGGGGACACGGGTGCCCGTGATCCGGAATGGTGGCTCCAACACCTTA
ATTTCCAGTTCCACGACCCCGCGCCAGGACTGTGTGCAATGGGGGCTACACACCAAGACGAGATGCTTC
CCAGCACC CGGACCTGCGTGGTATCAGACCTGGCCAGGCCCTGGGAGCAAGCCCTCTGCAAGCACAAAG
60 ATCCCTGCCTCCAGCACACCCAGAACTGGTCAGCCACGTGGACCAAGGACAGCAAGCGTCGGGACAAGC

GCTGGGTCAAGTACGAGGGAATCGGGCCCGTGGACGAGAGCGGCATGCCCATTTGCCCCCGATCCAGCGT
 TGACAGACCCAGAGACTGGTACCGGAGAATGTTCCAGCAGATTACCGGAAAATGCCAGACTTGCAGCTG
 GACTGGACCTTCGAGGAGCCACCCAGAGACCCAGGCATCTAGGAGGCCAGCAAAGACCTGCCACAGGC
 CCGGCCCCGGAACATCTTCCAGTGGAAAGAGCTGGGACCACTCTGAAGAGTTACCTAGAAGCACCTTCAA
 5 CTACAGACCTGGAGCATTCTCCACTGTGCTGCAGCCCTCAAATCAGGTGCTCAGACGCCGGGAAAAAGTA
 GACAATGTCTGGACGGAAGAGTCTTGAACCAAGTTTCTGCAGGAAGTAGAGACTGGGCAGAGGCCCAAGA
 AACCGCTGGTGGACGACCTGGTGAGAAGCCCTCCAGCCCATTTAGAGGTGCTGCTGGAGAGAGAGCTGGC
 CGAGCTGAGCGCCGAGCTGGACAAGGACCTGCGGGCAATTGAGACCCGACTGCCGTCCCCCAAGAGCTCG
 10 CCGGCGCCCCGACGGGCCCCGGAGCAGCGGCCCGGCCGCGCCTCAGCCTGGAGCTCCAGCTACC
 CACATGCACCTTACCTGGGTTCCGCCCCGGTCCCTGAGTCCCCACAAAATGGCTGATGGAGGAAGCCCCCTT
 CCTAGGTCCGAGGGACTTTGTCTACCTTCCCTCAACCCGAGACCCCTAGTGCCTCTAACGGAGGGGGCAGC
 CCAGCCAGGAGGAAGAGAAGAAGAGAAAGGCCCGCAGGCTCAAGTTTGACTTCCAGGCGCAGTCCCCCA
 AGGAGCTGACTCTGCAGAAGGGTGACATTGTCTACATCCACAAGGAGGTGGACAAGAAGTGGCTGGAGGG
 AGAGCACCACGGCCGCCTGGGCATCTTCCCTGCTAATTATGTGGAGGTGCTGCCCGCAGATGAGATCCCT
 15 AAGCCCATCAAGCCCCGACCTACCAGGTGCTGGAGTATGGAGAGGCTGTGGCCAGTACACCTTCAAGG
 GGGACCTGGAGGTGGAGCTGTCTTCCGCAAGGGAGAGCACATCTGCCTGATCCGCAAGGTGAACGAGAA
 CTGGTACGAGGGACGCATCACGGGCACGGGGCGCCAAGGCATATTCCTGCCAGCTACGTGCAGGTGTCT
 CGTGAACCCCGGCTCCGGCTCTGTGACGACGGCCCCCAGCTCCCCACGTCTCCCCGCCTGACCGCTGCCG
 CCGCTCAGCCCGTCAACCCAGCTCCCCCTCAGCCCTGCGCAGCCAGCTGACCCACCGACTTGGGGGG
 20 ACAGACCTCCCCCGTTCGCACTGGCTTCTCCTTCCCCACCCAGGAGCCTAGACCCAGACCCAGAATCTT
 GGCACCCCTGGTCCAGCTCTGTCCCACCTCGAGGTCCCAGCCATCCCCTGGACCTGGGGACCTCCTCTC
 CTAACACCTCTCAGATACACTGGACCTGACCCCGTACCGGGCGATGTACCAAGTACAGGCCCCAGAAGACGA
 GCTGGAGCTGCGCGAGGGGGACAGGGTGGATGTCTATGCAGCAGTGTGACGATGGCTGGTTTGTGGGTGTC
 TCCCGGAGGACCCAGAAATTCGGAACGTTCCCTGGAAATTACGTTGCCCGGTGTGAGTGGTCTCCATGG
 25 CAACTTGGAGCCAGCCAGGATGGGGTGGGGAGCGGTGGCACTCGTGGGAGGGAGAGGACCCCGCCACA
 TCCTCCTTCCCAGGACCTGAGCTCCCAGCATCTGCAGACGACCCCGCAGCATTTCCCTCGGACCCCCC
 TCGAAGCCCCCTGGACTGATTCCCACCCACGACTCACAGGCATTCCTCCACAGCCCTTTTCATTTCTCC
 CCACCCCACTCCCCAAATACAGAGGTCTGCTTTGAAGCGGAGACCATTTCAGGCCTTATTGAGACCAGA
 CCCCAGTCCCCCACCCCCATCCTGCTCCAGCGTTTCTCTAACAGGGACCAGCTCTCCGCTTTGCCCCC
 30 ACGGGTTCTCTAACAGAACAGCTTCTAGCCTCGTAGAGACCAAAGGCCGCCCGCCCTGCTGGGG
 TTCCTCCAGCACCCAGCTTGGCTGGCTGCCCTCTTTGCTTCTGGCCTCCAGCTGGGTGTGGGGGGGCG
 GAGCAAGGCGGGGACAGCAGCAGCACTTCTTAGCGATCTAGGCCTGGCAAGAGCTCTGGCCCCAAGGC
 CTCCTCTTCCCAGGGGCTGCCAAGTCTGGCCCTGGCCCTGGCATATCACCCCGCACTGTGGGGGCCAGGC
 ACCACTAGCCTGGCTCAAATATTCCCAGGGAGACTGCTGTGTGCTGCCCGCCTGCCTGCTGGCTCTCC
 35 CCAGCCCCACATCCCCTCTGGAAGAGAATGTAAATAAACCTGGACACAAGGGCCTTCGTGGCCTCGA

SEQ ID NO:520

>gi|19923335|ref|NP_005766.2| vinexin beta (SH3-containing adaptor
 molecule-1) [Homo sapiens]
 40 MQGPPRSLRAGLSLDDFIPGHLQSHIGSSSRGTRVPVIRNGGSNTLNFQFHDPAAPRTVCNGGYTPRRDAS
 QHPDPAWYQTPGPGSKPSASTKIPASQHTQNSATWTKDSKRDRKRWVKYEGIGPVDESMPPIAPRSSV
 DRPRDWYRRMFQQIHRKMPDLQLDWTFRFEPDRPHLQAQQRPAHRPGPATSSSGRSWDHSEELPRSTFN
 YRPGAFSTVLQPSNQVLRREKVDNVWTEESWNQFLQLELTGQRPKKPLVDDPGEKPSQPIEVLLERELA
 45 ELSAELDKDLRAIETRLPSPKSSPAPRRAPQRPPAGPASAWSSSYPHAPYLGSARSLSPHKMADGGSPF
 LGRRDFVYPSSTRDPSASNGGSPARREEKKRKAARLKFDFOAQSPKELTLQKGDIVYIHKEVDKNWLEG
 EHHGRLGIFPANYVEVLPADIEIPKPIKPPTYQVLEYGEAVAQYTFKGDLEVELSFRKGEHICLIRKVNEN
 WYEGRITGTGRQGIFFASYVQVSREPRLRLCDDGPQLPTSPRLTAAARSARHPSSPSALRSPADPTDLGG
 QTSPPRTGFSFPTQEP RPQTQNLGTPGPALSHSRGPSHPLDLGTSSPNTSQIHWTPIRYAMYQYRPQNEDE
 50 LELREGDRDVMQQCDDGWFVGVSRRTQKFGTFPGNYVAPV

SEQ ID NO: 521

NM_004265 (Homo sapiens fatty acid desaturase 2 (FADS2))NM_004265.2
 GI:14141180
 1 agggggcgcg gtgggaggag taggagaaga caaaagccga aagcgaagag ggccccgggct
 55 61 gcacacaccg gctgggaggc agcgtctgt gcagcgagca gccggcgcg ggaggccgca
 121 gtgcacgggg cgtcacagtc ggcagcgagc atgggggaagg gagggaaacca gggcgagggg
 181 gccgcccagc gcgaggtgtc ggtgccacc ttcagctggg aggagattca gaagcataac
 241 ctgcgcaccg acaggtggct ggtcattgac cgcaagggtt acaacatcac caaatggtcc
 301 atccagcacc cggggggcca gcgggctatc gggcactacg ctggagaaga tgcaacggat
 60 361 gccttccgcg ccttccacc tgacctgaa ttcgtgggca agttcttgaa acccctgctg
 421 attggtgaac tggccccgga ggagcccagc caggaccacg gcaagaactc aaagatcact

481 gaggacttcc gggccctgag gaagacggct gaggacatga acctgttcaa gaccaaccac
 541 gtgtttctcc tctctctcct ggccacatc atcgccctgg agagcattgc atggttcact
 601 gtcttttact ttggcaatgg ctggattcct accctcatca cggcctttgt ccttgctacc
 661 tctcaggccc aagctggatg gctgcaacat gattatggcc acctgtctgt ctacagaaaa
 5 721 cccaagtgga accaccttgt ccacaaattc gtcattggcc acttaaaggg tgcctctgcc
 781 aactggtgga atcatcgcca cttccagcac caccgccaagc ctaacatctt ccacaaggat
 841 cccgatgtga acatgctgca cgtgtttgtt ctgggcgaat ggcagcccat cgagtacggc
 901 aagaagaagc tgaaataacct gccctacaat caccagcacg aatacttctt cctgattggg
 961 ccgccgctgc tcatcccat gtatttccag taccagatca tcatgacct gatcgtccat
 10 1021 aagaactggg tggacctggc ctgggcctgc agctactaca tccggttctt catcacctac
 1081 atccctttct acggcatcct gggagccctc cttttcctca acttcatcag gttcctggag
 1141 agccactggg ttgtgtgggt cacacagatg aatcacatcg tcatggagat tgaccaggag
 1201 gcctaccgtg actggttcag tagccagctg acagccacct gcaacgtgga gcagtccttc
 1261 ttcaacgact ggttcagtgg acaccttaac ttccagattg agcaccacct cttccccacc
 15 1321 atgccccggc acaacttaca caagatcgcc ccgctggtga agtctctatg tgccaagcat
 1381 ggcattgaat accaggagaa gccgctactg agggccctgc tggacatcat caggtccctg
 1441 aagaagtctg ggaagctgtg gctggacgcc taccttcaca aatgaagcca cagcccccg
 1501 gacaccgtgg ggaaggggtg caggtggggt gatggccaga ggaatgatgg gcttttgttc
 1561 tgaggggtgt ccgagagggt ggtgtatgca ctgctcacgg accccatggt ggatctttct
 20 1621 ccttttctcc tctccttttt cttctcact ctccccata gcacctgccc ctcatgggac
 1681 ctgccctccc tcagccgtca gccatcagcc atggccctcc cagtgcctcc tagcccttc
 1741 ttccaaggag cagagagggt gccaccgggg gtggctctgt cctacctcca ctctctgccc
 1801 ctaaagatgg gaggagacca gcggtccatg ggtctggcct gtgagtctcc ccttgcagcc
 1861 tggctactag gcatcacccc cgctttggtt cttcagatgc tcttgggggt cataggggca
 25 1921 ggtcctagtc gggcagggcc cctgaccctc ccggcctggc ttcactctcc ctgacggctg
 1981 ccattggtcc accctttcat agagaggcct gctttgttac aaagctcggg tctccctcct
 2041 gcagctcggg taagtaccgg aggcctctct taagatgtcc agggccccag gcccgcgggc
 2101 acagccagcc caaaccttgg gccctggaag agtccctccac cccatcata gagtgtctctg
 2161 accctgggct ttcacgggcc ccattccacc gcctcccaa cttgagcctg tgaccttggg
 30 2221 accaaagggg gagtccctcg tctctgtga ctcagcagag gcagtggcca cgttcaggga
 2281 ggggcgggct ggcctggagg ctcagcccac cctccagctt ttcctcaggg tgtcctgagg
 2341 tccaagattc tggagcaatc tgacccttct ccaaaggctc tgttatcagc tgggcagtgc
 2401 cagccaatcc ctggccattt ggccccaggg gacgtgggcc ctgcaggctg caggagggca
 2461 ctggagctgg gaggtctcgt ccagccctc cccatctcgg ggctgctgtg tggacggcgc
 35 2521 tgcctcaggc actctcctgt ctgaacctgc ccttactgtg tttaacctgt tgetccagga
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 2641 tggccttgcc tgggtggccc tgactgtcag ggagggccag ggaggcagag cgggagggag
 2701 tctcaggagg aggctgccct gaggggctgg ggagggggta cctcatgagg accagggtgg
 2761 agctcagaag agggagggtg ggggctgga ggtgctggta gctgagggga cgggcaagt
 40 2821 agaggggagg gaggggaagt ctgggaggat cctgagctgc tgttgcagtc taaccacta
 2881 atcagttctt agattcaggg gaagggcagg caccaacaac tcagaatggg ggctttcggg
 2941 gagggcgccct agtcccccca gctctaagca gccaggaggg acctgcatct aagcatctgg
 3001 gttgccatgg caatggcatg cccccagct actgtatgcc cccgaccccc gcagaggcag
 3061 aatgaacca tagggagctg atcgtaatgt ttatcatgtt acttccccac ccctacattt
 45 3121 tttgaaataa aataaggaat tttattctc

SEQ ID NO:522

NP_004256 (fatty acid desaturase 2; linoleoyl-CoA desaturase (delta-6-
 desaturase)-like 2; delta-6 fatty acid desaturase) [Homo
 sapiens].NP_004256.1 GI:4758334

50 1 mgkgnqgeg aaerevspt fsweeiqkhn lrtdrwlvid rkvnitkws iqhpggqrvi
 61 ghyagedatd afrahpdl fvgkflkpl igelapeeps qdhgknskit edfralrkta
 121 edmnlfktnh vffllllahi ialesiawft vfyfngwip tlitaflvat sqagagwlqh
 181 dyghlsvyrk pkwnhlvhkf vighlkgasa nwnnrhfhq hakpnifhkd pdvnmhvf
 55 241 lgewqpieyg kkkllkylpyn hqheyfflig ppllipyf yqiimtmivh knwvdlawav
 301 syirffity ipfygilgal lflnfirfle shwfvwtqm nhivmeidqe ayrdwfssql
 361 tatenveqsf fndwfsghln fqiehhlfpt mprhnlhkia plvkslcakh gileyqekpl
 421 ralldiirsl kksghklwlda ylhk

SEQ ID NO:523

AF134404 (Homo sapiens delta-6 fatty acid desaturase (CYB5RP) mRNA),
AF134404.1 GI:4868365

```

5      1 cttcgcttcc ctcgggggtct tgctcggacc tcggccaccg cctgggattcc ccaggactcg
      61 tgcgtgcagc atgggcggcg tcggggagcc gggaccgcgg gagggaccgc cgcagccggg
      121 ggcaccgctg cccaccttct gctgggagca gatccgcgcg caccgaccag cccgcgacaa
      181 gtggctggtc atcgagcgcc gcgtctacga catcagccgc tgggcacagc ggcaccagg
      241 gggcagccgc ctcatcggcc accacggcgc tgaggacgcc acggatgcct tccgtgcctt
      301 ccatcaagat ctcaattttg tgcgcaagtt cctacagccc ctggttgatt gagagctggc
10     361 tccggaagaa cccagccagg atggaccctt gaatgcgcag ctggtcgagg acttccgagc
      421 cctgcaccag gcagccgagg acatgaagct gtttgatgcc agtcccacct tctttgcttt
      481 cctactgggc cacatcctgg ccatggaggt gctggcctgg ctccctatct acctcctggg
      541 tcctggctgg gtgcccagtg ccctggccgc cttcctcctg gccatctctc aggetcagtc
      601 ctggtgtctg cagcatgacc tgggcatgc ctccatcttc aagaagtcct ggtggaacca
15     661 cgtggcccag aagttcgtga tggggcagct aaagggttc tccgccact ggtggaactt
      721 ccgccacttc cagcaccacg ccaagcccaa catcttcac aaagaccag acgtgacggt
      781 ggcgcccgtc ttctcctggg gggagtcac cgtcgagtat ggcaagaaga aacgcagata
      841 cctaccctac aaccagcagc acctgtactt cttcctgata ggcccgcgc tgctcaccct
      901 ggtgaacttt gaagtggaaa atctggcgta catgctggtg tgcattgagc gggcggtatt
20     961 gctctggggc gccagcttct atgcccgtt cttcttatcc tacctccct tctacggcgt
      1021 ccctgggggtg ctgctcttct ttgttgctgt cagggtcctg gaaagccact ggttcgtgtg
      1081 gatcacacag atgaaccaca tccccaaagga gatcggccac gagaagcacc gggactgggt
      1141 cagctctcag ctggcagcca cctgcaacgt ggagccctca cttttcacca actggttcag
      1201 cgggcaccct aacttcaga tcagacacca cctcttcccc aggatgccga gacacaacta
25     1261 cagccgggtg gccccgctgg tcaagtcgct gtgtgccaa cagggcctca gctacgaagt
      1321 gaagcccttc ctcaccgcgc tgggtggacat cgtcaggtcc ctgaagaagt ctggtgacat
      1381 ctggctggac gcctacctcc atcagtgaag gcaacaccca ggccggcaga gaagggtcga
      1441 gggcaccagc aaccaagcca gccccggcg ggatcgatac cccaccctt cactggcca
      1501 gcctgggggt gactgcctg ccctcctggt actgttgtct tcccctcggc cccctcacat
30     1561 gtgtattcag cagccctatg gccttggtc tgggcctgat gggacaggg tagagggag
      1621 gtgagcatag cacattttcc tagagcgaga attgggggaa agctgttatt tttatattaa
      1681 aatacattca gatgtaaaa aaaaa

```

SEQ ID NO:524

35 AAD31282 (delta-6 fatty acid desaturase) [Homo sapiens]. AAD31282.1
GI:4868366

```

      1 mggvgpgrp egpaqpgapl ptfcweqira hdqpgdkwlv ierrydisr waqrhpggsr
      61 lighhgaeda tdafrfhqd lnfvrkflqp lligelapee psqdgplnaq lvedfralhq
40     121 aaedmklfda sptffafllg hilamevlaw lliyllgpgw vpsalaafil aisqaqswcl
      181 qhdlghasif kkswnnhvaq kfvmgqlkgf sahwnfrhf qhhakpnifh kdpdvtvapv
      241 flgessvey gkkkrrylpy nqghlyffli gpplltlvnf evenlaymlv cmqwadllwa
      301 asfyarffls ylpfygvpv llffvavrvi eshwfvwitq mnhipkeigh ekhrdwvssq
      361 laatcnveps lftnwfsghl nfqiehhfip rmprhnysrv aplvkslcak hglsyevkpf
45     421 ltalvdivrs lkksqdiwld aylhq

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